Supplementary File S4. Corrected alignment files in FastA format.

Supplementary file S4a

```
>ab736_10
---------------------MTQAIQNETRSVRDMLIAAK-----VLAKDGKATESPCKTCRV--------
------------------------------------------------------------------------
---------------------PVWVS---FFFDG------------------------------TGNNKDAD
AATLNQSNVVALFEAHKQDS--------------------------------KNGIEKFYYEGL-GTQFRFD
KYSV---------------------VDSGKITAAARSLQGRKIDITDAEWRKQGYSESGKGVQGALGLGVAL
GIKQRLQK--------------------------------------------------------------
------------AIFELVDYLDKIYTQKGITEINIS----------------------------AFGFSRGA
TEARIFMN-WLQHAPNVTTQGTGSGKKLFYRG--------------------------------------
----KPLKAKFLGI----------------------------------------------FDTVESIGNAAQNK
NP--------------------------------ELYRTRIEDYIEHSMHLVASLEMRQSFPLTPTGKPTA
NTVKGLIHDQKVYPGVHSNVGGGYMPMEQARILGLSRITLHAMYNRACAYGLKFF-----------------
------------------------------------------------------------------------TL
NELNAAKQRK------------------------------------------------------------
-------------IVFTRFYAFDSKWQQDLNNF--------------------------------------
MAYVKGGT-----------------------------------SFEQQMQGQIALY-----------------
-------------------------HQWIREGGYARFIHRKTRERIGRKEKITAITKLNDGLFENIRQALNV
YVPE-------------------------------------------------------------GARPYDVIKGR
DRKSTLPKEVIYYFENYVCDSVGGFIAEASDFQAILNDGKAPNYFIPRGIVRPT------------------
----------------------------
>ATCC19606_10
---------------------MTQAIQNETRSVRDMLIAAK-----VLAKDGKATESPCKTCRV--------
------------------------------------------------------------------------
---------------------PVWVS---FFFDG------------------------------TGNNKDAD
AATLNQSNVVALFEAHKQDS--------------------------------KNGIEKFYYEGL-GTQFRFD
KYSV---------------------VDSGKITAAARSLQGRKIDITDAEWRKQGYSESGKGVQGALGLGVAL
GIKQRLQK--------------------------------------------------------------
------------AIFELVDYLDKIYTQKGITEINIS----------------------------AFGFSRGA
TEARIFMN-WLQHAPNVTTQGTGSGKKLFYRG--------------------------------------
----KPLKAKFLGI----------------------------------------------FDTVESIGNAAQNK
```

```
NP--------------------------------ELYRTRIEDYIEHSMHLVASLEMRQSFPLTPTGKPTA
NTVKGLIHDQKVYPGVHSNVGGGYMPMEQARILGLSRITLHAMYNRACAYGLKFF-----------------
-----------------------------------------------------------------------TL
NELNAAKQRK----------------------------------------------------------------
-------------IVFTRFYAFDSKWQQDLNNF-------------------------------------
MAYVKGGT---------------------------------SFEQQMQGQIALY-----------------
-------------------------HQWIREGGYARFIHRKTRERIGRKEKITAITKLNDGLFENIRQALNV
YVPE-------------------------------------------------------GARPYDVIKGR
DRKSTLPKEVIYYFENYVCDSVGGFIAEASDFQAILNDGKAPNYFIPRGIVRPT------------------
----------------------------
>AF-401_30
-------------------------------------MNDA-----AIALESFAKQTCGRACVMPPIQP---
-----------------------------------------------------------------------
---------------------VVLDV-YKQSFTA-----------------------------FVGGAADK
Y----QFLGRPL-----------------------------------------DIDFPDDIGAGPTGI-----
-MKS---------------------CMRKFKEASSSQITKAK----FE-----------------------
-----------------------------------------------------------------------
------------YYGYEEAYSTDSVVKRYRGKLLLN---------------------------LLTDIKNI
LKEEPNTQINLV----------------------------------------------------------
----GHSLGGWNVA-----GLSEELSKAKICTVHTL----------------------ITIDPVGIRLSKSG
VG-----------------------------------------------------------------N
DRARIYYLEPDPVAKKWINIFSQPLKNYRDDYIAI-------------------------------------
-----------------------------------------------------------------------LG
GRWNDDDTAK-------------------ANFNSVSTYHHGEA----------------------------
-----------------SEMFFEKKFLENKMSA-------------------------------------
----------------------------------------SDLLVSELKKVIK-------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
----------------------------
>3207_1
------------------------MDNVIDANKDIKKQATE-----LLKKAHGKVSNVPPVIPVKLTTYTHS
LTI--------------------------------------------------------------------
```

```
--------------------FIGGA-ADKYVFT------------------------------PGDVPVGW
G--------------DFRPIGPTYFV-------------------------GNYVNNYFATIKGGS-----
------------------------------------------------------------------
------------------------------------------------------------------
------------KNAFVKYYGYEEAYVSDTRELTV----------------------------NTNKDKKL
NAFNDVKNFLKTYPQTQVNIVGH-----------------------------------------------
----SLGGWNAAGL-----------------------------------AEILHKNNICKVNVLVTIDPVG
EI-------------------------------------------------------------LSKIGLG
SRTSIYYSRPKPVFNLWISISCDPKSYEWNNDLIAD----------------------------------
-----------------------------------------------------------------LG
GQWSSYPSSN------------------------------------------------------------
-----------------SSYYYVTRYSHADFRL-------------------------------------
-----------------------------------------MMQEKIVNNLSVQ-----------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------DILSKELSRIK----------------------------------------------
----------------------------
>AR_0088_1
------------------------MDNVIDANKDIKKQATE-----LLKKAHGKVSNVPPVIPVKLTTYTHS
LTI-------------------------------------------------------------------
--------------------FIGGA-ADKYVFT------------------------------PGDVPVGW
G--------------DFRPIGPTYFV-------------------------GNYVNNYFATIKGGS-----
------------------------------------------------------------------
------------------------------------------------------------------
------------KNAFVKYYGYEEAYVSDTRELTV----------------------------NTNKDKKL
NAFNDVKNFLKTYPQTQVNIVGH-----------------------------------------------
----SLGGWNAAGL-----------------------------------AEILHKNNICKVNVLVTIDPVG
EI-------------------------------------------------------------LSKIGLG
SRTSIYYSRPKPVFNLWISISCDPKSYEWNNDLIAD----------------------------------
-----------------------------------------------------------------LG
GQWSSYPSSN------------------------------------------------------------
-----------------SSYYYVTRYSHADFRL-------------------------------------
-----------------------------------------MMQEKIVNNLSVQ-----------------
```

```
------------------------------------------------------------------
------------------------------------------------------------------
-----------DILSKELSRIK--------------------------------------------
----------------------------
>HWAB8_1
------------------------MDNVIDANKDIKKQATE-----LLKKAHGKVSNVPPVIPVKLTTYTHS
LTI---------------------------------------------------------------
---------------------FIGGA-ADKYVFT-----------------------------PGDVPVGW
G--------------DFRPIGPTYFV-------------------------GNYVNNYFATIKGGS-----
------------------------------------------------------------------
------------------------------------------------------------------
------------KNAFVKYYGYEEAYVSDTRELTV----------------------------NTNKDKKL
NAFNDVKNFLKTYPQTQVNIVGH-------------------------------------------
----SLGGWNAAGL-----------------------------------AEILHKNNICKVNVLVTIDPVG
EI-----------------------------------------------------------LSKIGLG
SRTSIYYSRPKPVFNLWISISCDPKSYEWNNDLIAD------------------------------------
------------------------------------------------------------------LG
GQWSSYPSSN--------------------------------------------------------
-----------------SSYYYVTRYSHADFRL--------------------------------------
-----------------------------------------MMQEKIVNNLSVQ-----------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------DILSKELSRIK--------------------------------------------
----------------------------
>AB042_1
------------------------MDNVIDANKDIKKQATE-----LLKKAHGKVSNVPPVIPVKLTTYTHS
LTI---------------------------------------------------------------
---------------------FIGGA-ADKYVFT-----------------------------PGDVPVGW
G--------------DFRPIGPTYFV-------------------------GNYVNNYFATIKGGS-----
------------------------------------------------------------------
------------------------------------------------------------------
------------KNAFVKYYGYEEAYVSDTRELTV----------------------------NTNKDKKL
NAFNDVKNFLKTYPQTQVNIVGH-------------------------------------------
```

```
----SLGGWNAAGL-----------------------------------AEILHKNNICKVNVLITIDPVG
EI------------------------------------------------------------LSKIGLG
SRTSIYYSRPKPVFNLWISISCDPKSYEWNNDLIAD-----------------------------------
---------------------------------------------------------------------LG
GQWSSYPSSN----------------------------------------------------------
-----------------SSYYYVTRYSHADFRL-------------------------------------
-------------------------------------------MMQEKIVNNLSVQ-----------------
---------------------------------------------------------------------
---------------------------------------------------------------------
-----------DILSKELSRIK-------------------------------------------------
----------------------------
>ATCC17978-mff_1
------------------------MDNVIDANKDIKKQATE-----LLKKAHGKVSNVPPVIPVKLTTYTHS
LTI------------------------------------------------------------------
---------------------FIGGA-ADKYVFT-----------------------------PGDVPVGW
G--------------DFRPIGPTYFV--------------------------GNYVNNYFATIKGGS-----
---------------------------------------------------------------------
---------------------------------------------------------------------
------------KNAFVKYYGYEEAYVSDTRELTV----------------------------NTNKDKKL
NAFNDVKNFLKTYPQTQVNIVGH----------------------------------------------
----SLGGWNAAGL-----------------------------------AEILHKNNICKVNVLITIDPVG
EI------------------------------------------------------------LSKIGLG
SRTSIYYSRPKPVFNLWISISCDPKSYEWNNDLIAD-----------------------------------
---------------------------------------------------------------------LG
GQWSSYPSSN----------------------------------------------------------
-----------------SSYYYVTRYSHADFRL-------------------------------------
-------------------------------------------MMQEKIVNNLSVQ-----------------
---------------------------------------------------------------------
---------------------------------------------------------------------
-----------DILSKELSRIK-------------------------------------------------
----------------------------
>ATCC17978-mff_2
-------------------------MPDPQNQQFWSKIAER-----PTEIQQQFWYGAEKLAKYLNDNP---
```

```
------------------------------------------------------------------
---------------------AMYKG-YMTYDTS------------------------------KPDPNLSW
WEKILFYSGQAHYNEAVTHYNTSKVI-------------------------ADQGSWLWGMLK-GD-----
-FNKDP-------------------SMSQIIVGGLISLIPVA----DQVCDIRDLIANFITLSDEKARTKDN
YMALALTSVG-------------------------------------------------------------
------------IIPEVGSAIKTIVKSS-----------------------------------RAKDVSKV
KLFKFME--YFEEALTKLKIKCPWGKAPEAWLRSRPWKGIATQAFNTLKNNIDRILSVINKCLIRFNGALKV
ALAKFQATLNHVLN-----TIKKYIDQLCDEVDKAI------------------GRLLPQQPLAMAHAGGGG
KN---------------------------------APTGRYEANVSSGKKTEASHRQKKETPPPPRKMKPK
HVVEPCLEPKKGLRNSWGKKTGKSQAELDAEFDRQLKRQEEGLNRLTVEEYQ--------------------
-----------------------------------------------------------------------QN
RQLYEKYKRA-------------------------------------------------------------
-----------------GTGTQQQRIREDMQRQ-------------------------------------
LEESEYKKL--------------------------------KTEQPQLSKGQIE------------------
-------RMAENNAKKTLEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGH---------------------
-------------------------------------------------------------SGVNRSIGSQM
AAKKRLANMDAAAAQAKAKGMGKDAMDVELKRCK--------------------------------------
----------------------------
>CIP70.10_2
-------------------------MPDPQNQQFWSKIAER-----PTEIQQQFWYGAEKLAKYLNDNP---
------------------------------------------------------------------------
---------------------AMYKG-YMTYDTS------------------------------KPDPNLSW
WEKILFYSGQAHYNEAVTHYNTSKVI-------------------------ADQGSWLWGMLK-GD-----
-FNKDP-------------------SMSQIIVGGLISLIPVA----DQVCDIRDLIANFITLSDEKARTKDN
YMALALTSVG-------------------------------------------------------------
------------IIPEVGSAIKTIVKSS-----------------------------------RAKDVSKV
KLFKFME--YFEEALTKLKIKCPWGKAPEAWLRSRPWKGIATQAFNTLKNNIDRILSVINKCLIRFNGALKV
ALAKFQATLNHVLN-----TIKKYIDQLCDEVDKAI------------------GRLLPQQPLAMAHAGGGG
KN---------------------------------APTGRYEANVSSGKKTEASHRQKKETPPPPRKMKPK
HVVEPCLEPKKGLRNSWGKKTGKSQAELDAEFDRQLKRQEEGLNRLTVEEYQ--------------------
-----------------------------------------------------------------------QN
RQLYEKYKRA-------------------------------------------------------------
-----------------GTGTQQQRIREDMQRQ-------------------------------------
```

```
LEESEYKKL--------------------------------KTEQPQLSKGQIE-----------------
-------RMAENNAKKTLEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGH--------------------
------------------------------------------------------------SGVNRSIGSQM
AAKKRLANMDAAAAQAKAKGMGKDAMDVELKRCK--------------------------------------
----------------------------
>R2091_2
-------------------------MPDPQNQQFWSKIAER-----PTEIQQQFWYGAEKLAKYLNDNP---
----------------------------------------------------------------------
---------------------AMYKG-YMTYDTS------------------------------KPDPNLSW
WEKILFYSGQAHYNEAVTHYNTSKVI--------------------------ADQGSWLWGMLK-GD-----
-FNKDP-------------------SMSQIIVGGLISLIPVA----DQVCDIRDLIANFITLSDEKARTKDN
YMALALTSVG----------------------------------------------------------
------------IIPEVGSAIKTIVKSS-----------------------------------RAKDVSKV
KLFKFME--YFEEALTKLKIKCPWGKAPEAWLRSRPWKGIATQAFNTLKNNIDRILSVINKCLIRFNGALKV
ALAKFQATLNHVLN-----TIKKYIDQLCDEVDKAI------------------GRLLPQQPLAMAHAGGGG
KN---------------------------------APTGRYEANVSSGKKTEASHRQKKETPPPPRKMKPK
HVVEPCLEPKKGLRNSWGKKTGKSQAELDAEFDRQLKRQEEGLNRLTVEEYQ--------------------
-----------------------------------------------------------------QN
RQLYEKYKRA----------------------------------------------------------
-----------------GTGTQQQRIREDMQRQ----------------------------------------
LEESEYKKL--------------------------------KTEQPQLSKGQIE-----------------
-------RMAENNAKKTLEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGH--------------------
------------------------------------------------------------SGVNRSIGSQM
AAKKRLANMDAAAAQAKAKGMGKDAMDVELKRCK--------------------------------------
----------------------------
>ZW85-1_19
------------------------------VTDFLPSKQDL-----LNALATISSPINKAIKKGQETARDVA
D-------------------------------------------------------------------
---------------------WLWVVIQGDFAEE------------------------------QTTAQTVT
G----TVISMIPFVDQICDVRDICA--------------------------NCIKIKEDSNNP--------
-WPW---------------------IGLILTLIGLFPVLGSL----FKGIFKVI------------------
----------------------------------------------------------------------
------------LAPVRRFMLRPATKALKFTGGNIY----------------------------KLAEPAIE
```

```
SGITEMNKFLARPAVKRTIKNSNITNIYKAIAK--------------------------------KIREVK
AGTNKQALLSVFDI-------LIDHLKESVKFIEKY---------------GSKAIGVKAKQMLQSVLDIRN
LA---------------------------------NQKLGEFLKPVQDFLEKLAVRIEKEGDQTFKATTNV
KNIHNFQRIGQNAELKSVLNNKPVWVDIVAKEKFKALSESPLIPKNYPD-----------------------
------------------------------------------------------------------------IS
EMSKNRALRD-------------------AFKTFHDLEPVHLSEGE--------------------------
-----------------ILYRVLDPKSADNSIC-------------------------------------
WMRASEYK---------------------------------KLKSKAD-----------------------
-------WRRYFAVFASWNNNGEVVKYRVPKGGMNVWEGPAASQTFKNSAG---------------------
-------------------------------------KVEKVNSKGEIFVLEGGG------IQIVLDPNDLV
RSNVSKREATPWGYDSGLIGEAKTSMVGVPRLEQNWYGDKK------------------------------
----------------------------
>ab736_9
--------------------------------------MNK-----LVTITTKFYDKSGNRI----------
------------------------------------------------------------------------
---------------------------INLNVQS------------------------------RYKGSLKA
NSQKTDKLGLFVFQASPNRTVEILAKPP-----------------------NQKDYTVFKTIN-SSMNSSE
IHPI--------------------KVQLPKTIDEYKQVKQS----KSTKGIVSTFFKIFDMNGKVMKNFPI
QSRPKGKG--------------------------------------------------------------
------------NSPDKYTNDEGIVEVRSSPNRDIEV---------------------------LVLTSNDT
FVLKSSINSANGSSQPVLIKLDEPYEKFKSASTIKILDR-------------DGSDYIVEKTNVKMLVVENG
KKQLFSISNGKLSL----------------------------------------QSMIGQKLEFTVYKPDG
KP----------------------------LKTQTYMATRVKNNLIEFHLDVDITKGSTAQNDPEINKKVKV
DILITMEQMKKMWPKALATKMQPILDELNSDLLGYKLDTR-------------------------------
------------------------------------------------------------------LR
QAHFMAQVRQ-----------------EVGSSFSLREQVEYMG----------------------------
-----------------PTALKQIGYYRTHPKQ-------------------------------------
-------------------------------------------AEIDGYKRG---------------------
----------QGPANGEVIANRMYDDNYRSAKYKLGNTSPGDGWKYL------GRGLKQLTGKNNYQDLTNM
YSTLWP---------------------------GEKVDFVKNPELIEQPKYAVRSAIRFWLKFKLYEVADRG
ANGEQVDAITKVINEATNSYADRRAHFVQARKIFI-------------------------------------
----------------------------
>ATCC19606_9
```

```
--------------------------------------MNK-----LVTITTKFYDKSGNRI----------
------------------------------------------------------------------------
---------------------------INLNVQS------------------------------RYKGSLKA
NSQKTDKLGLFVFQASPNRTVEILAKPP-----------------------NQKDYTVFKTIN-SSMNSSE
IHPI---------------------KVQLPKTIDEYKQVKQS----KSTKGIVSTFFKIFDMNGKVMKNFPI
QSRPKGKG--------------------------------------------------------------
------------NSPDKYTNDEGIVEVRSSPNRDIEV---------------------------LVLTSNDT
FVLKSSINSANGSSQPVLIKLDEPYEKFKSASTIKILDR-------------DGSDYIVEKTNVKMLVVENG
KKQLFSISNGKLSL----------------------------------------QSMIGQKLEFTVYKPDG
KP---------------------------LKTQTYMATRVKNNLIEFHLDVDITKGSTAQNDPEINKKVKV
DILITMEQMKKMWPKALATKMQPILDELNSDLLGYKLDTR-------------------------------
------------------------------------------------------------------LR
QAHFMAQVRQ-----------------EVGSSFSLREQVEYMG----------------------------
-----------------PTALKQIGYYRTHPKQ-------------------------------------
-------------------------------------------AEIDGYKRG---------------------
----------QGPANGEVIANRMYDDNYRSAKYKLGNTSPGDGWKYL------GRGLKQLTGKNNYQDLTNM
YSTLWP---------------------------GEKVDFVKNPELIEQPKYAVRSAIRFWLKFKLYEVADRG
ANGEQVDAITKVINEATNSYADRRAHFVQARKIFI-------------------------------------
-----------------------------
>Ab04-mff_11
------------------------MSYSEDFKIFVATINGE-----AENCSETSWKVIAHTMRNRVGFANW-
------------------------------------------------------------------------
---------------------KSWST-IIQIVTK------------------------------TGYDAYTQ
KNSPYKRAKKALDSGDISPKLMSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYP-SLVPDFV
VSKS---------------------NPTQQVQIPGTEKDDMR----WYKVLTSIFDVSFVDNAGNPLVGVTV
DVVYNDKKPVP-------------------------------------------------------------
------------LFKDLITDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVIVVNNGK
GGIKSKTDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPNFSYFLKY
KNAEKKHSVGANGI-------ENNLVALSGEEITVLISGLDSKQEIIRFTAQEGMGEKTIKLNLHTFNILFR
HKDTKKPITNLNLIQKYRN----QIKQKKTDGNGKITVSAMPGFELNYKLRDERNLLTIKVDKNKSLRVIDV
DSSAIEQASKNIKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDN-------
------------------------------------------------------------------GE
TEFIVYTYDQ-------------------KTNQLFSGGNYSIE----------------------------
```

```
----YKGNKKRHSSGIHGIGKKIHKGEIGQKIK---------------------------------------
ITASSGGK---------------------------EFIAFDGNLSRGMKAFELKIDRSVIPSVSDVIISFKG
VNEQSRQAIVSQKTKNVLAYLAKEANMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECI----
-----------------------------AKGLGKEATIQKMVEKIVEFQNKGVRVSKHCVSEEQYRKNNII
DLGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIISGFISADVAGEGAMHIEIIQ-----------------
----------------------------
>BJAB0715_11
------------------------MSYSEDFKIFVATINGE-----AENCSETSWKVIAHTMRNRVGFANW-
----------------------------------------------------------------------
---------------------KSWST-IIQIVTK------------------------------TGYDAYTQ
KNSPYKRAKKALDSGDISPKLMSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYP-SLVPDFV
VSKS---------------------NPTQQVQIPGTEKDDMR----WYKVLTSIFDVSFVDNAGNPLVGVTV
DVVYNDKKPVP---------------------------------------------------------
------------LFKDLITDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVIVVNNGK
GGIKSKTDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPNFSYFLKY
KNAEKKHSVGANGI-------ENNLVALSGEEITVLISGLDSKQEIIRFTAQEGMGEKTIKLNLHTFNILFR
HKDTKKPITNLNLIQKYRN----QIKQKKTDGNGKITVSAMPGFELNYKLRDERNLLTIKVDKNKSLRVIDV
DSSAIEQASKNIKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDN-------
-----------------------------------------------------------------------GE
TEFIVYTYDQ-------------------KTNQLFSGGNYSIE-----------------------------
----YKGNKKRHSSGIHGIGKKIHKGEIGQKIK---------------------------------------
ITASSGGK---------------------------EFIAFDGNLSRGMKAFELKIDRSVIPSVSDVIISFKG
VNEQSRQAIVSQKTKNVLAYLAKEANMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECI----
-----------------------------AKGLGKEATIQKMVEKIVEFQNKGVRVSKHCVSEEQYRKNNII
DLGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIISGFISADVAGEGAMHIEIIQ-----------------
----------------------------
>LAC-4_11
------------------------MSYSEDFKIFVATINGE-----AENCSETSWKVIAHTMRNRVGFANW-
----------------------------------------------------------------------
---------------------KSWST-IIQIVTK------------------------------TGYDAYTQ
KNSPYKRAKKALDSGDISPKLMSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYP-SLVPDFV
VSKS---------------------NPTQQVQIPGTEKDDMR----WYKVLTSIFDVSFVDNAGNPLVGVTV
DVVYNDKKPVP---------------------------------------------------------
```

```
------------LFKDLITDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVIVVNNGK
GGIKSKTDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPNFSYFLKY
KNAEKKHSVGANGI-------ENNLVALSGEEITVLISGLDSKQEIIRFTAQEGMGEKTIKLNLHTFNILFR
HKDTKKPITNLNLIQKYRN----QIKQKKTDGNGKITVSAMPGFELNYKLRDERNLLTIKVDKNKSLRVIDV
DSSAIEQASKNIKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDN-------
----------------------------------------------------------------------GE
TEFIVYTYDQ-------------------KTNQLFSGGNYSIE-----------------------------
----YKGNKKRHSSGIHGIGKKIHKGEIGQKIK--------------------------------------
ITASSGGK---------------------------EFIAFDGNLSRGMKAFELKIDRSVIPSVSDVIISFKG
VNEQSRQAIVSQKTKNVLAYLAKEANMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECI----
------------------------------AKGLGKEATIQKMVEKIVEFQNKGVRVSKHCVSEEQYRKNNII
DLGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIISGFISADVAGEGAMHIEIIQ-----------------
----------------------------
>WKA02_11
------------------------MSYSEDFKIFVATINGE-----AENCSETSWKVIAHTMRNRVGFANW-
----------------------------------------------------------------------
---------------------KSWST-IIQIVTK------------------------------TGYDAYTQ
KNSPYKRAKKALDSGDISPKLMSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYP-SLVPDFV
VSKS---------------------NPTQQVQIPGTEKDDMR----WYKVLTSIFDVSFVDNAGNPLVGVTV
DVVYNDKKPVP----------------------------------------------------------
------------LFKDLITDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVIVVNNGK
GGIKSKTDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPNFSYFLKY
KNAEKKHSVGANGI-------ENNLVALSGEEITVLISGLDSKQEIIRFTAQEGMGEKTIKLNLHTFNILFR
HKDTKKPITNLNLIQKYRN----QIKQKKTDGNGKITVSAMPGFELNYKLRDERNLLTIKVDKNKSLRVIDV
DSSAIEQASKNIKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDN-------
----------------------------------------------------------------------GE
TEFIVYTYDQ-------------------KTNQLFSGGNYSIE-----------------------------
----YKGNKKRHSSGIHGIGKKIHKGEIGQKIK--------------------------------------
ITASSGGK---------------------------EFIAFDGNLSRGMKAFELKIDRSVIPSVSDVIISFKG
VNEQSRQAIVSQKTKNVLAYLAKEANMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECI----
------------------------------AKGLGKEATIQKMVEKIVEFQNKGVRVSKHCVSEEQYRKNNII
DLGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIISGFISADVAGEGAMHIEIIQ-----------------
----------------------------
```

```
>XH858_11
------------------------MSYSEDFKIFVATINGE-----AENCSETSWKVIAHTMRNRVGFANW-
------------------------------------------------------------------------
---------------------KSWST-IIQIVTK------------------------------TGYDAYTQ
KNSPYKRAKKALDSGDISPKLMSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYP-SLVPDFV
VSKS---------------------NPTQQVQIPGTEKDDMR----WYKVLTSIFDVSFVDNAGNPLVGVTV
DVVYNDKKPVP-----------------------------------------------------------
------------LFKDLITDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVIVVNNGK
GGIKSKTDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPNFSYFLKY
KNAEKKHSVGANGI-------ENNLVALSGEEITVLISGLDSKQEIIRFTAQEGMGEKTIKLNLHTFNILFR
HKDTKKPITNLNLIQKYRN----QIKQKKTDGNGKITVSAMPGFELNYKLRDERNLLTIKVDKNKSLRVIDV
DSSAIEQASKNIKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDN-------
-------------------------------------------------------------------GE
TEFIVYTYDQ-------------------KTNQLFSGGNYSIE-----------------------------
----YKGNKKRHSSGIHGIGKKIHKGEIGQKIK-------------------------------------
ITASSGGK---------------------------EFIAFDGNLSRGMKAFELKIDRSVIPSVSDVIISFKG
VNEQSRQAIVSQKTKNVLAYLAKEANMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECI----
-----------------------------AKGLGKEATIQKMVEKIVEFQNKGVRVSKHCVSEEQYRKNNII
DLGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIISGFISADVAGEGAMHIEIIQ-----------------
----------------------------
>AB030_24
--MKNGKSINQKSYPLTRYGFICAVSRMESSSDLSLPLTAP-----VNIRASQNKNSRGYIGFFQFGEAA--
------------------------------------------------------------------------
---------------------LIDLGYYKHWNDN-----------------------------SDKTKANDW
TGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLR-------------NRSFNEYYGKIINGI-----
-------------------------EITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIE
MFNHYDLE-----------------------------------------------------------SCCSRK
IYII--LKNQIGQIAKNKKVTIESEYSGKFKQS-------------------------------KFIVSAES
DEQGLLPVIIRHPGSKIIIKVDGKQSAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQK
TVDLKKDEVKTNAP-------KDIKFDIAIIESDTNRKITNMRFFIRYKGKIKEHTSDSSGIKTGIIAEEGE
NL-------DILVNGSKGY---QKLKTISITKGMENSCISVPLGLVSVKLKIHDSKGKILKNNKFFVSYRGR
EIEKITDSNGFIQLKMLNAFVYKLLLSNKKPILTLRNDPSISVINVNLNSAATTIQ----------------
-------------------------------------------------------------------MP
```

```
RVASNPPSKT-------------------VPAKTKPAKE--------------------------------
-----------------TSSKREESFVDYLIDF----------------------------------IPSLG
KTENVHTE---------------------------------KNGNPLTKQYGSDVVFTIKTINKETGKEEN
LAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVDSKEQVLYTAILKNPMPVIEIRMDKPKDDDSY
LFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTEIRAMADGKVRVVKGFYSGTDVIEIVHKKHII
RYGEVLAGKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLEMYSNPKDTSPLTVRGNNAYQRRSDLIDPTT
FLDNSTL---------------------
>AbH12O-A2_24
--MKNGKSINQKSYPLTRYGFICAVSRMESSSDLSLPLTAP-----VNIRASQNKNSRGYIGFFQFGEAA--
------------------------------------------------------------------------
---------------------LIDLGYYKHWNDN-----------------------------SDKTKANDW
TGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLR-------------NRSFNEYYGKIINGI-----
-------------------------EITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIE
MFNHYDLE-----------------------------------------------------------SCCSRK
IYII--LKNQIGQIAKNKKVTIESEYSGKFKQS-------------------------------KFIVSAES
DEQGLLPVIIRHPGSKIIIKVDGKQSAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQK
TVDLKKDEVKTNAP-------KDIKFDIAIIESDTNRKITNMRFFIRYKGKIKEHTSDSSGIKTGIIAEEGE
NL-------DILVNGSKGY---QKLKTISITKGMENSCISVPLGLVSVKLKIHDSKGKILKNNKFFVSYRGR
EIEKITDSNGFIQLKMLNAFVYKLLLSNKKPILTLRNDPSISVINVNLNSAATTIQ----------------
-----------------------------------------------------------------------MP
RVASNPPSKT-------------------VPAKTKPAKE--------------------------------
-----------------TSSKREESFVDYLIDF----------------------------------IPSLG
KTENVHTE---------------------------------KNGNPLTKQYGSDVVFTIKTINKETGKEEN
LAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVDSKEQVLYTAILKNPMPVIEIRMDKPKDDDSY
LFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTEIRAMADGKVRVVKGFYSGTDVIEIVHKKHII
RYGEVLAGKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLEMYSNPKDTSPLTVRGNNAYQRRSDLIDPTT
FLDNSTL---------------------
>AF-401_24
--MKNGKSINQKSYPLTRYGFICAVSRMESSSDLSLPLTAP-----VNIRASQNKNSRGYIGFFQFGEAA--
------------------------------------------------------------------------
---------------------LIDLGYYKHWNDN-----------------------------SDKTKANDW
TGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLR-------------NRSFNEYYGKIINGI-----
-------------------------EITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIE
```

```
MFNHYDLE-------------------------------------------------------------SCCSRK
IYII--LKNQIGQIAKNKKVTIESEYSGKFKQS--------------------------------KFIVSAES
DEQGLLPVIIRHPGSKIIIKVDGKQSAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQK
TVDLKKDEVKTNAP-------KDIKFDIAIIESDTNRKITNMRFFIRYKGKIKEHTSDSSGIKTGIIAEEGE
NL-------DILVNGSKGY---QKLKTISITKGMENSCISVPLGLVSVKLKIHDSKGKILKNNKFFVSYRGR
EIEKITDSNGFIQLKMLNAFVYKLLLSNKKPILTLRNDPSISVINVNLNSAATTIQ----------------
-----------------------------------------------------------------------MP
RVASNPPSKT-------------------VPAKTKPAKE---------------------------------
-----------------TSSKREESFVDYLIDF-----------------------------------IPSLG
KTENVHTE---------------------------------KNGNPLTKQYGSDVVFTIKTINKETGKEEN
LAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVDSKEQVLYTAILKNPMPVIEIRMDKPKDDDSY
LFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTEIRAMADGKVRVVKGFYSGTDVIEIVHKKHII
RYGEVLAGKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLEMYSNPKDTSPLTVRGNNAYQRRSDLIDPTT
FLDNSTL---------------------
>AR_0101_24
--MKNGKSINQKSYPLTRYGFICAVSRMESSSDLSLPLTAP-----VNIRASQNKNSRGYIGFFQFGEAA--
-----------------------------------------------------------------------
---------------------LIDLGYYKHWNDN----------------------------SDKTKANDW
TGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLR-------------NRSFNEYYGKIINGI-----
-------------------------EITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIE
MFNHYDLE-------------------------------------------------------------SCCSRK
IYII--LKNQIGQIAKNKKVTIESEYSGKFKQS--------------------------------KFIVSAES
DEQGLLPVIIRHPGSKIIIKVDGKQSAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQK
TVDLKKDEVKTNAP-------KDIKFDIAIIESDTNRKITNMRFFIRYKGKIKEHTSDSSGIKTGIIAEEGE
NL-------DILVNGSKGY---QKLKTISITKGMENSCISVPLGLVSVKLKIHDSKGKILKNNKFFVSYRGR
EIEKITDSNGFIQLKMLNAFVYKLLLSNKKPILTLRNDPSISVINVNLNSAATTIQ----------------
-----------------------------------------------------------------------MP
RVASNPPSKT-------------------VPAKTKPAKE---------------------------------
-----------------TSSKREESFVDYLIDF-----------------------------------IPSLG
KTENVHTE---------------------------------KNGNPLTKQYGSDVVFTIKTINKETGKEEN
LAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVDSKEQVLYTAILKNPMPVIEIRMDKPKDDDSY
LFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTEIRAMADGKVRVVKGFYSGTDVIEIVHKKHII
RYGEVLAGKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLEMYSNPKDTSPLTVRGNNAYQRRSDLIDPTT
```

```
FLDNSTL---------------------
>AR_0063_24
--MKNGKSINQKSYPLTRYGFICAVSRMESSSDLSLPLTAP-----VNIRASQNKNSRGYIGFFQFGEAA--
------------------------------------------------------------------------
---------------------LIDLGYYKHWNDN-----------------------------SDKTKANDW
TGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLR-------------NRSFNEYYGKIINGI-----
-------------------------EITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIE
MFNHYDLE-------------------------------------------------------SCCSRK
IYIILLLKNQIGQIAKNKKVTIESEYSGKFKQS-------------------------------KFIVSAES
DEQGLLPVIIRHPGSKIIIKVDGKQSAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQK
TVDLKKDEVKTNAP-------KDIKFDIAIIESDTNRKITNMRFFIRYKGKIKEHTSDSSGIKTGIIAEEGE
NL-------DILVNGSKGY---QKLKTISITKGMENSCISVPLGLVSVKLKIHDSKGKILKNNKFFVSYRGR
EIEKITDSNGFIQLKMLNAFVYKLLLSNKKPILTLRNDPSISVINVNLNSAATTIQ----------------
-----------------------------------------------------------------------MP
RVASNPPSKT-------------------VPAKTKPAKE---------------------------------
-----------------TSSKREESFVDYLIDF-----------------------------------IPSLG
KTENVHTE---------------------------------KNGNPLTKQYGSDVVFTIKTINKETGKEEN
LAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVDSKEQVLYTAILKNPMPVIEIRMDKPKDDDSY
LFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTEIRAMADGKVRVVKGFYSGTDVIEIVHKKHII
RYGEVLAGKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLEMYSNPKDTSPLTVRGNNAYQRRSDLIDPTT
FLDNSTL---------------------
>AB031_25
MKKTIKFEKDSKSFETNLAGFIEAVSFKESSSNLLLPLTHP-----INMEAASITNEMGFIGLFQWGEEALY
DLGYYLGDQGISYADIKNTDKNSSLRISWKNQFNSNNWVGKWSGKRNINSKKDFLKHPEIQYEIIKEWIKYL
CNQLRNNNFNEYFGTTIQNIEITESG-AIAGMHL------------------------------VGIGGLGA
F----LGIPKFHGKKQTDGNGTHIKK--------------------------YIENFGGFDLEQ-CC-----
-NRK---------------------IYVTLKDNLGLELKDKE----VIIVSQNKGKYVSGETKVKVKSDENG
NLPVIVRS-------------------------------------------------------PNTEIKICADGKE
SNTI--------IQKANEKQKAILSDFKVSSHP-------------------------------ATLEKNST
PQPKPQTNKTPQEVRNEQTQPSTAPEKEKDSSSKDVDFNIQIVEGDS-------------------GKAISN
M---NFFITYKGNI-------KKHTAD-GHGIKQNII--------------AEIGQDIEVSVQGTGHKQVIH
HF-------TANAA----------------------LKNKTVKVSLPVHSFNISVTQDNKPVPNTLFSIFYR
GREISKRTDSRGMLNVRMLTGFVFGFGIKGKSLILSRVEKNTITKA--FTVNGSAVHASKAYEANDAK----
```

```
------------------QKQNENLNKHKKEKQEEAAKKQADQAKTQKNSKNEVKQSNTYTENGGKPLTTVS
NQASVTSDTT-------------------NYIIYPNGTIDRINKD---------------------------
-----------------ATGFAAYYYVANNQPI--------------------------------------
LIGKSRIY---------------------------T----ADRWLKKGKKGSGISHLVS-IREIFGDSGSKP
NNKWEKKIGNLNISIHNDTQQQHRYWLSTVAFAAYIGAVCKFG--EKVRFS--GFSDRNGSPGGSSSHLNGE
VGDIGY----------IRVDRNNSVGVNFEMADYDHDASLRFVNILISFGWGKTK------NMLSEHYPAHL
VNKYKLNQGYILPRCSQWTNPRHNNHLHLQGLSVTFNKDE--------------------------------
----------------------------
>6200_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
------------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVISSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSSISHR----FNCKTSEIVHLNKLKNPDHIDVGQII
KI-----------------------------------------------------------------PYKGES
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD-----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINQTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM------------------------------------
----------------------------
>ZW85-1_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
------------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVISSKILL--------------------------DNIILAKSTNKP-GN-----
```

```
-YRY---------------------LTHKVKKGENLSSISHR----FNCKTSEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGES
SDSK--------KSPDNKQSKHENNKSSSTQKVN-----------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT--------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINQTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>A1_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
-----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN-----------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT--------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
```

```
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>A388_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>A85_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
```

```
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD-----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>AB307-0294_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
-----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-----------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT--------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD-----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>AB5075-UW_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
-----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
```

```
K----VRHTVIYKKEIVRVTSSKILL-------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN-----------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>AR_0083_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
-----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL-------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN-----------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
```

```
----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>AYE_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-----------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK----------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>D36_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-----------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
```

```
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>WCHAB005078_17
----------MNKKGLIQFRFVELFTGNNIPNLYHVIKNEK-----GTTIASGMTNSNGLTVMISR------
-----------------------------------------------------------------------
---------------------DVGDT-LYVYLKN------------------------------IITGDLKE
K----VRHTVIYKKEIVRVTSSKILL--------------------------DNIILAKSTNKP-GN-----
-YRY---------------------LTHKVKKGENLSLISHR----FNCKISEIVHLNKLKNPDHIDVGQII
KI-----------------------------------------------------------------PYKGGS
SDSK--------KSPDNKQSKHENNKSSSTQKVN------------------------------SHENNNKN
TSDKPQKRIESKDITDEYTKESGKPMKVATNAT---------------------------------SPCICK
Q---YNLAWGSKVS-------CEFRKRVIKIAQNLW---------------PNDSENMASQLMAVMHLESAG
TF-------SPKIGTFISK----KLTD---------DAKGGYVGLIQFGKFASIDLKVKRSDLAKMSAVQQL
DYVEKYYKLNSAHTKIKNLTGLYLWVNYPKNVKENRLEDEDIVYAAPKDAEV--------------------
-----------------------------------------------------------------------TS
KKFLESPYHQ-------------------NPSFMKENEEYKRD----------------------------
-----------------GKKVIRQGFKNGSTKV-------------------------------------
WEVEQEIK---------------------------K------HLTEGIKSQ---------------------
-------NLEKNYNCAYINHTEIKNTQKINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADTSGHPVA-
-----------------------------ASDWGPTLKKIGYKEIPEEFNKPQLG------DIYIITKTDKH
QYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM-----------------------------------
----------------------------
>A1_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
-----------------------------------------------------------------------
```

```
---------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR--------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------------
-----------------SQARDKVANLQSSMRL------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>A388_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
---------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR--------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------------
-----------------SQARDKVANLQSSMRL------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>A85_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
---------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------------
-----------------SQARDKVANLQSSMRL------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB0057_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
---------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------IQ
REFESKKITA-------------------------------------------------------------
-----------------SQARDKVANLQSSMRL-------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB307-0294_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
--------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K----------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------IQ
REFESKKITA-------------------------------------------------------------
-----------------SQARDKVANLQSSMRL-------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB5075-UW_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
```

```
------------------------------------------------------------------
--------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------AEN-GV-----
------------------------------------------------------------------
------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------
-----------------SQARDKVANLQSSMRL-----------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>AR_0083_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------
--------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------AEN-GV-----
------------------------------------------------------------------
------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------
-----------------SQARDKVANLQSSMRL-----------------------------------
```

```
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>D36_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
--------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ---------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------IQ
REFESKKITA------------------------------------------------------------
-----------------SQARDKVANLQSSMRL-----------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>USA15_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
------------------------------------------------------------------------
--------------------EIWAK-RKDFLDD-----------------------------IGIGGNRD
K-------------------------------------------------------AEN-GV-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
```

```
PIYSAGINQKLGQ------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------IQ
REFESKKITA---------------------------------------------------------------
-----------------SQARDKVANLQSSMRL----------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
----------------------------
>WCHAB005078_16
----------------------------CSTTLNRNLGGVK-----GDHLQAHHIIPE--------------
-------------------------------------------------------------------------
---------------------EIWAK-RKDFLDD------------------------------IGIGGNRD
K-----------------------------------------------------------AEN-GV-----
-------------------------------------------------------------------------
-------------------------------------------------------------------------
------------LMPDSEAKAKQMKR-------------------------------------QLYHCGSH
PIYSAGINQKLGQ------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------IQ
REFESKKITA---------------------------------------------------------------
-----------------SQARDKVANLQSSMRL----------------------------------------
-----------------------------------------VLITPGTKPIRLS-----------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
----------------------------
>AR_0078_29
```

```
----------MNKKSLVTIQILDLFGSPISKAQYEVKNQRT-----GQVIAAGTTNSSGCIVEISR------
------------------------------------------------------------------------
---------------------DKGTA-LDVYIKS------------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL---------------------------NLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRVLERLNKIDDPNKISIGQVI
KL-------------------------------------------------------------PVHIPASGN
HSHQ--------DKPKHKHSAQSTNKPTASSTKTTP---APAAKRPANPASQTKQENGLPEKAHQLYEDTKK
ALNEAASSVSKILTIDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIRQFQRDYMGV-PDTGKICGSVLVALDQFYDEY------------------PISSFMGKAACNCGKCSG
FG-------NGKMGVQSGI-----------------NTANEYPGIHRSLIWILKSLNFYLKNEFKDKKINVA
YIESGYRCIENNKKHERTSVNHMGLALDIHFHKNGVRTRELSDMEFIRKNI---------------------
----------------------------------------------------------------------MA
KKMGASEQRI-------------------RDKIYLEPKVFRSG-----------------------------
------EAGATSWVHFDITMFLAKYFNNNMFKT-------------------------------------
KVSDLNGV----------------------------------KLVNLAASSRILSCGGI-VALP--------
-------KSQNNITDELVLSNEDIIDIMKVTETEVIKFKTEKY--FLEQAA--GVVDTIMNRTKSGVWGNSV
RKVVNA------------DRQFSKITGPKSLDPYGSVENMPMSHVSRKVRNFVNS------YLLERANGKKS
IIGENLNYANKYYSDEKNRKAWVDKFHNEAVKNGMILGTGKAIHAHGTVRELRDKMPKPFKIVLPKDFKGI-
----------------------------
>AR_0088_14
----------MNKKSLVTIQILDLFGSPISKAQYVVKNQRT-----GKVIAAGPTNSSGCIVEISQ------
------------------------------------------------------------------------
---------------------DKGTT-LDVYIKS------------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL----------------------------DLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRALERLNKIDDPNKISVGQVI
KL-------------------------------------------------------------PVHIPASGN
HSHQ--------DKPKHKHSAQSTNKPTASSAKTTP---APAAKRPANPASQTKQENGLPEKAHQLYEDTKK
ALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIKQFQRDYMGV-PDTGKICGSVLAALDRFRDEY------------------GIASYFESMKCPCGECSG
FG-------RSRSGNFRFE----MYNKTTRQYVEVYRDAKEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIV
KISSGYRCIDNNWKNRRPTTNHMGCA--LDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTSLGWSPDKFGL
ERISD----------------------------------------------------------------GA
KTWVHLDVRE-------------------FNKKYKIDKLFSTS-----------------------------
```

```
----KDGLNGDYLINLFKADEKANKILGCSGIV--------------------------------------
VSPNKNPN------------------------------LNDSSLEDLIRQLGSVISHGE---------GNYE
SYNTGTKNVKGDKVGYSFKNPGKGTVTSKRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFT
GSEVYD--------------------ANMQEQVFREFLISKRTKLSQFVRKGIG-------SLRDAQYDAAQ
EWASVAVPKGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVLEILEKIHRFHKDGK---------------
----------------------------
>CIP70.10_14
----------MNKKSLVTIQILDLFGSPISKAQYVVKNQRT-----GKVIAAGPTNSSGCIVEISQ------
----------------------------------------------------------------------
---------------------DKGTT-LDVYIKS------------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL----------------------------DLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRALERLNKIDDPNKISVGQVI
KL-------------------------------------------------------------PVHIPASGN
HSHQ--------DKPKHKHSAQSTNKPTASSAKTTP---APAAKRPANPASQTKQENGLPEKAHQLYEDTKK
ALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIKQFQRDYMGV-PDTGKICGSVLAALDRFRDEY------------------GIASYFESMKCPCGECSG
FG-------RSRSGNFRFE----MYNKTTRQYVEVYRDAKEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIV
KISSGYRCIDNNWKNRRPTTNHMGCA--LDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTSLGWSPDKFGL
ERISD-----------------------------------------------------------------GA
KTWVHLDVRE-------------------FNKKYKIDKLFSTS------------------------------
----KDGLNGDYLINLFKADEKANKILGCSGIV--------------------------------------
VSPNKNPN------------------------------LNDSSLEDLIRQLGSVISHGE---------GNYE
SYNTGTKNVKGDKVGYSFKNPGKGTVTSKRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFT
GSEVYD--------------------ANMQEQVFREFLISKRTKLSQFVRKGIG-------SLRDAQYDAAQ
EWASVAVPKGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVLEILEKIHRFHKDGK---------------
----------------------------
>HWBA8_14
----------MNKKSLVTIQILDLFGSPISKAQYVVKNQRT-----GKVIAAGPTNSSGCIVEISQ------
----------------------------------------------------------------------
---------------------DKGTT-LDVYIKS------------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL----------------------------DLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRALERLNKIDDPNKISVGQVI
KL-------------------------------------------------------------PVHIPASGN
```

```
HSHQ--------DKPKHKHSAQSTNKPTASSAKTTP---APAAKRPANPASQTKQENGLPEKAHQLYEDTKK
ALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIKQFQRDYMGV-PDTGKICGSVLAALDRFRDEY------------------GIASYFESMKCPCGECSG
FG-------RSRSGNFRFE----MYNKTTRQYVEVYRDAKEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIV
KISSGYRCIDNNWKNRRPTTNHMGCA--LDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTSLGWSPDKFGL
ERISD-------------------------------------------------------------GA
KTWVHLDVRE-------------------FNKKYKIDKLFSTS-----------------------------
----KDGLNGDYLINLFKADEKANKILGCSGIV--------------------------------------
VSPNKNPN------------------------------LNDSSLEDLIRQLGSVISHGE---------GNYE
SYNTGTKNVKGDKVGYSFKNPGKGTVTSKRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFT
GSEVYD--------------------ANMQEQVFREFLISKRTKLSQFVRKGIG-------SLRDAQYDAAQ
EWASVAVPKGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVLEILEKIHRFHKDGK---------------
----------------------------
>R2091_14
----------MNKKSLVTIQILDLFGSPISKAQYVVKNQRT-----GKVIAAGPTNSSGCIVEISQ------
---------------------------------------------------------------------
---------------------DKGTT-LDVYIKS------------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL----------------------------DLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRALERLNKIDDPNKISVGQVI
KL-----------------------------------------------------------PVHIPASGN
HSHQ--------DKPKHKHSAQSTNKPTASSAKTTP---APAAKRPANPASQTKQENGLPEKAHQLYEDTKK
ALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIKQFQRDYMGV-PDTGKICGSVLAALDRFRDEY------------------GIASYFESMKCPCGECSG
FG-------RSRSGNFRFE----MYNKTTRQYVEVYRDAKEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIV
KISSGYRCIDNNWKNRRPTTNHMGCA--LDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTSLGWSPDKFGL
ERISD-------------------------------------------------------------GA
KTWVHLDVRE-------------------FNKKYKIDKLFSTS-----------------------------
----KDGLNGDYLINLFKADEKANKILGCSGIV--------------------------------------
VSPNKNPN------------------------------LNDSSLEDLIRQLGSVISHGE---------GNYE
SYNTGTKNVKGDKVGYSFKNPGKGTVTSKRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFT
GSEVYD--------------------ANMQEQVFREFLISKRTKLSQFVRKGIG-------SLRDAQYDAAQ
EWASVAVPKGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVLEILEKIHRFHKDGK---------------
----------------------------
```

```
>TYTH-1_14
----------MNKKSLVTIQILDLFGSPISKAQYEVKNQRT-----GQVIAAGTTNSSGCIVEISR------
------------------------------------------------------------------------
---------------------DKGTA-LDVYIKS-----------------------------MFKGSMVK
V----QSFVMSKDRMVVKITSPKVLL---------------------------NLKTLTNQGNNGQ-----
-YKR---------------------KTHIVKKGDTLFEIAQK----NHTTVRALERLNKIDDPNKISIGQVI
KL-----------------------------------------------------------PVHIPASGN
HSHQ--------DKSKHKHSAQPVNKPTASSTKTTP---AAAAKRPANPTSQTKQENGLPEKVHQLYEDTKK
ALNEAASSASKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELI-REVNIRLAGFGGALPTDEFTELT
ATCIKQFQRDYMGV-PDTGKICGSVLAALDRFRDEY------------------GIASYFESMKCPCGECSG
FG-------RSRSGNFRFE----MYNKTTRQYVEVYRDAKEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIV
KISSGYRCIDNNWKNRRPTTNHMGCA--LDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTSLGWSPDKFGL
ERISD-------------------------------------------------------------GA
KTWVHLDVRE-------------------FNKKYKIDKLFSTS----------------------------
----KDGLNGDYLINLFKADEKANKILGCSGIV-------------------------------------
VSPNKNPN------------------------------LNDSSLEDLIRQLGSVISHGE---------GNYE
SYNTGTKNVKGDKVGYSFKNPGKGTVTSKRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFT
GSEVYD--------------------ANMQEQVFREFLISKRTKLSQFVRKGIG-------SLRDAQYDAAQ
EWASVAVPKGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVLEILEKIHRFHKDGK---------------
----------------------------
>15A5_28
-------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY------------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH---------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------FV
```

```
NAEKVLPTTV------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-----------------------------------------LPDNLNDYLMK------------------
---------------------------------------------------------------------
---------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK----------------------------------------
-----------------------------
>Ab4568_28
-------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
---------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA----------------------
---------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS----------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM-------------------------------------------------------------------
---------------------------------------------------------------------
------------------------------------------------------------------FV
NAEKVLPTTV------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-----------------------------------------LPDNLNDYLMK------------------
---------------------------------------------------------------------
---------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK----------------------------------------
-----------------------------
>Ab4977_28
-------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
---------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA----------------------
```

```
------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------FV
NAEKVLPTTV--------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-----------------------------------------
-----------------------------
>JBA13_28
-----------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------
---------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------FV
NAEKVLPTTV--------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-----------------------------------------
```

```
----------------------------
>KAB04_28
------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------------
---------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------FV
NAEKVLPTTV--------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF--------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK----------------------------------------
----------------------------
>KAB07_28
------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------------
---------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-----------------------------------------------------------------------FV
NAEKVLPTTV-------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-----------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-------------------------------------------
---------------------------
>KAB08_28
-----------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
-----------------------------------------------------------------------
--------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL--------------------EGANSPRGEGILRIWSS----FDA----------------------
-----------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM---------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------FV
NAEKVLPTTV-------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-----------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-------------------------------------------
---------------------------
>KBN10P02143_28
-----------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
-----------------------------------------------------------------------
--------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
```

```
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------FV
NAEKVLPTTV--------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF--------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK----------------------------------------
----------------------------
>SAA14_28
------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
------------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------FV
NAEKVLPTTV--------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF--------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-------------SPDVKVDIKNTYHLKK-------------------------------------------
----------------------------
>SMC_Paed_Ab_BL01_28
------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
-----------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
-----------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM---------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------FV
NAEKVLPTTV-------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF--------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-------------------------------------------
----------------------------
>SSA12_28
------------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
-----------------------------------------------------------------------
---------------------KPEAE-LHLLVGS-----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
-----------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM---------------------------------------------------------------------
```

```
------------------------------------------------------------------
-------------------------------------------------------------------FV
NAEKVLPTTV-------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-------------------------------------------
----------------------------
>SSMA17_28
-----------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------
---------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA----------------------
------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-------------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM----------------------------------------------------------------
------------------------------------------------------------------
-------------------------------------------------------------------FV
NAEKVLPTTV-------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-------------------------------------
-------------------------------------------LPDNLNDYLMK------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-------------------------------------------
----------------------------
>YU-R612_28
-----------------------------------MGNNS-----TTSTTTNTANPPTQKVPL--------
------------------------------------------------------------------
---------------------KPEAE-LHLLVGS----------------------------AYGEGDRES
```

```
P----YGHTAVYIKLKGKDYIY-----------------------------DFGRYGKTKPESFGI-----
-FTL---------------------EGANSPRGEGILRIWSS----FDA-----------------------
----------------------------------------------------------------------
------------YIADENSQGKGTSKTRTTH--------------------------------AYGYRIFD
SQAMLVLNYYNNLLKTATLRRNEKYYKS-----------------------------------------
----YALSQDYFAL-----------------------------------APNCTTQSLEATKKAIPSMAKSG
HM--------------------------------------------------------------------
----------------------------------------------------------------------
-----------------------------------------------------------------FV
NAEKVLPTTV------------------------------------------------------------
-----------------KLAFKASKYEMPKYLF-----------------------------------
-----------------------------------------LPDNLNDYLMK------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------SPDVKVDIKNTYHLKK-----------------------------------------
----------------------------
>15A34_23
------MNTELKHKLYNITFTLHDLTHKPIPNLYYEIKNGK-----DLVKKGNTNAQGEITLKY--------
----------------------------------------------------------------------
---------------------VGGNT-LTLFVRK------------------------------DIDNTLKE
I----GKVHTPSKNIKVKLISPKMKF--------------------------DVTLLPHQKQGK--------
-YWR---------------------GTYKVKSGDTLSKIAKE---HHTTISALLALNPNIKSPHEIYQNENI
DIVEGNAD-----------------------------------------------------AIIKLDEN
MTVK--------VPPHKKTGTVSIDRKSKSTSITP-----------------------------QTDTTNKT
AEPKVGQTKLQPPVTKKEQSAASDSKSIPQQKTSTATTQKIEVQQEHNEDKKPVAVASL-------SGCVCK
D---YDLIWGKTTK----FVNCEFRKKVIQICKDMW---------------PNDTKNMANYLMACMHLETGG
SF-------DPAQPNGLGY----------------------YGLIQFGPDVRKDLNNISVEKLTKMSGAQQL
DLVKQHFTRSDRHKLMKSLTDMYLYINYPNALLSGKNKPNDIL-----------------------------
-----------------------------------------------------------------YE
GGSERSAYHA-------------------NPAFMKEKGEYQNI-----------------------------
-FAYRKDKNGNFKLDKNKKKIPIRGFEDGKTYI-------------------------------------
WEVTQEIN---------------------------K------HLTTGLDSKNKENNF---------------
-------ACSIKPVQPIQDICPNCQTKHVDLSASVEWISQFTQPRPNVACARTCVLILKNSKLSSSAGSPTG
```

```
LFQVAL-----------------ENSNHSTIEATSNFQNGLNYLDKELNVGHPVMIGVDHKLGYGINEGTTD
HFIVVVGRGCENGKVYYRFYDVGTRHKEKGTSNSNKLYIINGFLRGKTAYNGSTYTMTQVRRN---------
----------------------------
>CIP70.10_31
--------------------------------MVDLNKDDVA-----LITQAIAIGFSPAGVAL---------
----------------------------------------------------------------------
---------------------DVADLARASYNLY------------------------------QEKSDDNY
F---------------------------------------------------EVILCVIGFIPGPGD-----
-----------------------------GLKAGLRIVNRKPEILFELIRFIMTHCKIYGNPEQWLSEIIS
DT--------------------------------------------------------------------
------------KIRELIRSGKREALNASNKNIGNRWAKYWIN---------------------QSIEITFN
FLEASISSLVQLLARKVLHWKTKIPKSSADKRHVGGGKGHQNNSAHGTT-----------------------
----YDGKTGQNGN--------------------------------GHGSKGKTLSKVDISKVLSNLEVGG
VG--------EHMADYWVA---------------------NKLAIPAVHDSGQQLTPKLQRPMTKLHIGIHD
QGIDAIWKSDKKNIGIMNTKSYAIIEAKASLSMGKGTGPGSLLNDLDKQQD--------------------
----------------------------------------------------------------------TR
ERHIERASAK------------------------------------------------------------
-----------------KEKRAEKKLIPKKKFL-----------------------------------
-----------------------------------------INQQMSDEWVKKRLRAT-------------
-------SLRNVEIAGFSRHLLYFNYAHPETVEHLNVLAISIQ-----------------------------
-------------------------------------------------------------DNQPVDHSEHL
NEHTPSNFWGAAKIDEALNNRVTRANIKNGHTK-------------------------------------
----------------------------
>R2091_31
--------------------------------MVDLNKDDVA-----LITQAIAIGFSPAGVAL---------
----------------------------------------------------------------------
---------------------DVADLARASYNLY------------------------------QEKSDDNY
F---------------------------------------------------EVILCVIGFIPGPGD-----
-----------------------------GLKAGLRIVNRKPEILFELIRFIMTHCKIYGNPEQWLSEIIS
DT--------------------------------------------------------------------
------------KIRELIRSGKREALNASNKNIGNRWAKYWIN---------------------QSIEITFN
FLEASISSLVQLLARKVLHWKTKIPKSSADKRHVGGGKGHQNNSAHGTT-----------------------
----YDGKTGQNGN--------------------------------GHGSKGKTLSKVDISKVLSNLEVGG
```

```
VG--------EHMADYWVA---------------------NKLAIPAVHDSGQQLTPKLQRPMTKLHIGIHD
QGIDAIWKSDKKNIGIMNTKSYAIIEAKASLSMGKGTGPGSLLNDLDKQQD---------------------
-----------------------------------------------------------------------TR
ERHIERASAK----------------------------------------------------------------
-----------------KEKRAEKKLIPKKKFL----------------------------------------
-----------------------------------------INQQMSDEWVKKRLRAT-------------
-------SLRNVEIAGFSRHLLYFNYAHPETVEHLNVLAISIQ-----------------------------
-------------------------------------------------------------DNQPVDHSEHL
NEHTPSNFWGAAKIDEALNNRVTRANIKNGHTK-------------------------------------
----------------------------
>ab736_7
------------------------------MSTSETYLNDE------------------------------
----------------------------------------------------------------------
---------------------EIFELVRDIPLDT---------------------------SIIYGEEDQEF
GICPYITFYIYHQDNEVDEVANKIIDLYEEFENE------------------IIDKPFKLRYRDTGVWKNAN
KW-----------------------RPSRQVMLDEMHESYKK----YFVYFIGATTGDSGGQSARWALQAII
RDNG-----------------------------------------------------------------
------------LRYTSLKISFGDKWFRENKKK------------------------------WYAFVENC
LIKLNPIQAYSGYEIGSPQSFNCVSPEFETVE--------------------------------------
----RIFSDYFYGL-----------------------------------------DIDHPSNMSFSHDDPSG
LI--------------------------------------YTPSLAAGIRTPTWCFLLSPYWIEKLGLSEE
QIRLKLNDPRIEITKLPDPADPEKYSLWIRLGELSLYPIEEGVPDLL-------------------------
----------------------------------------------------------------------VM
ANELIKPIRC------------------------------------------------------------
--------------NDLKLTTLDAWDDDPNPRF---------------------------------------
-----------------------------------DIDNSPQWIARFDEDSHWPEG---------------
-------KRVNKIHAVLLEQNAIKVLGGEICPKTGEWYSPANNMKKRYFA----------------------
-------------------------------------------------------------EGEIMPEIKDN
PWGETIWYLEVTNKTE------------------------------------------------------
----------------------------
>ACICU_7
------------------------------MSTSETYLNDE------------------------------
----------------------------------------------------------------------
```

```
---------------------EIFELVRDIPLDT---------------------------SIIYGEEDQEF
GICPYITFYIYHQDNEVDEVANKIIDLYEEFENE------------------IIDKPFKLRYRDTGVWKNAN
KW-----------------------RPSRQVMLDEMHESYKK----YFVYFIGATTGDSGGQSARWALQAII
RDNG-------------------------------------------------------------------
------------LRYTSLKISFGDKWFRENKKK------------------------------WYAFVENC
LIKLNPIQAYSGYEIGSPQSFNCVSPEFETVE---------------------------------------
----RIFSDYFYGL-------------------------------------------DIDHPSNMSFSHDDPSG
LI---------------------------------------YTPSLAAGIRTPTWCFLLSPYWIEKLGLSEE
QIRLKLNDPRIEITKLPDPADPEKYSLWIRLGELSLYPIEEGVPDLL-------------------------
-----------------------------------------------------------------------VM
ANELIKPIRC-------------------------------------------------------------
--------------NDLKLTTLDAWDDDPNPRF----------------------------------------
------------------------------------DIDNSPQWIARFDEDSHWPEG---------------
-------KRVNKIHAVLLEQNAIKVLGGEICPKTGEWYSPANNMKKRYFA----------------------
-------------------------------------------------------------EGEIMPEIKDN
PWGETIWYLEVTNKTE-------------------------------------------------------
----------------------------
>ATCC19606_7
------------------------------MSTSETYLNDE------------------------------
-----------------------------------------------------------------------
---------------------EIFELVRDIPLDT---------------------------SIIYGEEDQEF
GICPYITFYIYHQDNEVDEVANKIIDLYEEFENE------------------IIDKPFKLRYRDTGVWKNAN
KW-----------------------RPSRQVMLDEMHESYKK----YFVYFIGATTGDSGGQSARWALQAII
RDNG-------------------------------------------------------------------
------------LRYTSLKISFGDKWFRENKKK------------------------------WYAFVENC
LIKLNPIQAYSGYEIGSPQSFNCVSPEFETVE---------------------------------------
----RIFSDYFYGL-------------------------------------------DIDHPSNMSFSHDDPSG
LI---------------------------------------YTPSLAAGIRTPTWCFLLSPYWIEKLGLSEE
QIRLKLNDPRIEITKLPDPADPEKYSLWIRLGELSLYPIEEGVPDLL-------------------------
-----------------------------------------------------------------------VM
ANELIKPIRC-------------------------------------------------------------
--------------NDLKLTTLDAWDDDPNPRF----------------------------------------
------------------------------------DIDNSPQWIARFDEDSHWPEG---------------
```

```
-------KRVNKIHAVLLEQNAIKVLGGEICPKTGEWYSPANNMKKRYFA----------------------
------------------------------------------------------------EGEIMPEIKDN
PWGETIWYLEVTNKTE------------------------------------------------------
----------------------------
>AB042_3
----MNPYTIFEYTIVFYNQRNKELPNVKYSIIFFCEDGTK-----KTYEGATNPKGQTKPIPLNQNGKLHI
FVEGHETIFSPKKTIKPILAEGSNIVEVNDIRLKSNTS----------------------------------
---------------------FLTKA-QYELMQK------------------------------KTSKDLEE
L----RKNAKAVKQKNFFNLSKIRPTFPLDLAEELNERINMSYEEYRKK---NTHIVKKTKYLKFKNYALYR
FVDSAGNGIPIVDYQIFAQGQSRPLINARPGPPDKKGYTQLV----YTHLKSRVTYTLGSARKNSEWYEPIT
CVDKQTIY-------------------------------------------------QIIFPTSIAVTQPD
INHK--------ENMEARQKPPIVINPTTNEVLILPSAVYAEFDKKTKILSDAV----------REVHKSNA
NLIKAIQSRDLDEIKELEKRLNINQEKAIEKINGEFKQTADLREVWVVETTGKTNEKISKYNLKRRYLKVTE
YEELKAKRRNPQTE--VDVTANQYTVQQPAQIRSSF-----EKLSQQLLTVKGNAGSDEKAVYNLIGGLGGE
IAEEYKNSRDVTVTQEAQW----MRMVAGASGEGSISAAPKGVSIKTSGDMSAKWTLFEGVKEWRKFYPCET
GWKLEYDNYDLGTIRFLIGAEISGFSGANLGIAGNLSVDISHQGAAQVIKAVVRPPERSMSQMVDRNKKPMF
QPAQGSLKI-------------------------------------------------------------IG
NNNQENAQNQ-------------------GNISINAFAGVQIQGLLKGAVEWFKPKGDGSGEGEFVAIASAA
AGGGVSAGVGAQGQFQIGYDQTSGNFKILVAAH---------------------------------------
LCWGMGAK------------GVASFVVGTEHLLSYLGFIKSQVAHAGFKTLLYINEAAF-LLAAQVLAYCIG
ENHPVISDINRIAASYGDWIRRLDIDQGRYKTAQNINSSSGKKELLYATPETKGILLYAVTHWTDRTAPIFD
MNVKFSDMKIEFFPTRKTAVINIFKTCISTEEWENTIQHIHPRGNKLTQTQLGKV------EGDIIRFLNYG
NDEKYAEDIIRCLNSGIEYKGTQINAWLQDYLKYRKGAKKIAGSLNYMLVKNQDDNRFKQLEIQQGVWGDSE
EITLIASNLNVLSPFDQDDTDKYETYNV
>ATCC17978-mff_3
----MNPYTIFEYTIVFYNQRNKELPNVKYSIIFFCEDGTK-----KTYEGATNPKGQTKPIPLNQNGKLHI
FVEGHETIFSPKKTIKPILAEGSNIVEVNDIRLKSNTS----------------------------------
---------------------FLTKA-QYELMQK------------------------------KTSKDLEE
L----RKNAKAVKQKNFFNLSKIRPTFPLDLAEELNERINMSYEEYRKK---NTHIVKKTKYLKFKNYALYR
FVDSAGNGIPIVDYQIFAQGQSRPLINARPGPPDKKGYTQLV----YTHLKSRVTYTLGSARKNSEWYEPIT
CVDKQTIY-------------------------------------------------QIIFPTSIAVTQPD
INHK--------ENMEARQKPPIVINPTTNEVLILPSAVYAEFDKKTKILSDAV----------REVHKSNA
NLIKAIQSRDLDEIKELEKRLNINQEKAIEKINGEFKQTADLREVWVVETTGKTNEKISKYNLKRRYLKVTE
```

```
YEELKAKRRNPQTE--VDVTANQYTVQQPAQIRSSF-----EKLSQQLLTVKGNAGSDEKAVYNLIGGLGGE
IAEEYKNSRDVTVTQEAQW----MRMVAGASGEGSISAAPKGVSIKTSGDMSAKWTLFEGVKEWRKFYPCET
GWKLEYDNYDLGTIRFLIGAEISGFSGANLGIAGNLSVDISHQGAAQVIKAVVRPPERSMSQMVDRNKKPMF
QPAQGSLKI-----------------------------------------------------------IG
NNNQENAQNQ-------------------GNISINAFAGVQIQGLLKGAVEWFKPKGDGSGEGEFVAIASAA
AGGGVSAGVGAQGQFQIGYDQTSGNFKILVAAH-------------------------------------
LCWGMGAK------------GVASFVVGTEHLLSYLGFIKSQVAHAGFKTLLYINEAAF-LLAAQVLAYCIG
ENHPVISDINRIAASYGDWIRRLDIDQGRYKTAQNINSSSGKKELLYATPETKGILLYAVTHWTDRTAPIFD
MNVKFSDMKIEFFPTRKTAVINIFKTCISTEEWENTIQHIHPRGNKLTQTQLGKV------EGDIIRFLNYG
NDEKYAEDIIRCLNSGIEYKGTQINAWLQDYLKYRKGAKKIAGSLNYMLVKNQDDNRFKQLEIQQGVWGDSE
EITLIASNLNVLSPFDQDDTDKYETYNV
>AR_0088_32
--------------------MSTAVAKSPAKTIRVTQKGEQSAADWIKGVLDGSGSSPAQIIVAVVIGC---
------------------------------------------------------------------------
---------------------IPFVG-QGVDVGN------------------------------VIVSIVKI
A--ENPNNKDNWFDLVFNLIAFVPVA--------------------------GDGLKIVFKQLRSGK-----
AMGA---------------------ILDAIPSKTMRGNVEKW----FRNLNWNAYTKELQTTSNKIIDGLID
V-----------------------------------------------------------------------
------------FDSWMTRAVLGQARLKTL----------------------------------VVQLRKMK
TVANRQIEMVMKDLQLAHKKALATPYPNTTAKA---------------------------------------
----PIHKTGSKPL-----------------------------------------------NRTSAPHTQQKG
QV----------------------------------LKNTSGNTAKTGSKNTSTKRTSKKRSNKELGSGGEH
ITDYYFVKRKKSRTKINNNGVLYEYHDTGHDGIDHAWYSNS-------------------------------
-----------------------------------------------------------------------IG
HKYRITDSKA----------------------------------------------------------------
-----------------TNLASHRKIMTPKAAM----------------------------------------
-----------------------------------D------ALSMGLDVYVKSSKE---------------
-------KKTKGALGKTVSDGAQMSHLWIANKIGSAKITSSHKVKLLEQIEAWKRVEFKPASERVFKNGKGQ
TVA-------------------------------------------------------------VKCPYDRSLVT
ITGNQFDHHSQCKGLDEPKCTRSVTSHAITLEFVLPNEMLRE-------------------------------
----------------------------
>Ab04-mff_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
```

```
------------------------------------------------------------------
--------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK----------------------------
------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIVPWHLA-------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW---------------------SSCLPSIKNLKVTK
EINDAFT----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGARMQRWFIGMPDATLVLSSDYSVDAVKKN-----------------------
-------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------
-----------------LVELKEDVYIAPLKGT-------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------
-----------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV-----------------------------------------
----------------------------
>LAC-4_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------
--------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK----------------------------
------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIVPWHLA-------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW---------------------SSCLPSIKNLKVTK
EINDAFT----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGARMQRWFIGMPDATLVLSSDYSVDAVKKN-----------------------
-------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------
-----------------LVELKEDVYIAPLKGT-------------------------------------
```

```
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV------------------------------------------
----------------------------
>WKA02_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFIKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV------------------------------------------
----------------------------
>BJAB0715_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
```

```
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
---------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV--------------------------------------------
----------------------------
>D1279779_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
---------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK--------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
---------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
---------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV--------------------------------------------
----------------------------
>KAB02_13
```

```
-----------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
--------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ-----------------------------------------------------------
-----------------LVELKEDVYIAPLKGT-----------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV----------------------------------------
-----------------------------
>KAB05_13
-----------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
--------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ-----------------------------------------------------------
```

```
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV------------------------------------------
----------------------------
>MDR-TJ_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI---------------------------NLFARGNL
WLFMDIAPWHLA-----------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN-----------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ-------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV------------------------------------------
----------------------------
>R2090_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
```

```
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
-------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV--------------------------------------------
----------------------------
>XH856_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
-------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK-------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
-------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
-------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV--------------------------------------------
----------------------------
```

```
>XH858_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK--------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWENCSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
GNYTGSKADQ---------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT---------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
------------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV--------------------------------------------
----------------------------
>KAB06_13
------------------------------MSNSLDWNSKT-----NISEHSCKDAHCDCL-----------
------------------------------------------------------------------------
---------------------TFWEI-YQQEAIK------------------------------RLSNLQKA
N----NYKLEPGYEARARRIASVYAK--------------------------IFLEIELGGNKN--------
-------------------------LLGRYYWM-GLGAFASK-----------------------------
------------------------------------------------------------------------
------------TVATIFKHW-GSLLGYNVGVQEAI----------------------------NLFARGNL
WLFMDIAPWHLA-------------------------------------------------------WSASSE
S---FKSCKGTRDT-------STFKFVKPALMNLPW----------------------SSCLPSIKNLKVTK
EINDAFT-----------------------------LLPAIEKAFLNGRDEKSKYRKASQNLFDHLMAIAVQ
EQHNILQVVVWE-CSVKFGAWMQRWFIGMPDATLVLSSDYSVDAVKKN------------------------
-----------------------------------------------------------------------WF
```

```
GNYTGSKADQ------------------------------------------------------------
-----------------LVELKEDVYIAPLKGT-------------------------------------
IAEDYDSR---------------------------M------KWIGKAAEKY--------------------
----------------------------------------------------------------------
-------------------------------------------------------------HRLMLDEKGRP
FLQQELKTISKWGNSKADFKIHSSSNEGKV----------------------------------------
-----------------------------
>AB030_22
----------------------------------NSKKTPAQ-----LTADRAR-------------------
----------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G--------------------------------------------------NVNITGISGRVG-KN-----
----------------------------------------------------------------------
----------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG---------------------------------------------------------
-----MNIEGATID--------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------------------------------------------------------------VV
NINSNDKRHG------------------------------------------------------------
-----------------------THKPACSSCS------------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-----------------------------
>AbH12O-A2_22
----------------------------------NSKKTPAQ-----LTADRAR-------------------
----------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G--------------------------------------------------NVNITGISGRVG-KN-----
----------------------------------------------------------------------
```

```
------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG------------------------------------------------------
-----MNIEGATID------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------VV
NINSNDKRHG----------------------------------------------------------
-----------------------THKPACSSCS-----------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>AF-401_22
---------------------------------NSKKTPAQ-----LTADRAR-------------------
------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G-------------------------------------------------NVNITGISGRVG-KN-----
------------------------------------------------------------------
------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG------------------------------------------------------
-----MNIEGATID------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------VV
NINSNDKRHG----------------------------------------------------------
-----------------------THKPACSSCS-----------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
```

```
----------------------------
>AR_0063_22
---------------------------------NSKKTPAQ-----LTADRAR-------------------
-----------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G-----------------------------------------------------NVNITGISGRVG-KN-----
-----------------------------------------------------------------------
-----------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG-----------------------------------------------------------
-----MNIEGATID----------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------VV
NINSNDKRHG--------------------------------------------------------------
-----------------------THKPACSSCS-------------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
----------------------------
>AR_0101_22
---------------------------------NSKKTPAQ-----LTADRAR-------------------
-----------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G-----------------------------------------------------NVNITGISGRVG-KN-----
-----------------------------------------------------------------------
-----------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG-----------------------------------------------------------
-----MNIEGATID----------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
```

```
-------------------------------------------------------------------VV
NINSNDKRHG-------------------------------------------------------------
-----------------------THKPACSSCS----------------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>IOMTU433_22
---------------------------------NSKKTPAQ-----LTADRAR-------------------
------------------------------------------------------------------------
---------------------------FELGKTS------------------------------GAAADLQV
G-----------------------------------------------------NVNITGISGRVG-KN-----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------VHPQLKKALRDVPKEE-----------------------------------QAPWHGAC
AEVDAINKALKKG----------------------------------------------------------
-----MNIEGATID---------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VV
NINSNDKRHG-------------------------------------------------------------
-----------------------THKPACSSCS----------------------------------------
-----------------------------------------NVLKQFGVKSNEK-----------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>A1296_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
------------------------------------------------------------------------
---------------------LIFVG-QKLKLKN------------------------------TPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
```

```
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTPTPTPTP
TPTP---------------------TPTPTPTL-------------------------------------
SNVLKEIK-----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>1656-2_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
-----------------------------------------------------------------------
---------------------LIFVG-QKLKLKNTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTP------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK-----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
```

```
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>ACICU_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
------------------------------------------------------------------------
---------------------LIFVG-QKLKLKN--------------------TPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS-------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTP--------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>AR_0056_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
------------------------------------------------------------------------
---------------------LIFVG-QKLKLKN----------------------TPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS-------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
```

```
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTPTPTP--
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>D1279779_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
-----------------------------------------------------------------------
---------------------LIFVG-QKLKLKN----------------TPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS-----------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKS--------------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>DU202_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
-----------------------------------------------------------------------
---------------------LIFVG-QKLKLKNTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPIQNL
```

```
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTPTPTP--
--------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>KAB03_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
-----------------------------------------------------------------------
---------------------LIFVG-QKLKLKN----------TPTPTPTPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS------------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTPTPTP--
--------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
```

```
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>NCGM237_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
---------------------------------------------------------------------------
---------------------LIFVG-QKLKLKN----------TPTPTPTPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS-----------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI-------------------------
-----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTP----------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK-----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>R2090_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
---------------------------------------------------------------------------
---------------------LIFVG-QKLKLKN--------------TPTPTPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFETKTDNHKKPINN
NVNNNGQS-----------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
```

```
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTPTPTPTP------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>AbPK1_8
--------------------------------MYIVKKGDT-----LTSIANKNGCTVEQIIKLNSIKNKN-
----------------------------------------------------------------------
---------------------LIFVG-QKLKLKN--------------TPTPTPTPTPTPTPTPTPTPIQNL
G----GKVGIAIVNKKGEPISNFKLKIQVGNNIYSNQLTN------------ARGVVTLPRQKS-GENIIIQ
GWSK---------------------TNNSYKLISNRFITENR----NLGIGISLDTIKFEAKTDNHKKPINN
NVNNNGQS-----------------------------------------------------------TTTNG
SNSQ--------NNPIARTSVEGCSNCTKITENELK----------------------------QIFTQANS
NDIKKIIDVYTNFSEKFGMNNCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLSYTKIKRKEYIIEKG
KRVEKMTHGGPFSA-------FRGNRQLCDKYGR-----------------NDNHPADQVMIANIAYANRNG
NG-------DIQSGDGWKY-------------------RGRGIIQITGKDKYDKINKAIKDNYPNVGISIDA
NNINNIYEGTLASMAYWKSFGLSKLATQKQVDIRTQLEVVDSLIDI--------------------------
----------------------------------------------------------------------IN
RDTASRSDRK-------------------KNFEYITAKVFKLNECKNSIVEANLLSKSTP------------
-------------------------TPTPTPTL-------------------------------------
SNVLKEIK----------------------------------QLVDRNIPYSQTGARGA-------------
-------GSNKNATSVITANDLKGLDCSETVAIYLLKLGVTDK--FYSIHT--GVMLTENDFRKAIRSNKIE
YVVG-----------------------------SKDLNFIPQIGDIFVWRNGGGH------CGIVYDVDRQN
DTVTILEAIGDVGSADENFNINNGGEKKVGCTRTAVYRRSGKALAQHRGWVGYFRPIISGKKI---------
----------------------------
>15A34_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
----------------------------------------------------------------------
```

```
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>15A5_6
------------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>1656-2_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>3027STDY5784958_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
```

```
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB07_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT-----------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB34299_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
```

```
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------
----FHSKQGHRGS----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI--------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>Ab4568_6
------------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------
----FHSKQGHRGS----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI--------------------------------------
```

```
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Ab4653_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Ab4977_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
```

```
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AbPK1_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AC29_6
```

```
----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AC30_6
----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-----------------TTNVSRGRLIDRQAMI---------------------------------------
-------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>ACICU_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI---------------------------------------
-------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AF-673_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
```

```
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AR_0056_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>AYP-A2_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>BJAB07104_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>BJAB0868_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>CBA7_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
```

```
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH--------------------------------------------------------
----FHSKQGHRGS-------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>CMC-CR-MDR-Ab4_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH--------------------------------------------------------
----FHSKQGHRGS-------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
```

```
----------------------------
>CMC-CR-MDR-Ab66_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>CMC-MDR-Ab59_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>DU202_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH----------------------------------------------------------
----FHSKQGHRGS---------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>HRAB-85_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
```

```
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>JBA13_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S---------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
----------------------------
>KAB01_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>KAB02_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
-------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB03_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
-------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB04_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
```

```
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
-----------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI------------------------------------
---------------------------------------------NQFNKGCSI------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
----------------------------
>KAB05_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
-----------------------------------------------------------------------
---------------------RAWSL-EKQLIQT-------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
-----------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI------------------------------------
---------------------------------------------NQFNKGCSI------------------
-----------------------------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB06_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB07_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB08_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KBN10P02143_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
```

```
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>MDR-TJ_6
------------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>MDR-ZJ06_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>NCGM237_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
-----------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
```

```
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SAA14_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT-----------------------------TGTGTRDW
S-----------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SMC_Paed_Ab_BL01_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
```

```
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>SSA12_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
```

```
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SSA6_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>TCDC-AB0715_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
```

```
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
----------------------------------------------NQFNKGCSI------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
----------------------------
>TYTH-1_6
------------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
--------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
--------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
----------------------------------------------NQFNKGCSI------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
----------------------------
>USA2_6
```

```
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>WCHAB005133_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-----------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-----------------TTNVSRGRLIDRQAMI----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>XDR-BJ83_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S---------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>XH386_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
--------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S---------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
```

```
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>XH856_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI-------------------------------VFLENPKH
PNSSPMPNAYNEH------------------------------------------------------------
----FHSKQGHRGS------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>XH857_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>XH859_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S--------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH---------------------------------------------------------
----FHSKQGHRGS--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>XH860_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH-----------------------------------------------------------
----FHSKQGHRGS----------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-------------------------------------
---------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>YU-R612_6
-----------------------------APCSLVRYKPDK-----VTPQAGSRQDAID-------------
------------------------------------------------------------------
---------------------RAWSL-EKQLIQT------------------------------TGTGTRDW
S-------------------------------------------------KAELDTILRTPS-GS-----
------------------------GKGHLSSVMSNLGYTGHH-----------------------------
```

```
------------------------------------------------------------------
------------INSVKNNGALGESWKGDPRNI------------------------------VFLENPKH
PNSSPMPNAYNEH--------------------------------------------------------
----FHSKQGHRGS-------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TTNVSRGRLIDRQAMI-----------------------------------
-----------------------------------------------NQFNKGCSI------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>15A34_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE--------------------------------------------------------
----YKSKSKARGI-------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY----------------------------------------------------
```

```
----------------------------
>15A5_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-----------------------------------------------------
----------------------------
>3027STDY5784958_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
------------------------------------------------------------------
----------------TISQGKEMVGNPNGPS----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>Ab4653_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------TISQGKEMVGNPNGPS----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>Ab4977_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
```

```
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-------------------------------------------------------
----YKSKSKARGI------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY----------------------------------------------------
----------------------------
>ACICU_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-------------------------------------------------------
----YKSKSKARGI------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>AF-673_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
-----------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
-----------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS----------------------------------------
-------------------------------------------IIHGPGHSW---------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>AR_0056_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
-----------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
-----------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
-----------------------------------------------------------------------
```

```
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW--------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>AR_0102_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW--------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>BJAB07104_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
```

```
A--------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-----------------------------------------------------
----------------------------
>BJAB0868_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A--------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>CMC-CR-MDR-Ab4_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>CMC-CR-MDR-Ab66_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-------------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>CMC-MDR-Ab59_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------------
----YKSKSKARGI----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-------------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>HRAB-85_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
```

```
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------EROVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>KBN10P02143_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------EROVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
```

```
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>MDR-TJ_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>MDR-ZJ06_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
```

```
----YKSKSKARGI------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY--------------------------------------------------------
----------------------------
>NCGM237_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------GRQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY--------------------------------------------------------
----------------------------
>SMC_Paed_Ab_BL01_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
```

```
------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------
------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------
----------------------------
>SSA6_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------
----YKSKSKARGI----------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
```

```
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>TCDC-AB0715_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------------
----YKSKSKARGI----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>TYTH-1_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
```

```
HTDKISPYIYKDE------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-------------------------------------------IIHGPGHSW---------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
-------DLGAHGFPSTY---------------------------------------------------------
----------------------------
>USA2_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
----------------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-------------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
----------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-------------------------------------------IIHGPGHSW---------------------
----------------------------------------------------------------------------
----------------------------------------------------------------------------
-------DLGAHGFPSTY---------------------------------------------------------
----------------------------
>WCHAB005133_5
```

```
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-----------------------------------------------------
----------------------------
>XDR-BJ83_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
-----------------TISQGKEMVGNPNGPS---------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY------------------------------------------------------
----------------------------
>XH386_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------GRQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE-----------------------------------------------------------
----YKSKSKARGI----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS---------------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY------------------------------------------------------
----------------------------
>XH856_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
--------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------------GVGVGIYANYKGNGE-----
------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
```

```
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-----------------------------------------IIHGPGHSW----------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
>YU-R612_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG-----------------------------KSVGGSAT
A-------------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE------------------------------------------------------------
----YKSKSKARGI------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------------
-----------------------------------------IIHGPGHSW----------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPSTY-------------------------------------------------------
----------------------------
```

```
>Ab4568_5
----------------------------ASTNSIGSYGSVK-----SASDTYEKYATSK-------------
------------------------------------------------------------------------
---------------------SLKDV-AERYAAG------------------------------KSVGGSAT
A-----------------------------------------------GVGVGIYANYKGNGE-----
-------------------------STLTMERKVGLGYEYGV----FERNYHYG------------------
------------------------------------------------------------------------
------------ERQVNRGYIEGCAATG-----------------------------------ESKYCAGS
HTDKISPYIYKDE---------------------------------------------------------
----YKSKSKARGI--------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------TISQGKEMVGNPNGPS-----------------------------------
-----------------------------------------IIHGPGHSW---------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------DLGAHGFPST-----------------------------------------------------
----------------------------
>6200_21
-----------------------------NFKSVGKIKEER-----ARRQTSSSAPYIKHT-----------
------------------------------------------------------------------------
---------------------MAKCKTQAQNISK------------------------------KEAQYWDM
S----KCESNVAQVTAFRNRLEKEGL-------------------------NKGYKVDLGDNK-GS-----
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------HY-----------------------------YIYDAGRN
IGFNEGKET-------------------------------------------------------------
----QYMRIEVS----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------ST
```

```
NEFHGHPISK------------------------------------------------------------
-----------------------QRYE-----------------------------------------
-------------------------------------------SWQSKT------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB031_27
---------------------------NNNPLVGIDLSNKS-----RSEIENILSNSSEVSY----------
------------------------------------------------------------------------
--------------------KGGSP-DKKFMQW-----------------------------------KW
N-------------------------------------------------DNGQTAVRLDPP--------
--------------------------------DKVTLYDHA-----------------------------
------------------------------------------------------------------------
-------------------------------------------------------------HLYDKNGN
PLDK------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------DGNIVPRESPDAHIPI-------------------------------------
-----------------------------------------------GDCK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>15A5_18
----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
--------------------NLRIG-QKIYLQN-----------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL--------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
```

```
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>3027STDY5784958_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
```

```
----------------------------
>AB07_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD----------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>Ab4568_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
```

```
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>Ab4977_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>AC29_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
```

```
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>AC30_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
```

```
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>AF-673_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>AR_0102_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
```

```
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL--------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>AYP-A2_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL--------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>CBA7_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
```

```
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>CMC-CR-MDR-Ab4_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
```

```
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>CMC-CR-MDR-Ab66_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD----------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>HRAB-85_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
```

```
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>JBA13_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB02_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
```

```
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB04_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
```

```
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB05_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK-------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB06_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK-------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
```

```
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL--------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB07_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
--------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL--------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>KAB08_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
```

```
H-----------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>SAA14_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
```

```
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>SSA12_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>SSMA17_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
```

```
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>XH386_18
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-----------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
----------------------------
>XH856_18
```

```
-----------------------------MSKIYIVKSGDT-----LWGISKKHHISVKELARINSLSGRMI
H-----------------------------------------------------------------------
---------------------NLRIG-QKIYLQN------------------------------DVNNTNNF
E----TQLKIILMDLSFKPILKATIQLEFDGKKIIRNTKNSIFEDINIQDH-SKGLKVFFKNLN-GT-----
-FDL---------------------IADHKVLPLGRKVLKLT----SRKMKVEGSHYAKDGILNETVNQIMS
NLKKVGKP-------------------------------------------------------IVESISTTSNKDE
LKNK--------QPPLKIPEEKIEQKRTDNGNSTHI-------------------------I--AAQFTEDN
FLLKPVNNKYRAYIVNAAKRHGFTPHSLAAVIEAEAAKIKKTGEWNTNSKANSSTAAGLTQFLDETWLAMCK
D---KSSLVGQYVM-------NNPKLTIQQKLNLRF---------------NAEMAIDAAAAYAISNFKSSG
LPYQKLT--EPSSIAKFAY----LLHH---------EGATGGKNFVLNTLSQERAKKLLFTQFGKNGAKQAA
DFLNRYKGDAKAAYGAWLRNYIDGHINIYQYVVDKSKTSGINLSTDETIKL---------------------
-----------------------------------------------------------------------LK
GQTISTPAPK-------------------ISTTTNNQQVTNVS-----------------------------
-----------------TIEKSESKIRINTSQA-------------------------------------
PTNNVGGD---------------------------N------KWHNPLAD-CKLRTAGL-------------
-------ANAKGATFGKVRNNGTKNHQGVD-----LQANPGTK--IYAVCG--GVIAFAGATGGAYGKVIVL
KVDIND-----------------------LPEKQKKYAQTKLTKNKYVYFFYAHL------SVIDVDKGDPV
DTGEVIGKTGATGNANKMTTISKGAHLHFEARSAPLLGVGLDGRFDPIPFINANLPY---------------
-----------------------------
>3207_4
-----------------------------MSNIHIVKKGDT-----LWGISNKYHIKLNELIEINGLYGRKK
N-----------------------------------------------------------------------
---------------------LLKIG-QQIYLKK--------------------------------DNVKKY
D----TTLVIKIYDLKWEPITHGKLLLEYDDKCHLATSNDKGVIEDIQIEDALKGIKISFYTLK-NK-----
-FEL---------------------IAHHKTLPLGKKILKLS----SRAMMIKGNTYKVEGIPRTNTKTIEK
ELKVNSKKVQHSSGASGASGASGASGASGASGASGASGASGASGASGASGASGASGASGASGASGASGASGA
SGASG-------ASGASGASGASETRIEGGLPAVTV----------------------------APVYSEEN
LYLHPDNEKYRKIIIDAAKKYNLAPQALAAKINAEAGTKKGSQEWNPQAQASTSSAVGLTQFLSGTWYEICT
VSTYKDTLLQQYVI-------KKKLISNFKENMALKLISNTDKAKLKALGTDPTFSVDSAAAYARANINIVK
KIYSKIDSLEPGDLAKVGY----VAHHD--------GPTGFGKIVEATNDPSWSKLQGQVCPKNNPNCDTYL
NYKERFSNGRDAYRWWLCTEYTDSKINVNRFTLSPKDGKKFKNARTMEEIIVF-------------------
-----------------------------------------------------------------------LG
GKPLVRPSRDFEKKGTTDNSKLNDNINIVITSLVNNKVQANIS----------------------------
```

```
-----------------YFVKSKYGLKPHSTNVNGHEIIHAKKGDKIEILFNDQVIASINAINDKEEFKINF
PSKNITNA------------STEKQSSNSEQKLNFN------RWRNPLNGICQIRRFGY-NSLPLKANASSY
NEKNLEQATKIASRFNRTSYRASGIHQGVD-----LEADNGVN--IYPVCV--GTIAKVIPAYPGYGKTIIL
ECDVND--------------------------LPSSKKVLAKNLDTIYFIYAHLN------SINVSEGDIIT
TLDTVLGKTGNSGNAGSMTRIEDGSHLHFEVRSEIMKSMGKSGMSYRLDPFPWLDNCMTTENGVKVNR----
----------------------------
>ATCC17978-mff_4
-----------------------------MSNIHIVKKGDT-----LWGISNKYHIKLNELIEINGLYGRKK
N-----------------------------------------------------------------------
---------------------LLKIG-QQIYLKK--------------------------------DNVKKY
D----TTLVIKIYDLKWEPITHGKLLLEYDDKCHLATSNDKGVIEDIQIEDALKGIKISFYTLK-NK-----
-FEL---------------------IAHHKTLPLGKKILKLS----SRAMMIKGNTYKVEGIPRTNTKTIEK
ELKVNSKKVQHSSGASGASGASGASGASGASGASGASG------------------------------
------------ASGASGASGASETRIEGGLPAVTV---------------------------APVYSEEN
LYLHPDNEKYRKIIIDAAKKYNLAPQALAAKINAEAGTKKGSQEWNPQAQASTSSAVGLTQFLSGTWYEICT
VSTYKDTLLQQYVI-------KKKLISNFKENMALKLISNTDKAKLKALGTDPTFSVDSAAAYARANINIVK
KIYSKIDSLEPGDLAKVGY----VAHHD--------GPTGFGKIVEATNDPSWSKLQGQVCPKNNPNCDTYL
NYKERFSNGRDAYRWWLCTEYTDSKINVNRFTLSPKDGKKFKNARTMEEIIVF-------------------
-----------------------------------------------------------------------LG
GKPLVRPSRDFEKKGTTDNSKLNDNINIVITSLVNNKVQANIS------------------------------
-----------------YFVKSKYGLKPHSTNVNGHEIIHAKKGDKIEILFNDQVIASINAINDKEEFKINF
PSKNITNA------------STEKQSSNSEQKLNFN------RWRNPLNGICQIRRFGY-NSLPLKANASSY
NEKNLEQATKIASRFNRTSYRASGIHQGVD-----LEADNGVN--IYPVCV--GTIAKVIPAYPGYGKTIIL
ECDVND--------------------------LPSSKKVLAKNLDTIYFIYAHLN------SINVSEGDSIT
TLDTVLGKTGNSGNAGSMTRIEDGSHLHFEVRSEIMKSMGKSGMSYRLDPFPWLDNCMTTENGVKVNR----
----------------------------
>6200_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
-----------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS------------------------------
-----------------------------------------------------------------------
```

```
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
----------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
>A1_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
----------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
----------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
----------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
```

```
>A388_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>A85_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VK
```

```
GTWASELGVG------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL---------------------------------------
-------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
>AB0057_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
----------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
----------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-----------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP--------------------------------------------------------------------
----------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL---------------------------------------
-------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
>AB030_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
----------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
```

```
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB307-0294_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
----------------------------
>AB5075-UW_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AbH12O-A2_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------VK
GTWASELGVG-------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
>AF-401_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
----------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
----------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP--------------------------------------------------------------------
----------------------------------------------------------------------
------------------------------------------------------------------VK
GTWASELGVG-------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK-------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------
>AR_0063_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
----------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
```

```
-------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-----------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK--------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AR_0078_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
-------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-----------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------------
---------------------------------------------DAVKPSKK--------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------
----------------------------
>AR_0083_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------
------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-----------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>AR_0101_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------
```

```
------------------------------------------------------------------
-----------------------------------------------------------------VK
GTWASELGVG-------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-------------------------------
---------------------------------------------DAVKPSKK-------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>D36_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------
------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC-------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP---------------------------------------------------------------
------------------------------------------------------------------
-----------------------------------------------------------------VK
GTWASELGVG-------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL-------------------------------
---------------------------------------------DAVKPSKK-------------
------------------------------------------------------------------
------------------------------------------------------------------
------------------------------------------------------------------
----------------------------
>IOMTU433_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------
------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
```

```
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-----------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP--------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL----------------------------------------
-------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>USA15_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY-----------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-----------------------------------------
----VTVGGGAYGA----------------------------------------------VANVVVPLVSKS
SP--------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL----------------------------------------
-------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>WCHAB005078_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMTMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
SP----------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------------VK
GTWASELGVG--------------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL------------------------------------
---------------------------------------------DAVKPSKK-------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SDF_15
--------------------------------NSFNYGEMF-----GIPASAQSG-----------------
------------------------------------------------------------------------
---------------------LAYQG-QRNYECY------------------------------AETGELCK
I--------------KVPPLFDYVAC--------------------------SGGGLGI------GV-----
--------------------------GFVKNQWTGEYYISGS-----------------------------
------------------------------------------------------------------------
------------KDSLLIPVAKSVAQNKQFSAKDL----------------------------AGASCVGG
NIHN-IPSYTKTTMAMGEITNEFVSGAS-------------------------------------------
----VTVGGGAYGA-----------------------------------------------VANVVVPLVSKS
```

```
SP-----------------------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------VK
GTWASELGVG------------------------------------------------------
---------------TPGFNVGVSGTVSVDTIL----------------------------------
-----------------------------------------DAVKPSKK-------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
---------------------------
>AB031_26
----------------------QPVGGKKSGLGIGFLFPNT-----MAGFAKNPEDARNLR-----------
-----------------------------------------------------------------
--------------------ALGAIRNNNLAAA-----------------------------SVAGYGPY
VVAGTAAAGSAAAPVVGRVAAPFI---------------------------GTGAQLEGAGLTAGT-----
--------------------VGKAAVTSAGIGGGMDVISQG----VKCKCLKDINLVR-------------
-----------------------------------------------------------------
------------TGGVAAVSAVTSGWGATTSAAA-----------------------------GFGQVGWK
SIALNAPNMGQFL---------------------------------------------------
----KNNASGMVIF--------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------AN
EQMIGQAG--------------------------------------------------------
-----------------SRAVKAATEKDKSSKK-----------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
-----------------------------------------------------------------
---------------------------
>ZW85-1_20
MDKKMSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
```

```
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK------------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-------------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNTLRNSEFKKVMDF----------------------------LAKKDGDF
TNEHRLHSSQCIDSIKICLENKLLNERS--QFSAQATKSIVLMGLWNELPKNLTDADDINYELEKIYKRKSK
AEQERLLKEAQEKQRANKGIYTEDMGKLSRGEGEQIWVKKYKPNLDMVAKSNFDKKINALIQECLAGARAIG
DDHIKWLLSKAVINALHAYDDQVQVPFGNIFYVHAMDMINGMSGVPSGQALLETWLGVEKIAKENIYMRAIC
YNQESLKNKYNAAAPSIIDISWDDGQNAAKTAIAAFVAADKAWQEWAADKTNNGYM----------------
-----------------------------------------------------------------------LH
GQKFSLLKTF-------------YWMSELTQSAVKWSMKYTPGSEFAKKLGRLTFYTFAHSGALVEHVAKNS
LYYLIPVQTLTGRVKLTPEMVQNNWKKYSSSAT-------------------------------------NP
SKAAKQID---------------------------------RIIANSSPSAGLRVSGVVAIFELINLGTQI
-------SKFNIDPSVDNTLSYMSGMMATTAAILEVGSSSMEKFSFAERAAYIAKCGAYFAIAGAIVSFFID
LKGLNKAFEESNGYAFALNLLKAASSFGTLAVGFSAFLNLPIMRNSTLYSMVERYAVGRALLGIKVVRVGAM
LSLAGIALVALEIYLKNYVLDNAMQDWCQKCAFKLKKENGEDAFKDVKEEEKEFNNAVVSV-----------
----------------------------
>D1279779_12
----MSENQKMILGKSKSNNLLNEIIAQQKQKQSQIPVIGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PATLGKNVKDIQLSHLKYAVEMIDTG-YIYRLVK------------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-------------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-----------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDKVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA-------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
```

```
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------------------------------
----------------------------
>R2090_12
----MSENQKMILGKSKSNNLLNEIIAQQKQKQSQIPVIGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PATLGKNVKDIQLSHLKYAVEMIDTG-YIYRLVK-----------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-------------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-----------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDKVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA---------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------------------------------
----------------------------
>Ab04-mff_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK-----------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-------------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
```

```
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHMKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA-------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI------------------------------------
----------------------------
>AR_0088_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK-----------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK-------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA-------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI------------------------------------
----------------------------
>CIP70.10_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
```

```
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK-----------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA-------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------------------------------
----------------------------
>HWBA8_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK-----------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA-------------------------------------
```

```
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------------------------------
----------------------------
>R2091_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK------------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-----------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA---------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------------------------------
----------------------------
>LAC-4_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK------------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
```

```
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA---------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-------------------------------------
----------------------------
>WKA02_12
----MSENQKMILGKSKSNNLFNEAIAQQKQKQSQIPVMGK-----TKAVGDMRNPTVAKNINKKIEESEIA
K-----------------------SAKQSTAANMQNSSAGQAQKECSNFCRKKGFNILPLRYTVVKDNPPAL
PPTLGKNVKDIQLSHLKYAVEMINTG-YIYRLVK------------------------------RTSGALEW
A----GYKVTPNGHLSYFPVGKEAPK--------------------------SVPEFACKGAGH-SFNSSVI
AVESNPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGK----WQKILINGGSAQEHCIAASQFKTTVY
NLNSFGKN-----------------------------------------------RIDATLNKFKDEPKSLA
CMAL--------YDPVGITRKLNDSRNSQFGKLTNY----------------------------LAKNVEKI
SNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYLSKIQEIWDRAPT
AERDKFLLQRNKKF-------AEGEQKLKEKIITQS----------------------KAEAKITWETKYAP
KI-------NWDTKKAFDK----EVKK---------LINEGRTLAQTYASDHIKWLKSKHLLNAFYVYDQTI
LKEYGALFHVHALAVMDGMTGCDEGQALMEKWLGVEEISDDNLYMRAVTYNQKNLIDQYNAKSSEITSLTWD
QTQSSLKSLIAAFVSADQ-------------------------------------------------------LW
EQWLADPNNKINELKWYNPAKSLLWISEITRSVAKWSLQYNINPLIAKRLSRVSFIAYAHSSLLTDRVPKWS
LLYNVDFKMTNASTQLNVTEIERRWKNAGQNTA---------------------------------------
AQKIKEILSKSPASVAIRISSIVALFELINFGVQSNKFIGERNWENGFQLISGLLASSA-AVLDIAGGGMDA
LSFQEKANKIRLYGARLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVGFGLLLNLPI
LQNSWV---------------VSSANKIAFTRILLRANFIRIAAYCNWIGIGFLV------IEYLLKTYVLD
DDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-------------------------------------
```

Supplementary file S4b

```
>Ab04-mff_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIVPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGARMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>LAC-4_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIVPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
```

```
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGARMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>WKA02_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS-------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFIKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>BJAB0715_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>D1279779_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
```

```
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB02_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS-------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB05_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>MDR-TJ_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
```

```
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>R2090_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS-------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>XH856_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XH858_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS--------------------------------
------------------------------------------------------------------------
```

```
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWENCSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB06_13
------------------------------------------------------------------------
-----MSNSLDWNSKTNISEHS-------CKDAHCDCLTF---WEIYQQEAIKRLSNLQKANNYK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------LEP-GYEARARRIASVYAKIFLEIELGGNKNLLGRYYWMGLGAFASKTVA-------------
------------------------------------------------------------------------
-----------------------------------TIFKHWGSLLGYN------------VGVQEAINLFAR
GN-----------LWLFMDIAPWHLAWSASS--ES--FKS------------------------------
------------------------------------------------------------------------
---------CKGTRDTSTFKFVKPA--------------------------------L---MNLPWSSCLP
SIKN------LKVTKEINDAFTLLPAIEKAFLNGRDEKSKYRKAS---------------------QNLFDH
LMAIAVQEQHNI--LQVVVWE-CSVKFGAWMQR----WFIGMPDA---------------------------
------------------------------------------------------------------------
-----------------TLVLSSDYSVDAVKKNWFGNYTGSKADQLVELKEDVYI-----------------
-------------APLKGTIAEDYDSRMKWIGKAAEKYHRLMLDE---------------------------
------------------------------------------------------------------------
-------------------------------------KGRPFLQQELKTISKWGNSKADFKIHSSSNEGKV-
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>15A34_23
-------------------------------------------------------------------MNTELK
HKLYNITFTLHDLTHKPIPNLY-------YEIKNGKDLV----KKGNTNAQGEITLKYVGGNTLT-------
----------------LFVRKDIDNTLKEIGKVHTPSKNIKVKLISPKMKFDVTLLPHQKQGKYWRGTYKVK
SGDTLSKIAKEHHTTISALLALNP------------------------------------------------
------------------------NIKSPHEIYQNENIDIVEGNADAIIKLDENMTVKVPPHKKTGTVSIDR
KSKSTSITPQTDTTNKTAEPKVGQTKLQPPVTKKEQSAASDSKSIPQQKTSTATTQKI--------------
----------------------------------------------------------------------
-----------------------------------EVQQEHNEDKKPV------------AVASLSGCVCKD
YD-----------LIWGKTTKFVNCEFRKKV--IQ--ICK--------------------------------
----------------------------------------------------------------------
-------DMWPNDTKNMANYLMACM--------------------------------H---LETGGSFDPA
QPNG---------------------LGYYGLIQFGPDVRKDLNNI--------------------SVEKLTK
MSGAQQLDLVKQ--HFTRSDRHKLMKSLTDMYL----YINYPNALLSGKNKPNDILYEGGS-----------
----------------------------------------------------------------------
----ERSAYHANPAFMKEKGEYQNIFAYRKDKNGNFKLDKNKKKIPIRGFEDGKT-----------------
-------------YIWEVTQEINKHLTTGLDSKNKENNFACSIKPVQPIQDICPNCQTKHVDLSASVEWISQ
FTQPRPNVACARTCVLILKNSKLSSSAGSPTGLFQVALENSNHSTIEATSNFQNG-----------------
-------------------------------------LNYLDKELNVGHPVMIGVDHKLGYGINEGTTDHFI
VVVGRGCENGKVYYRFYDVGTRHKEKGTSNSNKLYIINGFLRGKTAYNGSTYTMTQVRRN------------
----------------------------------------------------------------------
---------------------------
>ab736_9
-----------------------------------------------------------MNKLVTITTKFYDKS
GNRIINLNVQSRYKGSLKANSQKTDKLGLFVFQASPNRTV---EILAKPPNQKDYTVFKTINSSM-------
------------------NSSEIHPIKVQLPKTIDEYKQVKQSKSTKGIVSTFFKIFDMNGKVMKNFPIQSR
PKGKGNSPDKYTNDEGIVEV----------------------------------------------------
------------------------RSSPNRDIEVLVLTSNDTFVLKSSINSANGSSQPVLIKLDEPYEKFKS
ASTIKILDRDGS-DYIVEKTNVKMLVVENGKKQLFSISNGKLSLQSMIGQK---------------------
----------------------------------------------------------------------
-----------------------------------LEFTVYKPDGKPL----------KTQTYMATRVKNNL
IE-----------FHLDVDITKGSTAQNDPE--INKKVKV--------------------------------
-------------------------------------------------------------------DIL
```

```
ITMEQMKKMWPKALATKMQPILDE-------------------------------------LNSDLLGYKL
DTRL-------------------RQAHFMAQVRQEVGSSFSLREQ----------------------VEYMG
PTALKQIGYYRT--HPKQAEIDGYKRGQGPANG--EVIANRMYDD---------------------------
------------------------------------------------------------------------
-------------NYRSAKYKLGNTSPGDGWKYLGRGLKQLTGKNNYQDLTNMYS-----------------
-------------TLWPGEKVDFVKNPELIEQPKYAVRSAIRFWLKFK------------------------
------------------------------------------------------------------------
-------------------------------------LYEVADRGANGEQVDAITKVINEATNSYADRRAHF
VQARKIFI--------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>ATCC19606_9
-----------------------------------------------------------MNKLVTITTKFYDKS
GNRIINLNVQSRYKGSLKANSQKTDKLGLFVFQASPNRTV---EILAKPPNQKDYTVFKTINSSM-------
------------------NSSEIHPIKVQLPKTIDEYKQVKQSKSTKGIVSTFFKIFDMNGKVMKNFPIQSR
PKGKGNSPDKYTNDEGIVEV--------------------------------------------------
------------------------RSSPNRDIEVLVLTSNDTFVLKSSINSANGSSQPVLIKLDEPYEKFKS
ASTIKILDRDGS-DYIVEKTNVKMLVVENGKKQLFSISNGKLSLQSMIGQK---------------------
------------------------------------------------------------------------
-----------------------------------LEFTVYKPDGKPL----------KTQTYMATRVKNNL
IE-----------FHLDVDITKGSTAQNDPE--INKKVKV------------------------------
-----------------------------------------------------------------------DIL
ITMEQMKKMWPKALATKMQPILDE-------------------------------------LNSDLLGYKL
DTRL-------------------RQAHFMAQVRQEVGSSFSLREQ----------------------VEYMG
PTALKQIGYYRT--HPKQAEIDGYKRGQGPANG--EVIANRMYDD---------------------------
------------------------------------------------------------------------
-------------NYRSAKYKLGNTSPGDGWKYLGRGLKQLTGKNNYQDLTNMYS-----------------
-------------TLWPGEKVDFVKNPELIEQPKYAVRSAIRFWLKFK------------------------
------------------------------------------------------------------------
-------------------------------------LYEVADRGANGEQVDAITKVINEATNSYADRRAHF
VQARKIFI--------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Ab04-mff_11
--------------------------------------------------MSYSEDFKIFVATINGEAENC
SETSWKVIAHTMRNRVGFANWKSWSTIIQIVTKTGYDAYT---QKNSPYKRAKKALDSGDISPKL-------
------------MSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYPSLVPDFVVSKSNPTQQV
QIPGTEKDDMRWYKVLTSIFDVSFVDNAGNPLVGVTVDVVYNDKKPVPLFKDLI------------------
------------------------TDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVI
VVNNGKGGIKSK-TDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPN
FSYFLKYKNAEKKHSVGANGIEN-------------------------------------------------
-----------------------------------NLVALSGEEITVL------------ISGLDSKQEIIR
FT-----------AQEGMGEKTIKLNLHTFN--ILFRHKD--------------------------------
---------------------------------------TKKPITNLNLIQKYRNQIKQKKTDGNGKITVSA
MPGFELNYKLRDERNLLTIKVDKNK---------------------------------SLRVIDVDSSAIEQ
ASKN--IKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDNGETEFIVYTYDQ
KTNQLFSGGNYS--IEYKGNKKRHSSGIHGIGK--KIHKGEIGQKIKITASSGGKEFIAFD-----------
------------------------------------------------------------------------
--GNLSRGMKAFELKIDRSVIPSVSDVIISFKGVNEQSRQAIVSQKTKNVLAYLAKEA--------------
-------------NMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECIAKGLGKEATIQKMVEK
IVEFQNKGVRVSKHCVSEEQYRKNNIID--------------------------------------------
-------------------------------------LGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIIS
GFISADVAGEGAMHIEIIQ-----------------------------------------------------
------------------------------------------------------------------------
---------------------------
>BJAB0715_11
--------------------------------------------------MSYSEDFKIFVATINGEAENC
SETSWKVIAHTMRNRVGFANWKSWSTIIQIVTKTGYDAYT---QKNSPYKRAKKALDSGDISPKL-------
------------MSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYPSLVPDFVVSKSNPTQQV
QIPGTEKDDMRWYKVLTSIFDVSFVDNAGNPLVGVTVDVVYNDKKPVPLFKDLI------------------
------------------------TDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVI
VVNNGKGGIKSK-TDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPN
FSYFLKYKNAEKKHSVGANGIEN-------------------------------------------------
-----------------------------------NLVALSGEEITVL------------ISGLDSKQEIIR
FT-----------AQEGMGEKTIKLNLHTFN--ILFRHKD--------------------------------
---------------------------------------TKKPITNLNLIQKYRNQIKQKKTDGNGKITVSA
```

```
MPGFELNYKLRDERNLLTIKVDKNK--------------------------------SLRVIDVDSSAIEQ
ASKN--IKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDNGETEFIVYTYDQ
KTNQLFSGGNYS--IEYKGNKKRHSSGIHGIGK--KIHKGEIGQKIKITASSGGKEFIAFD-----------
------------------------------------------------------------------------
--GNLSRGMKAFELKIDRSVIPSVSDVIISFKGVNEQSRQAIVSQKTKNVLAYLAKEA--------------
-------------NMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECIAKGLGKEATIQKMVEK
IVEFQNKGVRVSKHCVSEEQYRKNNIID-------------------------------------------
-------------------------------------LGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIIS
GFISADVAGEGAMHIEIIQ----------------------------------------------------
------------------------------------------------------------------------
---------------------------
>LAC-4_11
---------------------------------------------------MSYSEDFKIFVATINGEAENC
SETSWKVIAHTMRNRVGFANWKSWSTIIQIVTKTGYDAYT---QKNSPYKRAKKALDSGDISPKL-------
------------MSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYPSLVPDFVVSKSNPTQQV
QIPGTEKDDMRWYKVLTSIFDVSFVDNAGNPLVGVTVDVVYNDKKPVPLFKDLI------------------
------------------------TDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVI
VVNNGKGGIKSK-TDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPN
FSYFLKYKNAEKKHSVGANGIEN------------------------------------------------
-----------------------------------NLVALSGEEITVL------------ISGLDSKQEIIR
FT-----------AQEGMGEKTIKLNLHTFN--ILFRHKD-------------------------------
----------------------------------------TKKPITNLNLIQKYRNQIKQKKTDGNGKITVSA
MPGFELNYKLRDERNLLTIKVDKNK--------------------------------SLRVIDVDSSAIEQ
ASKN--IKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDNGETEFIVYTYDQ
KTNQLFSGGNYS--IEYKGNKKRHSSGIHGIGK--KIHKGEIGQKIKITASSGGKEFIAFD-----------
------------------------------------------------------------------------
--GNLSRGMKAFELKIDRSVIPSVSDVIISFKGVNEQSRQAIVSQKTKNVLAYLAKEA--------------
-------------NMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECIAKGLGKEATIQKMVEK
IVEFQNKGVRVSKHCVSEEQYRKNNIID-------------------------------------------
-------------------------------------LGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIIS
GFISADVAGEGAMHIEIIQ----------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>WKA02_11
--------------------------------------------------MSYSEDFKIFVATINGEAENC
SETSWKVIAHTMRNRVGFANWKSWSTIIQIVTKTGYDAYT---QKNSPYKRAKKALDSGDISPKL-------
------------MSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYPSLVPDFVVSKSNPTQQV
QIPGTEKDDMRWYKVLTSIFDVSFVDNAGNPLVGVTVDVVYNDKKPVPLFKDLI------------------
------------------------TDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVI
VVNNGKGGIKSK-TDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPN
FSYFLKYKNAEKKHSVGANGIEN-------------------------------------------------
-----------------------------------NLVALSGEEITVL------------ISGLDSKQEIIR
FT-----------AQEGMGEKTIKLNLHTFN--ILFRHKD--------------------------------
---------------------------------------TKKPITNLNLIQKYRNQIKQKKTDGNGKITVSA
MPGFELNYKLRDERNLLTIKVDKNK---------------------------------SLRVIDVDSSAIEQ
ASKN--IKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDNGETEFIVYTYDQ
KTNQLFSGGNYS--IEYKGNKKRHSSGIHGIGK--KIHKGEIGQKIKITASSGGKEFIAFD-----------
----------------------------------------------------------------------
--GNLSRGMKAFELKIDRSVIPSVSDVIISFKGVNEQSRQAIVSQKTKNVLAYLAKEA--------------
-------------NMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECIAKGLGKEATIQKMVEK
IVEFQNKGVRVSKHCVSEEQYRKNNIID--------------------------------------------
-------------------------------------LGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIIS
GFISADVAGEGAMHIEIIQ-----------------------------------------------------
----------------------------------------------------------------------
---------------------------
>XH858_11
--------------------------------------------------MSYSEDFKIFVATINGEAENC
SETSWKVIAHTMRNRVGFANWKSWSTIIQIVTKTGYDAYT---QKNSPYKRAKKALDSGDISPKL-------
------------MSLIKAVEPIFNGTEPDFTGGVVYYYSPKAQAQLHKSDPSNYPSLVPDFVVSKSNPTQQV
QIPGTEKDDMRWYKVLTSIFDVSFVDNAGNPLVGVTVDVVYNDKKPVPLFKDLI------------------
------------------------TDQKGKIKKVRVCNYMGARFKVNGVLVKDKNNKEISLLGDGKNYASVI
VVNNGKGGIKSK-TDIHNQESIPGQKQESVKIDSKAEVNNEKKAEVSDNNTKQKNVNFSIKVIDSENKAIPN
FSYFLKYKNAEKKHSVGANGIEN-------------------------------------------------
-----------------------------------NLVALSGEEITVL------------ISGLDSKQEIIR
FT-----------AQEGMGEKTIKLNLHTFN--ILFRHKD--------------------------------
---------------------------------------TKKPITNLNLIQKYRNQIKQKKTDGNGKITVSA
```

```
MPGFELNYKLRDERNLLTIKVDKNK--------------------------------SLRVIDVDSSAIEQ
ASKN--IKIGTKVVEIAQSKQPVPSSKQKHPVETHDSTPKRDEKVKISTDGHPKTLVNDNGETEFIVYTYDQ
KTNQLFSGGNYS--IEYKGNKKRHSSGIHGIGK--KIHKGEIGQKIKITASSGGKEFIAFD-----------
------------------------------------------------------------------------
--GNLSRGMKAFELKIDRSVIPSVSDVIISFKGVNEQSRQAIVSQKTKNVLAYLAKEA--------------
-------------NMDKLYITSTIRTPRAQAEAMYIKATKYAKPGEDVKKVKAECIAKGLGKEATIQKMVEK
IVEFQNKGVRVSKHCVSEEQYRKNNIID-------------------------------------------
-------------------------------------LGTNSNGFGTGNTLNSVGKRFKAVCEKALKDGIIS
GFISADVAGEGAMHIEIIQ----------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0088_32
-----------------------------------------------------------------MSTAVAKS
PAKTIRVTQKGEQSAADWIKGV-------LDGSGSSPAQI---IVAVVIGCIPFVGQGVDVGNVI-------
------------VSIVKIAENPNNKDNWFDLVFNLIAFVPVAGDGLKIVFKQLRSGKAMGAILDAIPSKTMR
GNVEKWFRNLNWNAYTKELQTTSNKIIDGLI----------------------------------------
------------------------DVFDSWMTRAVLGQARLKTLVVQLRKMKTVANRQIEMVMKDLQLAHKK
ALATPYPNTTAK-APIHKTGSKPLNRTSAPHTQQKGQVLKNTSGNTAKTGSKNTSTKRTSKK----------
------------------------------------------------------------------------
-----------------------------------RSNKELGSGGEHI------------TDYYFVKRKKSR
TK-----------INNNGVLYEY-HDTGHDG--IDHAWYS-------------------------------
------------------------------------------------------------------------
-------NSIGHKYRITDSKATNLA---------------------------------SHRKIMTPKAAMDA
LSMG-----------------LDVYVKSSKEKKTKGALGKTVSDG---------------------AQMSHL
WIANKIGSAKIT--SSHKVKLLEQIEAWKRVEF--KPASERVFKN---------------------------
------------------------------------------------------------------------
--------------------------GKGQTVAVKCPYDRSLVTITGNQFDHHSQC----------------
-------------KGLDEPKCTRSVTSHAITLEFVLPNEMLRE-----------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Tfe1
------------------------------------------------------------------------
MHWLNFKRYKSDVAKQAVPP---------HLNAAEFARHY---ADKPQTDTEEYLSLSGEMCWDA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----VVLCAHR-SGALSKAKYKQLWQT------------------------------------------
------------------------------------------------------------------------
-----------------------------------VFDKQYKHFVSPD------------DTEIRTMADMLR
AP-----------QGCFIGIFSLRDAAAPRL--LH-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------A---MIGTGAGFAA
GNKN----------------------LCIGVGGAVGWENLNLARD---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LRWQPEGGFLRQGDNEVLRIFYRPFPA--------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB031_25
-------------------------------------------------------MKKTIKFEKDSKSFETNL
AGFIEAVSFKESSSNLLLPLTH-------PINMEAASITN---EMGFIGLFQWGEEALYDLGYYL-------
---------GDQGISYADIKNTDKNSSLRISWKNQFNSNNWVGKWSGKRNINSKKDFLKHPEIQYEIIKEWI
KYLCNQLRNNNFNEYFGTTIQNIEITESGAIAGMHLVGIGGLGAFLGIPKFHGKKQTDGNGTHIKKYIENFG
GFDLEQ------------------CCNRKIYVTLKDNLGLELKDKEVIIVSQNKGKYVSGETKVKVKSDENG
NLPVIVRSPNTE-IKICADGKESNTIIQKANEKQKAILSDFKVSSHPATLE--KNSTPQPKP----QTNKTP
QEVRNEQTQPSTAPEKEKDSSSKDVDF-------------------------------------------
-----------------------------------NIQIVEGDSGKAI----------SNMNFFITYKGNIK
KH-----------TADGHGIKQNIIAEIGQD--IEVSVQG-------------------------------
------------------------------TGHKQVIHHFTANAALKNKTVKVSLPVHSFNISVTQDNKPVP
```

```
NTLFSIFYRGREISKRTDSRGMLNV--------------------------------R---MLTGFVFGFG
IKGK----SLILSRVEKNTITKAFTVNGSAVHASKAYEANDAKQK---------------------QNENLN
KHKKEKQEEAAK--KQADQAKTQKNSKNEVKQS--NTYTENGGKPLTTVSNQASVTSDTTN-----------
-------------------------------------------------------------------YIIYPN
GTIDRINKDATGFAAYYYVANNQPILIGKSRIYTADRWLKKGKKGSGISH----------------------
-------------LVSIREIFGDSGSKPNNKWEKKIGNLNISIHNDTQQQHRYWLSTVAFAAYIGAVCKFGE
KVRFSGFSDRNGSPGGSSSHLNGEVGDIGYIRVDRNNSVGVNFEMADYDHDASLR-----------------
-------------------------------------FVNILISFGWGKTKNMLSEHYPAHLVNKYKLNQGY
ILPRCSQWTNPRHNNHLHLQGLSVTFNKDE------------------------------------------
---------------------------------------------------------------------------
---------------------------
>RhsB
---------------------------------------------------------------------------
-------------------------------------------------AGCAMGEILADADKWSL-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------AKIGDRQKGMIKDKLS-------------------------------------------
---------------------------------------------------------------------------
-----------------------------------TVKERSKALNTKM------------REHFNANEQKII
SE-----------WEKQTGMNWPTLSSGSRA-----------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------------TPHHVIPIK
NGGS-------------------------------------------------------------------NEW
WNIIPVQHPHTG--TIHGTGSALRTHLPYQKDGG--------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------KLWNLLGY-----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------
```

```
>ZW85-1_19
------------------------------------------------------------------VTDFLPSK
QDLLNALATISSPINKAIKKGQ-------ETARDVADWLW---VVIQGDFAEEQTTAQTVTGTVI-------
--------------SMIPFVDQICDVRDICANCIKIKEDSNNPWPWIGLILTLIGLFPVLGSLFKGIFKVIL
APVRRFMLRPATKALKFTGGNIYKLAEPAIES----------------------------------------
------------------------GITEMNKFLARPAVKRTIKNSNITNIYKAIAKKIREVKAGTNKQALLS
VFDILIDHLKESVKFIEKYGSKAIGVKAKQMLQSVLDIRNLANQKLGEFLK---------------------
----------------------------------------------------------------------
-----------------------------------PVQDFLEKLAVRI----------EKEGDQTFKATTNV
KN-----------IHNFQRIGQNAELKSVLN--NKPVWVD--------------------------------
----------------------------------------------------------------------
-------IVAKEKFKALSESPL-----------------------------------------IPKNYPDISE
MSKN--------------------RALRDAFKTFHDLEPVHLSEG----------------EILYRVLDPKS
ADNSICWMRASE--YKKLKSKADWRRYFAVFAS----WNNNGEVV---------------------------
----------------------------------------------------------------------
-----KYRVPKGGMNVWEGPAASQTFKNSAGKVEKVNSKGEIFVLEGGGIQIVLDPN---------------
-------------DLVRSNVSKREATPWGYDSGLIGEAKTSM------------------------------
----------------------------------------------------------------------
-------------------------------------VGVPRLEQNWYGDKK--------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>Tfe2
----------------------------------------------------------------------
-MPLEVDGIIRGDRGSEPSRWQ------HASTKPLITLTW---HHTIPWNCLRNVWNGLVAGQHW-------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------NALDEFMNLIGVPNRAEVITQIKNKNLQDRDGLHTL-----------------------
----------------------------------------------------------------------
-----------------------------------VTWQGWNIVEGPG------------NEYRAQGDDPGE
-------------NFDGWSGKGMSTNQQATL--QQ-------------------------------------
----------------------------------------------------------------------
```

```
------------------------------------------------------------VNVLYQVMAP
LGSR-------------------------ALDAARQAPNISAEEA-----------------------SVLQ
RTIKQTRPTLRG--KEPIRWQEDMWHQVQPGKE--AKHFARWDTK---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PVWRKRLHSDLAQAG--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Tke9
---------------MDSLSETLELCRRITSGYRPALRNSPVADCTRRFELLPLRYAAVGGNPAQRARLPKL
PSYLSPFQEVGELTHSSYAIRPLREGFLYLLIKRHSAPAYEWHSQYRVAPNGSLLYISADAPWEP-------
-------------APLTGNLDDIIRSFGWTITLYDLDDIQELRPLFSPSPLTPRLLDNYRLLEDEYRNSLPA
IDIARFIQPSDAPPQPHVLKHDQLNWVADFKAQDDADLQALLDLQPFNNDQIVSPHASRLALAPPVNQTKPR
GAAIVIEDAIGITQELNAWRNAAVDDVKTKWLERTVEPGVDNERKLLVAQSFLEIEKLYPQMVAEEIVKREV
MAEKVRNQLHLH-PEIYLFSERARQQADAHDERLKPHMAQFERGVRSKVQARQDAGEFRKRFDQKYGHLVDR
QAMHDQLDGFEQAMQHAQQAAEDRANDHTRWV---------------------------------------
-----------------------------------VSERLLQALDRYD------------NADLINGLAFAE
QT-----------GQCVIGMEL--SEGGTKV--LDHWWRS-------------------------------
---------------------------------------DVADRGNLAIRGITYNQEDLREELAALLEAAKA
EPPSASSFALPEALARQAHAAANAFGR-----------------------------------INTLYEQMQA
QSST-------------ASIGLYAWYVALGRQVLRTATPNSMDRA------------LHQGLRLTLFASVHE
TAVDIRLSEAAR--SGQPINPQRSAGQVSRYLD--QAWAEGLMQARNSDFYKVRVSGLVCL-----------
-----------------------------------------------------------------LEGM
LMAFKARELPDSDARVKTELLAAAMTTAAAGFEVGASYVDQVVARYGANSVTGRGAAAALGRL---------
-------------KLWGASLAVTGGFVLAWWDFADAAQQLIYRQQNLTKHSTKKPGTLALAYASRALATITI
SLAEAGTAIAIAKPLFDHLSQNAKTKLVRMMTTSMGALANKLGTQAARLL----------------------
-------------------------------------LARLVLGAFWIGVILTLIIYILEDDALEKWCKRSC
FRTHKNIKPYEEQEELSALHTAIGEVL---------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>Tse2
------------------------------------------------------------------------
---------------MSYDYEK---------------------TSLTLYRAVFKANYDGDVGRYL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------HPD-KELAEAAEVAPLLH-----------------------------------------
------------------------------------------------------------------------
-----------------------------------PTFDSPNTPGVPA-----------RAPDIVAGRDGLY
AP----------------------DTGGTSV-----------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------FDRAGVLRRA
DGDF--------------------------VIPDGTDIPPDLKVK---------------------------
------QDSYNK--RLQATHYTIMPAKPMYREV-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LMGQLDNFVRNAIRRQWEKARGL-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AF-401_30
------------------------------------------------------------------------MN
DAAIALESFAKQTCGRACVM---------PPIQPVVLDVY---KQSFTAFVGGAADKYQFLGRPL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------DI-DFPDDIGAGPTGIMKSCMRKFKEASSSQITKAKFEYYG--YEEAY--------------
------------------------------------------------------------------------
-----------------------------------STDSVVKRYRGKL------------LLNLLTDIKNIL
KE------------EPNTQINLVGHSLGGWN--VA-----------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------GLSEELSKAK
ICTV----------------HTLITIDPVGIRLSKSGVGND-------------------------RARIYY
LEPDPVAKKWIN--IFSQPLKNYRDDYIAILGG--RWNDDDTAKA---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------NFNSVSTYHHGEASEMFFEKKFLENKM--------------------------------
------------------------------------------------------------------------
-------------------------------------SASDLLVSELKKVIK--------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>3207_1
-----------------------------------------------------------------MDNVIDA
NKDIKKQATELLKKAHGKVSNV-------PPVIPVKLTTY---THSLTIFIGGAADKYVFTPG---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVPVGWGDFRPIGPTYFVGNYVNNYFATIKGGSKN------------------------
------------------------------------------------------------------------
-----------------------------------AFVKYYGYEEAYV----------SDTRELTVNTNKDK
K------------LNAFNDVKNFLKTYPQTQ--VN-------------------------------------
------------------------------------------------------------------------
--------IVGHSLGGWNAAGLAEI-------------------------------------LHKNNICKVN
VLVT--------------------------IDPVGEILSKIGLGS----------------------RTSIYY
SRPKPVFNLWIS--ISCDPKSYEWNNDLIADLG--GQWSSYPSSN---------------------------
------------------------------------------------------------------------
------------------------------SSYYYVTRYSHADFR---------------------------
-------------LMMQEKIVNNLSVQDILSKELSRIK---------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>AR_0088_1
------------------------------------------------------------------MDNVIDA
NKDIKKQATELLKKAHGKVSNV-------PPVIPVKLTTY---THSLTIFIGGAADKYVFTPG---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVPVGWGDFRPIGPTYFVGNYVNNYFATIKGGSKN------------------------
------------------------------------------------------------------------
-----------------------------------AFVKYYGYEEAYV----------SDTRELTVNTNKDK
K------------LNAFNDVKNFLKTYPQTQ--VN-------------------------------------
------------------------------------------------------------------------
--------IVGHSLGGWNAAGLAEI-------------------------------------LHKNNICKVN
VLVT--------------------------IDPVGEILSKIGLGS---------------------RTSIYY
SRPKPVFNLWIS--ISCDPKSYEWNNDLIADLG--GQWSSYPSSN---------------------------
------------------------------------------------------------------------
-----------------------------SSYYYVTRYSHADFR----------------------------
-------------LMMQEKIVNNLSVQDILSKELSRIK---------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>HWAB8_1
------------------------------------------------------------------MDNVIDA
NKDIKKQATELLKKAHGKVSNV-------PPVIPVKLTTY---THSLTIFIGGAADKYVFTPG---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVPVGWGDFRPIGPTYFVGNYVNNYFATIKGGSKN------------------------
------------------------------------------------------------------------
-----------------------------------AFVKYYGYEEAYV----------SDTRELTVNTNKDK
K------------LNAFNDVKNFLKTYPQTQ--VN-------------------------------------
------------------------------------------------------------------------
```

```
--------IVGHSLGGWNAAGLAEI-------------------------------------LHKNNICKVN
VLVT--------------------------IDPVGEILSKIGLGS---------------------RTSIYY
SRPKPVFNLWIS--ISCDPKSYEWNNDLIADLG--GQWSSYPSSN--------------------------
------------------------------------------------------------------------
-----------------------------SSYYYVTRYSHADFR----------------------------
-------------LMMQEKIVNNLSVQDILSKELSRIK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB042_1
-----------------------------------------------------------------MDNVIDA
NKDIKKQATELLKKAHGKVSNV-------PPVIPVKLTTY---THSLTIFIGGAADKYVFTPG---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVPVGWGDFRPIGPTYFVGNYVNNYFATIKGGSKN------------------------
------------------------------------------------------------------------
-----------------------------------AFVKYYGYEEAYV----------SDTRELTVNTNKDK
K------------LNAFNDVKNFLKTYPQTQ--VN-------------------------------------
------------------------------------------------------------------------
--------IVGHSLGGWNAAGLAEI-------------------------------------LHKNNICKVN
VLIT--------------------------IDPVGEILSKIGLGS---------------------RTSIYY
SRPKPVFNLWIS--ISCDPKSYEWNNDLIADLG--GQWSSYPSSN--------------------------
------------------------------------------------------------------------
-----------------------------SSYYYVTRYSHADFR----------------------------
-------------LMMQEKIVNNLSVQDILSKELSRIK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>ATCC17978-mff_1
------------------------------------------------------------------MDNVIDA
NKDIKKQATELLKKAHGKVSNV-------PPVIPVKLTTY---THSLTIFIGGAADKYVFTPG---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVPVGWGDFRPIGPTYFVGNYVNNYFATIKGGSKN------------------------
------------------------------------------------------------------------
-----------------------------------AFVKYYGYEEAYV----------SDTRELTVNTNKDK
K------------LNAFNDVKNFLKTYPQTQ--VN-------------------------------------
------------------------------------------------------------------------
--------IVGHSLGGWNAAGLAEI-------------------------------------LHKNNICKVN
VLIT--------------------------IDPVGEILSKIGLGS---------------------RTSIYY
SRPKPVFNLWIS--ISCDPKSYEWNNDLIADLG--GQWSSYPSSN---------------------------
------------------------------------------------------------------------
-----------------------------SSYYYVTRYSHADFR----------------------------
-------------LMMQEKIVNNLSVQDILSKELSRIK---------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>ab736_7
-----------------------------------------------------------------MSTSETYLND
EEIFELVRDIPLDTSIIYGEED-------QEFGICPYITF---YIYHQDNEVDEVANKIIDLYEE-------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------------FENEIIDKPFKLRYRDTGVWKNANKWRPSRQVMLDEMHE
SYKKYFVYFIGA-TTGDSGGQSARWALQAIIRDNGLRYTSLKISFGDKWFRENKKKWYAFVE----------
------------------------------------------------------------------------
-----------------------------------NCLIKLNPIQAYS------------GYEIGSPQSFNC
VS-----------PEFETVERIFSDYFYGLD--ID-------------------------------------
-----------------------------------------------------------------HPSNMS
```

```
FSHDDPSGLIYTPSLAAGIRTPTWCFL-----------------------------------LSPYWIEKLG
LSEE-----------QIRLKLNDPRIEITKLPDPADPEKYSLWIR---------------------LGELSL
YPIEEGVPDLLV--MANELIKPIRCNDLKLTTL--DAWDDDPNPR---------------------------
------------------------------------------------------------------------
-------------------FDIDNSPQWIARFDEDSHWPEGKRVNKIHAVLLEQ------------------
-------------NAIKVLGGEICPKTGEWYSPANNMKKRYFAEGE--------------------------
------------------------------------------------------------------------
-------------------------------------IMPEIKDNPWGETIWYLEVTNKTE-----------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>ACICU_7
-------------------------------------------------------------MSTSETYLND
EEIFELVRDIPLDTSIIYGEED-------QEFGICPYITF---YIYHQDNEVDEVANKIIDLYEE-------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------------FENEIIDKPFKLRYRDTGVWKNANKWRPSRQVMLDEMHE
SYKKYFVYFIGA-TTGDSGGQSARWALQAIIRDNGLRYTSLKISFGDKWFRENKKKWYAFVE----------
------------------------------------------------------------------------
-----------------------------------NCLIKLNPIQAYS------------GYEIGSPQSFNC
VS-----------PEFETVERIFSDYFYGLD--ID-------------------------------------
-----------------------------------------------------------------HPSNMS
FSHDDPSGLIYTPSLAAGIRTPTWCFL-----------------------------------LSPYWIEKLG
LSEE-----------QIRLKLNDPRIEITKLPDPADPEKYSLWIR---------------------LGELSL
YPIEEGVPDLLV--MANELIKPIRCNDLKLTTL--DAWDDDPNPR---------------------------
------------------------------------------------------------------------
-------------------FDIDNSPQWIARFDEDSHWPEGKRVNKIHAVLLEQ------------------
-------------NAIKVLGGEICPKTGEWYSPANNMKKRYFAEGE--------------------------
------------------------------------------------------------------------
-------------------------------------IMPEIKDNPWGETIWYLEVTNKTE-----------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>ATCC19606_7
------------------------------------------------------------MSTSETYLND
EEIFELVRDIPLDTSIIYGEED-------QEFGICPYITF---YIYHQDNEVDEVANKIIDLYEE-------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------------------------------FENEIIDKPFKLRYRDTGVWKNANKWRPSRQVMLDEMHE
SYKKYFVYFIGA-TTGDSGGQSARWALQAIIRDNGLRYTSLKISFGDKWFRENKKKWYAFVE----------
------------------------------------------------------------------------
-----------------------------------NCLIKLNPIQAYS------------GYEIGSPQSFNC
VS-----------PEFETVERIFSDYFYGLD--ID-------------------------------------
-----------------------------------------------------------------HPSNMS
FSHDDPSGLIYTPSLAAGIRTPTWCFL-----------------------------------LSPYWIEKLG
LSEE-----------QIRLKLNDPRIEITKLPDPADPEKYSLWIR---------------------LGELSL
YPIEEGVPDLLV--MANELIKPIRCNDLKLTTL--DAWDDDPNPR---------------------------
------------------------------------------------------------------------
-------------------FDIDNSPQWIARFDEDSHWPEGKRVNKIHAVLLEQ------------------
-------------NAIKVLGGEICPKTGEWYSPANNMKKRYFAEGE--------------------------
------------------------------------------------------------------------
-------------------------------------IMPEIKDNPWGETIWYLEVTNKTE-----------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>ATCC17978-mff_2
-----------------------------------------------------MPDPQNQQFWSKIAERPTEIQ
QQFWYGAEKLAKYLNDNPAMYK--GYMTYDTSKPDPNLSW---WEKILFYSGQAHYNEAVTHYNT-------
-----------------SKVIADQGSWLWGMLKGDFNKDPSMSQIIVGGLISLIPVADQVCDIRDLIANFIT
LSDEKARTKDNYMALALTSVGIIP-------------------------------------------------
------------------------EVGSAIKTIVKSSRAKDVSKVKLFKFMEYFEEALTKLKIKCPWGKAPE
AWLRSRPWKGIA-TQAFNTLKNNIDRILSVINKCLIRFNGALKVALAKFQATLNHVLNTIKKYIDQLCDEVD
K------------------------------------------------------------------------
-----------------------------------AIGRLLPQQPLAM----------AHAGGGGKNAPTGR
YE-----------ANVSSGKKTEASHRQKKE--TPPPPRK--------------------------------
-----------------------------------------------------------------MKPKHVV
```

```
EPCLEPKKGLRNSWGKKTGKSQAE-------------------------------------LDAEFDRQLK
RQEE-----------------GLNRLTVEEYQQNRQLYEKYKRAG---------------------TGTQQQ
RIREDMQRQLEE--SEYKKLKTEQPQLSKGQIE--RMAENNAKKT---------------------------
------------------------------------------------------------------------
------LEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGHSGVNRSIGSQMAAKK-----------------
-------------RLANMDAAAAQAKAKGMGKDAMDVELKRCK----------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CIP70.10_2
---------------------------------------------------MPDPQNQQFWSKIAERPTEIQ
QQFWYGAEKLAKYLNDNPAMYK--GYMTYDTSKPDPNLSW---WEKILFYSGQAHYNEAVTHYNT-------
-----------------SKVIADQGSWLWGMLKGDFNKDPSMSQIIVGGLISLIPVADQVCDIRDLIANFIT
LSDEKARTKDNYMALALTSVGIIP-------------------------------------------------
------------------------EVGSAIKTIVKSSRAKDVSKVKLFKFMEYFEEALTKLKIKCPWGKAPE
AWLRSRPWKGIA-TQAFNTLKNNIDRILSVINKCLIRFNGALKVALAKFQATLNHVLNTIKKYIDQLCDEVD
K------------------------------------------------------------------------
-----------------------------------AIGRLLPQQPLAM----------AHAGGGGKNAPTGR
YE-----------ANVSSGKKTEASHRQKKE--TPPPPRK--------------------------------
-------------------------------------------------------------MKPKHVV
EPCLEPKKGLRNSWGKKTGKSQAE-------------------------------------LDAEFDRQLK
RQEE-----------------GLNRLTVEEYQQNRQLYEKYKRAG---------------------TGTQQQ
RIREDMQRQLEE--SEYKKLKTEQPQLSKGQIE--RMAENNAKKT---------------------------
------------------------------------------------------------------------
------LEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGHSGVNRSIGSQMAAKK-----------------
-------------RLANMDAAAAQAKAKGMGKDAMDVELKRCK----------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>R2091_2
--------------------------------------------------MPDPQNQQFWSKIAERPTEIQ
QQFWYGAEKLAKYLNDNPAMYK--GYMTYDTSKPDPNLSW---WEKILFYSGQAHYNEAVTHYNT-------
-----------------SKVIADQGSWLWGMLKGDFNKDPSMSQIIVGGLISLIPVADQVCDIRDLIANFIT
LSDEKARTKDNYMALALTSVGIIP------------------------------------------------
------------------------EVGSAIKTIVKSSRAKDVSKVKLFKFMEYFEEALTKLKIKCPWGKAPE
AWLRSRPWKGIA-TQAFNTLKNNIDRILSVINKCLIRFNGALKVALAKFQATLNHVLNTIKKYIDQLCDEVD
K-----------------------------------------------------------------------
-----------------------------------AIGRLLPQQPLAM----------AHAGGGGKNAPTGR
YE-----------ANVSSGKKTEASHRQKKE--TPPPPRK--------------------------------
-----------------------------------------------------------------MKPKHVV
EPCLEPKKGLRNSWGKKTGKSQAE--------------------------------------LDAEFDRQLK
RQEE-----------------GLNRLTVEEYQQNRQLYEKYKRAG---------------------TGTQQQ
RIREDMQRQLEE--SEYKKLKTEQPQLSKGQIE--RMAENNAKKT---------------------------
-----------------------------------------------------------------------
------LEGLDVLHNPDMQLGGFDVKYDPKKPPTLDDFGHSGVNRSIGSQMAAKK-----------------
-------------RLANMDAAAAQAKAKGMGKDAMDVELKRCK----------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
>TseF
-----------------------------------------------------------------------
------------------------------MAASGKLDL---VRGDSHLAGNLLDGSLEGPLRI-------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------DEH-DRPQASLGYRQGQLHGASTLFHPNGKVSAQLAF-------------------------
-----------------------------------------------------------------------
-----------------------------------VDGKLHGPASFHA------------AEGWLQRKAHYR
NG-----------LLHGEAFNYFANGQVAER--EH--YRD--------------------------------
-----------------------------------------------------------------------
```

```
------------------------------------------------------------GVRDGVYQRF
HGNG-------------------------QLAFDGRYLNGQLLDG---------------------------
--AQPFADDGRP--LDSEGKPMARWRW----------WWTRLAEP---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CIP70.10_31
---------------------------------------------------MVDLNKDDVALITQAIAIGFS
PAGVALDVADLARASYNLYQEK-------SDDNYFEVILC---VIGFIPGPGDGLKAGLRIVNRK-------
-------------------PEILFELIRFIMTHCKIYGNPEQWLSEIISDTKIRELIRSG------------
------------------------------------------------------------------------
------------------------KREALNASNKNIGNRWAKYWINQSIEITFNFLEASISSLVQLLARKVL
HWKTKIPKSSAD-KRHVGGGKGHQNNSAHGTTYDGKTGQNGNGHG---------------------------
------------------------------------------------------------------------
-----------------------------------SKGKTLSKVDISK----------VLSNLEVGGVGEHM
AD-----------YWVANKLAIPAVHDSGQQ--LT-------------------------------------
------------------------------------------------------------------------
-------PKLQRPMTKLHIGIHDQG-------------------------------------IDAIWKSDKK
NIGI-------------------MNTKSYAIIEAKASLSMGKGTG--------------PGSLLNDLDKQQD
TRERHIERASAK--KEKRAEKKLIPKKKFLINQ--QMSDEWVKKR---------------------------
------------------------------------------------------------------------
-----------------------LRATSLRNVEIAGFSRHLLYFNYAHPETVEHL-----------------
-------------NVLAISIQDNQPVDHSEHLNEHTPSNFWGAAK---------------------------
------------------------------------------------------------------------
-------------------------------------IDEALNNRVTRANIKNGHTK---------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>R2091_31
--------------------------------------------------MVDLNKDDVALITQAIAIGFS
PAGVALDVADLARASYNLYQEK-------SDDNYFEVILC---VIGFIPGPGDGLKAGLRIVNRK-------
-------------------PEILFELIRFIMTHCKIYGNPEQWLSEIISDTKIRELIRSG------------
------------------------------------------------------------------------
------------------------KREALNASNKNIGNRWAKYWINQSIEITFNFLEASISSLVQLLARKVL
HWKTKIPKSSAD-KRHVGGGKGHQNNSAHGTTYDGKTGQNGNGHG---------------------------
------------------------------------------------------------------------
-----------------------------------SKGKTLSKVDISK----------VLSNLEVGGVGEHM
AD-----------YWVANKLAIPAVHDSGQQ--LT-------------------------------------
------------------------------------------------------------------------
-------PKLQRPMTKLHIGIHDQG-------------------------------------IDAIWKSDKK
NIGI------------------MNTKSYAIIEAKASLSMGKGTG--------------PGSLLNDLDKQQD
TRERHIERASAK--KEKRAEKKLIPKKKFLINQ--QMSDEWVKKR---------------------------
------------------------------------------------------------------------
----------------------LRATSLRNVEIAGFSRHLLYFNYAHPETVEHL-----------------
-------------NVLAISIQDNQPVDHSEHLNEHTPSNFWGAAK---------------------------
------------------------------------------------------------------------
-------------------------------------IDEALNNRVTRANIKNGHTK---------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tse5
------------------------------------------------------------------------
----------------------------IIPLVVIGAFAA---RAAIGAALGAGIELGMQTGKQV-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------LGQM------------KDNWDSDRDLTD
IK-----------------------------------WKC--------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IDINWKHVGA
SAAI-----------------------------GTVAPGMLSTG---------------------KTVVQS
AKAIRTLSGQAA--NTANRAAKLAARKAAHADT----IKKAVATQ---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------AAWQTGKQIVKCPLKDEEEECPPQ-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>VasX
MSNPNQAAKTGQTNDAQNPASACPFKQPLIGIIPVRYAFDVYDDQGQALHPLPKADRQWKGQFSIKQRSYTL
RQLRDGWLYVYDETAKTLHEYE-------VVGCKLTKIDW---SDDEANKPTHERGSKGESKSCL-------
---------------LYPAQHTLSIGYAHQRWTWRVCEHMRSNTSSRHAVMRKVSLKQFESNGTHPHAHFAQ
YLEDYVADIGTPAEQDIFKDTCTPSLPVEKSEEAVKGTEFKFVADKAVVSSSDYLQDLPEQNCGLFVALNDP
LADVSDLFVTFTTQVAKRTKAI--GDETQQHKMQMAELTRTLGRIRLEEKEIPDFVKQDPIRILELERAITE
YCATAKLAEIES-HHLASEGHSPSGNYALMQQQAEQKLAELKTLYRFEPTSAQMRKWRKKDNSFIDEVRWAD
LDNFLVEHYTELKGLDEQIKQHYAQFMSAFNQLGLDPLLFGMDNQDEVQQAYLLALTSQFLVVVTQVNHDEK
SL---------------------------------EILKKDLSFDSPK----------NLMALASTGFSLQA
NQAINNHIQGFSTAFLSTSNPSDMVAFATAI--AN--WDT--------------------------------
-------------------------------------------------------FTGDERIQEKAWFKRWIE
PAQSSFGALQKAVANQAKESWQAVM---------------------------------E---LLFPYQNQPK
GGTP-------------SLLANLRLLLVESLVREEAVLQHNPKYAAELKQFETKLNAILQEMNDALELKPGN
VSPKNHQIATAQ--SAQRKLGQLLSSELPMMLT--LKNQAAMNTFQQSVNEKLSALSKNVK-----------
-----------------------------------------------------------TSSASVSQKLG
GLGGLLFALNLWNTMTVLENIRYKVAQYPSWNPFKNPALGEAIYATGNTIVVAGAISAGRAWV---------
-------------TIAEQGLLDRTLKNALNTTKVLGTKDALKTFAKSIALVATVGMIASALETWESWGKFND
SSKTDLERFGYLLKAGATGAQGIIFYIQFFTLLGSGIGGPSIAAISAGWMLAGFAV----------------
-------------------------------------IGIVYLIGVILTNVFKRSELEIWLSKSTWGKESAH
WPVGKELTELEHLLHRPSLRLSQVTQRKAAQWMDSGSLQWQLELTLPDYLKGQTIGLQITRLPAQPAYYQPQ
REAVTPILINEQQGKWSIEDNQPVYRITLGGSEKDTVGVCVALPLRWGKELSLKFYASGTRAGELDLQSAEA
NDIATRNLVVGKG--------------
```

```
>15A5_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Ab4568_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
```

```
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Ab4977_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN-------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>JBA13_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE---------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB04_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE---------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
```

```
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>KAB07_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN-------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>KAB08_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KBN10P02143_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
```

```
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SAA14_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN-------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>SMC_Paed_Ab_BL01_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE---------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>SSA12_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE---------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
```

```
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SSMA17_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE----------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN-------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>YU-R612_28
------------------------------------------------------------------------
--MGNNSTTSTTTNTANPPTQK-------VPLKPEAELHL---LVGSAYGEGDRESPYGHTAVYI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------KLKGK-DYIYDFGRYGKTKPESFGIFTLEGANSPRGE---------------------------
------------------------------------------------------------------------
-----------------------------------GILRIWSSFDAYI------------ADENSQGKGTSK
TR-----------TTHAYGYRIF-DSQAMLV--LN--YYN--------------------------------
------------------------------------------------------------------------
-------NLLKTATLRRNEKYYKSY--------------------------------A---LSQDYFALAP
NCTT------------------------QSLEATKKAIPSMAKSG------------------------HMF
VNAEKVLPTTVK--LAFKASKYEMPKYLFLPDN----LNDYLMKS---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDVKVDIKNTYHLKK--------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>RhsA
------------------------------------------------------------------------
---------------AKCPTLA----------HGANGEIL---SAKATVSKAELRTGSGTNQSSR-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DYARSLGN-----------------------------------------------------
------------------------------------------------------------------------
-----------------------------------QTDDAGHILGNVL------------GGQGGKGNVFPQ
LP-----------AINRGQYRDFEKVVKDYI--GQ--HGS--------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VDIEWAFKYG
NGGT-------------------------------------------------------------RPTEIY
YDVYQNGQKVFG------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------RIFNN------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tke4
------------------------------------------------------------------------
--------------------------------CPENVKEY-------------DITPYRPSNSPL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ENHH-------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GILDIWAAQNVPS-----------YGGKYPKGSPTIV
LS-----------SKNHAATKAVYREWLREK--TG-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------KPVGGKVDWSQISN
REVM-----------------------------------------------------------QLSERM
FDVAGVPATSRT--SYYRALNRYLHTGTF-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>A1_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------KPIRLS-----------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>A388_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
>A85_16
-----------------------------------------------------------------------
-----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------WAKRK-DFLDDIGI-----------------------------------------------
-----------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ----------LYHCGSHPIYSAGINQKL--GQ-----------------------------------
-----------------------------------------------------------------------
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
```

```
>AB0057_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------KPIRLS-----------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------------------------
>AB307-0294_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT--------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>AB5075-UW_16
----------------------------------------------------------------------
-----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------WAKRK-DFLDDIGI----------------------------------------------
----------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ----------LYHCGSHPIYSAGINQKL--GQ-----------------------------------
----------------------------------------------------------------------
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT--------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
```

```
>AR_0083_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------KPIRLS-----------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------------------------
>D36_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
>USA15_16
-----------------------------------------------------------------------
-----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------WAKRK-DFLDDIGI-----------------------------------------------
-----------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ----------LYHCGSHPIYSAGINQKL--GQ-----------------------------------
-----------------------------------------------------------------------
------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT-------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------KPIRLS-------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
```

```
>WCHAB005078_16
------------------------------------------------------------------------
----------------------------------CSTTL---NRNLGGVKGDHLQAHHIIPEEI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------WAKRK-DFLDDIGI-------------------------------------------------
------------------------------------------------------------------------
-----------------------------------GGNRDKAENGVLM-------------PDSEAKAKQMK
RQ-----------LYHCGSHPIYSAGINQKL--GQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------IQREFESKKI
TASQ-----------------------------------------------------------------
----------AR--DKVANLQSSMRLVLITPGT----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------KPIRLS-----------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB030_24
--------------------------------------------------MKNGKSINQKSYPLTRYGFICA
VSRMESSSDLSLPLTAPVNIRA-------SQNKNSRGYIG---FFQFGEAALIDLGYYKHWNDNS-------
---------------DKTKANDWTGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLRNRSFNEYYGK
IINGIEITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIEMFNHYDLESCCSRKIYII--
------------------------LKNQIGQIAKNKKVTIESEYSGKFKQSKFIVSAESDEQGLLPVIIRHP
GSKIIIKVDGKQ-SAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQKTVDLKKDEVKTN
APKDIKFDIAIIESDTNRKI--------------------------------------------------
-----------------------------------TNMRFFIRYKGKI------------KEHTSDSSGIKT
GIIAEEGENLDILVNGSKGYQKLKTISITKG--MENSCIS------------------------------
-----------------------------------------------------------------------V
```

```
PLGLVSVKLKIHDSKGKILKNNKFF-------------------------------------VSYRGREIEK
ITDS-----------NGFIQLKMLNAFVYKLLLSNKKPILTLRND---------------PSISVINVNLNS
AATTIQMPRVASNPPSKTVPAKTKPAKETSSKR-EESFVDYLIDFIPSLGKTENVHTEKNG-----------
------------------------------------------------------------------------
----NPLTKQYGSDVVFTIKTINKETGKEENLAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVD
SKEQVLYTAILKNPMPVIEIRMDKPKDDDSYLFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTE
IRAMADGKVRVVKGFYSGTDVIEIVHKKHIIRYGEVLA----------------------------------
-------------------------------------GKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLE
MYSNPKDTSPLTVRGNNAYQRRSDLIDPTTFLDNSTL-----------------------------------
------------------------------------------------------------------------
----------------------------
>AbH12O-A2_24
--------------------------------------------------MKNGKSINQKSYPLTRYGFICA
VSRMESSSDLSLPLTAPVNIRA-------SQNKNSRGYIG---FFQFGEAALIDLGYYKHWNDNS-------
---------------DKTKANDWTGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLRNRSFNEYYGK
IINGIEITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIEMFNHYDLESCCSRKIYII--
------------------------LKNQIGQIAKNKKVTIESEYSGKFKQSKFIVSAESDEQGLLPVIIRHP
GSKIIIKVDGKQ-SAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQKTVDLKKDEVKTN
APKDIKFDIAIIESDTNRKI-----------------------------------------------------
-----------------------------------TNMRFFIRYKGKI------------KEHTSDSSGIKT
GIIAEEGENLDILVNGSKGYQKLKTISITKG--MENSCIS--------------------------------
-----------------------------------------------------------------------V
PLGLVSVKLKIHDSKGKILKNNKFF-------------------------------------VSYRGREIEK
ITDS-----------NGFIQLKMLNAFVYKLLLSNKKPILTLRND---------------PSISVINVNLNS
AATTIQMPRVASNPPSKTVPAKTKPAKETSSKR-EESFVDYLIDFIPSLGKTENVHTEKNG-----------
------------------------------------------------------------------------
----NPLTKQYGSDVVFTIKTINKETGKEENLAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVD
SKEQVLYTAILKNPMPVIEIRMDKPKDDDSYLFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTE
IRAMADGKVRVVKGFYSGTDVIEIVHKKHIIRYGEVLA----------------------------------
-------------------------------------GKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLE
MYSNPKDTSPLTVRGNNAYQRRSDLIDPTTFLDNSTL-----------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AF-401_24
--------------------------------------------------MKNGKSINQKSYPLTRYGFICA
VSRMESSSDLSLPLTAPVNIRA-------SQNKNSRGYIG---FFQFGEAALIDLGYYKHWNDNS-------
---------------DKTKANDWTGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLRNRSFNEYYGK
IINGIEITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIEMFNHYDLESCCSRKIYII--
------------------------LKNQIGQIAKNKKVTIESEYSGKFKQSKFIVSAESDEQGLLPVIIRHP
GSKIIIKVDGKQ-SAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQKTVDLKKDEVKTN
APKDIKFDIAIIESDTNRKI-----------------------------------------------------
-----------------------------------TNMRFFIRYKGKI------------KEHTSDSSGIKT
GIIAEEGENLDILVNGSKGYQKLKTISITKG--MENSCIS--------------------------------
-----------------------------------------------------------------------V
PLGLVSVKLKIHDSKGKILKNNKFF-------------------------------------VSYRGREIEK
ITDS-----------NGFIQLKMLNAFVYKLLLSNKKPILTLRND---------------PSISVINVNLNS
AATTIQMPRVASNPPSKTVPAKTKPAKETSSKR-EESFVDYLIDFIPSLGKTENVHTEKNG-----------
-----------------------------------------------------------------------
----NPLTKQYGSDVVFTIKTINKETGKEENLAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVD
SKEQVLYTAILKNPMPVIEIRMDKPKDDDSYLFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTE
IRAMADGKVRVVKGFYSGTDVIEIVHKKHIIRYGEVLA----------------------------------
--------------------------------------GKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLE
MYSNPKDTSPLTVRGNNAYQRRSDLIDPTTFLDNSTL-----------------------------------
-----------------------------------------------------------------------
---------------------------
>AR_0101_24
--------------------------------------------------MKNGKSINQKSYPLTRYGFICA
VSRMESSSDLSLPLTAPVNIRA-------SQNKNSRGYIG---FFQFGEAALIDLGYYKHWNDNS-------
---------------DKTKANDWTGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLRNRSFNEYYGK
IINGIEITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIEMFNHYDLESCCSRKIYII--
------------------------LKNQIGQIAKNKKVTIESEYSGKFKQSKFIVSAESDEQGLLPVIIRHP
GSKIIIKVDGKQ-SAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQKTVDLKKDEVKTN
APKDIKFDIAIIESDTNRKI-----------------------------------------------------
-----------------------------------TNMRFFIRYKGKI------------KEHTSDSSGIKT
GIIAEEGENLDILVNGSKGYQKLKTISITKG--MENSCIS--------------------------------
-----------------------------------------------------------------------V
```

```
PLGLVSVKLKIHDSKGKILKNNKFF-------------------------------------VSYRGREIEK
ITDS-----------NGFIQLKMLNAFVYKLLLSNKKPILTLRND---------------PSISVINVNLNS
AATTIQMPRVASNPPSKTVPAKTKPAKETSSKR-EESFVDYLIDFIPSLGKTENVHTEKNG-----------
------------------------------------------------------------------------
----NPLTKQYGSDVVFTIKTINKETGKEENLAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVD
SKEQVLYTAILKNPMPVIEIRMDKPKDDDSYLFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTE
IRAMADGKVRVVKGFYSGTDVIEIVHKKHIIRYGEVLA----------------------------------
-------------------------------------GKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLE
MYSNPKDTSPLTVRGNNAYQRRSDLIDPTTFLDNSTL-----------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0063_24
--------------------------------------------------MKNGKSINQKSYPLTRYGFICA
VSRMESSSDLSLPLTAPVNIRA-------SQNKNSRGYIG---FFQFGEAALIDLGYYKHWNDNS-------
---------------DKTKANDWTGSWVGHNGVNSLSDFLKSPAKQIQIIGEWIDLLCKRLRNRSFNEYYGK
IINGIEITESGAIAGAHLVGEGGLGSFLGISGFKGNYKEVDGNNVHISRYIEMFNHYDLESCCSRKIYIILL
------------------------LKNQIGQIAKNKKVTIESEYSGKFKQSKFIVSAESDEQGLLPVIIRHP
GSKIIIKVDGKQ-SAVITQASDKKQSIELSVSEDIKIQSVLQKPAEPEPKQEKVVVVEQKTVDLKKDEVKTN
APKDIKFDIAIIESDTNRKI-----------------------------------------------------
-----------------------------------TNMRFFIRYKGKI------------KEHTSDSSGIKT
GIIAEEGENLDILVNGSKGYQKLKTISITKG--MENSCIS--------------------------------
-----------------------------------------------------------------------V
PLGLVSVKLKIHDSKGKILKNNKFF-------------------------------------VSYRGREIEK
ITDS-----------NGFIQLKMLNAFVYKLLLSNKKPILTLRND---------------PSISVINVNLNS
AATTIQMPRVASNPPSKTVPAKTKPAKETSSKR-EESFVDYLIDFIPSLGKTENVHTEKNG-----------
------------------------------------------------------------------------
----NPLTKQYGSDVVFTIKTINKETGKEENLAYSIKYNGAKRTHYTGQDGIGLKKHRGEEGKKIEIVVDVD
SKEQVLYTAILKNPMPVIEIRMDKPKDDDSYLFPLKARTNSYKNGFARFGSNRSGGKRKHAGCDLYAPTGTE
IRAMADGKVRVVKGFYSGTDVIEIVHKKHIIRYGEVLA----------------------------------
-------------------------------------GKSLVKVGDDVKRGQTIGYVGKLTVQVPSMMLHLE
MYSNPKDTSPLTVRGNNAYQRRSDLIDPTTFLDNSTL-----------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>ZW85-1_20
----------------------------------------MDKKMSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNTLR----NSEFKK
VMDFLAKKDGDFTNEHRLHSSQCIDSIKICLENKLLNERSQFSAQATKSI----------------------
-----------------------------------VLMGLWNELPKNL----------TDADDINYELEKIY
KR-----------KSKAEQERLLKEAQEKQR--ANKGIYT--------------------------------
---------EDMGKLSRGEGEQIWVKKYKPNLDMVAKSNFDKKINALIQECLAGARAIGDDHIKWLLSKAVI
NALHAYDDQVQVPFGNIFYVHAMDM----------------------INGMSGVPSGQA---LLETWLGVEK
IAKE---NIYMRAICYNQESLKNKYNAAAPSIIDISWDDGQNAAK--------------------TAIAAF
VAADKAWQEWAA--DKTNNGYMLHGQKFSLLKT--FYWMSELTQSAVKWSMKYTPGSEFAK-----------
------------------------------------------------------------KLGRLTFYTFA
HSGALVEHVAKNSLYYLIPVQTLTGRVKLTPEMVQNNWKKYSSSATNPSKAAKQIDRIIANSSPSAGLRVSG
VVAIFE-------LINLGTQISKFNIDPSVDNTLSYMSGMMATTAAILEVGSSSMEKFSFAERAAYIAKCGA
YFAIAGAIVSFFIDLKGLNKAFEESNGYAFALNLLKAASSFGTLA-VG------------------------
-------------------------------------FSAFLNLPIMRNSTLYSMVERYAVGRALLGIKVVR
VGAMLSLAGIALVALEIYLKNYVLDNAMQDWCQKCAFKLKKENGEDAFKDVKEEEKEFNNAVVSV-------
---------------------------------------------------------------------------
---------------------------
>D1279779_12
---------------------------------------------MSENQKMILGKSKSNNLLNEIIAQQKQKQ
SQIPVIGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPATLGKNVKDIQLSHLKYAVEMIDTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S-----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET-------------------------------
-------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
```

```
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDKVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
>R2090_12
-------------------------------------------MSENQKMILGKSKSNNLLNEIIAQQKQKQ
SQIPVIGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPATLGKNVKDIQLSHLKYAVEMIDTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET-------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDKVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
```

```
>Ab04-mff_12
--------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET--------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHMKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
--------------------------------------------------------------------------
---------------------------
>AR_0088_12
--------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET--------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
```

```
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
----------------------------
>CIP70.10_12
-------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET-------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
----------------------------
```

```
>HWBA8_12
--------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET--------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
>R2091_12
--------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQVADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET--------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
```

```
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
>LAC-4_12
-------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYL
S----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET-------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
```

```
>WKA02_12
-------------------------------------------MSENQKMILGKSKSNNLFNEAIAQQKQKQ
SQIPVMGKTKAVGDMRNPTVAK-------NINKKIEESEI---AKSAKQSTAANMQNSSAGQAQK-------
---------------ECSNFCRKKGFNILPLRYTVVKDNPPALPPTLGKNVKDIQLSHLKYAVEMINTGYIY
RLVKRTSGALEWAGYKVTPNGHLSYFPVGKEA------------PKSVPEFACKGAGHSFNSSVIAVES---
------------------------NPKDEAKIAYIIHTHVPMSKAKISEYEKNADKFVTEGKWQKILINGGS
AQEHCIAASQFK-TTVYNLNSFGKNRIDATLNKFKDEPKSLACMALYDPVG--ITRKLNDSR----NSQFGK
LTNYLAKNVEKISNEHRLQSSQLVDSIKIVVENKLINQQLSARSQIADLSAKIEYAKDKIPKFGSMDQREYL
S-----------------------------------KIQEIWDRAPTAE------------RDKFLLQRNKKF
AE-----------GEQKLKEKIITQSKAEAK--IT--WET--------------------------------
--------------------------KYAPKINWDTKKAFDKEVKKLINEGRTLAQTYASDHIKWLKSKHLL
NAFYVYDQTILKEYGALFHVHALAV---------MDGMTGCDEGQ-------------A---LMEKWLGVEE
ISDD---NLYMRAVTYNQKNLIDQYNAKSSEITSLTWDQTQSSLK---------------------SLIAAF
VSADQLWEQWLA--DPNNKINELKWYNPAKSLL----WISEITRSVAKWSLQYNINPLIAK-----------
-------------------------------------------------------------RLSRVSFIAYA
HSSLLTDRVPKWSLLYNVDFKMTNASTQLNVTEIERRWKNAGQNTAAQKIKEILSKSPASVAIRISSIVALF
E------------LINFGVQSNKFIGERNWENGFQLISGLLASSAAVLDIAGGGMDALSFQEKANKIRLYGA
RLAVSAAIISFCIDAFAVYKEKEGDKDKILMAFLFTKATVSLVMVGVG------------------------
-------------------------------------FGLLLNLPILQNSWVVSSANKIAFTRILLRANFIR
IAAYCNWIGIGFLVIEYLLKTYVLDDDLQKWCEKSIFGKDSSKFKLFKDEEEAFSKAIMSI-----------
---------------------------------------------------------------------------
---------------------------
>ab736_10
-----------------------------------------------------------------MTQAIQNE
TRSVRDMLIAAKVLAKDGKATE-------SPCKTCRVPVW---VSFFFDGTGNNKDADAATLNQS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------NVVALFEAHKQDSKNGIEKFYYEGLGTQFRFDKYSVVDSGKITAAARS
LQGRKIDITDAE-WRKQGYSESGKGVQGALGLGVALGIKQRLQKAIFELVD--YLDKIYTQK----GITEIN
ISAFGFSRGA----------------------------------------------------------------
-----------------------------------TEARIFMNWLQHA------------PNVTTQGTGSGK
KL-----------FYRGKPLKAKFLGIFDTV--ES--IGN-------------------------------
---------------------------------------------------------------------------
```

```
AAQNKNPELYRTRIEDYIEHSMHLV-------------------------------ASL---EMRQSFPLTP
TGKP----------------TANTVKGLIHDQKVYPGVHSNVGGG----------------------YMPMEQ
ARILGLSRITLH--AMYNRACAYGLKFFTLNEL----NAAKQRKI--------VFTRFYAF-----------
------------------------------------------------------------------------
------------------------DSKWQQDLNNFMAYVKGGTSFEQQMQGQIALY----------------
-------------HQWIREGGYARFIHRKTRERIGRKEKITAITKLNDGLFEN-------------------
------------------------------------------------------------------------
-------------------------------------IRQALNVYVPEGARPYDVIKGRDRKSTLPKEVIYY
FENYVCDSVGGFIAEASDFQAILNDGKAPNYFIPRGIVRPT------------------------------
------------------------------------------------------------------------
---------------------------
>ATCC19606_10
-----------------------------------------------------------------MTQAIQNE
TRSVRDMLIAAKVLAKDGKATE-------SPCKTCRVPVW---VSFFFDGTGNNKDADAATLNQS-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------NVVALFEAHKQDSKNGIEKFYYEGLGTQFRFDKYSVVDSGKITAAARS
LQGRKIDITDAE-WRKQGYSESGKGVQGALGLGVALGIKQRLQKAIFELVD--YLDKIYTQK----GITEIN
ISAFGFSRGA-------------------------------------------------------------
-------------------------------------TEARIFMNWLQHA------------PNVTTQGTGSGK
KL-----------FYRGKPLKAKFLGIFDTV--ES--IGN------------------------------
------------------------------------------------------------------------
AAQNKNPELYRTRIEDYIEHSMHLV-------------------------------ASL---EMRQSFPLTP
TGKP----------------TANTVKGLIHDQKVYPGVHSNVGGG----------------------YMPMEQ
ARILGLSRITLH--AMYNRACAYGLKFFTLNEL----NAAKQRKI--------VFTRFYAF-----------
------------------------------------------------------------------------
------------------------DSKWQQDLNNFMAYVKGGTSFEQQMQGQIALY----------------
-------------HQWIREGGYARFIHRKTRERIGRKEKITAITKLNDGLFEN-------------------
------------------------------------------------------------------------
-------------------------------------IRQALNVYVPEGARPYDVIKGRDRKSTLPKEVIYY
FENYVCDSVGGFIAEASDFQAILNDGKAPNYFIPRGIVRPT------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Hcp-ET1
------------------------------------------------------------------------MSN
IVYLTVTGEQQGSISAGCGTSESTGNRWQSGHEDEIFTFS---LLNNINNTGLGSQFHGITFCKL-------
-----------------------------------IDKSTPLFINSI-------------------------
------------------------------------------------------------------------
------------------------NNNEQLFMGFDFYRINRFGRLEKYYYIQLRGAFLSAIHHQIIENQLDT
ETITISYEFILCQHLIANTEFSYLALPENYNRLFLPNSKNQTNNRFKTLNSK--------------------
------------------------------------------------------------------------
-----------------------------------AIGRLLAAGGVYN----------GNIEGFRDTAEKLG
GD-----------AIKGYDQILNEKTAGIAI--AT-------------------------------------
------------------------------------------------------------------------
-----------ASILLTKRSNVDTY-------------------------------------TEINSYLGKL
RGQQ-----------------KLLDGIDIIEIIYIKRPSKDLANL---------------------RKEFNK
TVRKNFLIKLAK--TSETSGRFNAEDLLRMRKG--NVPLNYNVHH---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------KLSLDDGGTNDFENLVLIENEPYHKVFTNMQSRIA------------------------
------------------------------------------------------------------------
-------------------------------------KGILVGESKITPWAIPSGSIYPPMKNIMDHTK---
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle1Ec
------------------------------------------------------------------MTKY
QGYDVTDATHKTSIHNDWKVVV-------AKKKPARGVTL---TIGIFFDGTGNNRENTASRLMK-------
---------------FNECSAARQGVNQKDAQSCEDFLKEINKNSISNGSYRGYYSNIHWLNILYHPDQVLK
KDQTSAQIKTYISGIGTAAGEADSVIGMGLG----------------------------------------
------------------------TSILDIFEGVVTKTDEAMERITQALSEFMGFNLSPDFCIAKIQFDVFG
FSRGAAAARHFANRVMEQDPAIARAIAKGLRGDFYDGKPSGEVRFLGLFDTVAAIG----------------
------------------------------------------------------------------------
-----------------------------------GISNFFDINGRSN------------PGVKLELRPSVA
KK-----------VFQITAMNEYRYNFSLNS--IKGMWPE--------------------------------
------------------------------------------------------------------------
```

```
-------LALPGAHSDIGGGYNPVG---------------------------------SPLQENESLFLSCP
EFEI-----------VSDDTREMDTRVYRKAEQVRKMLMTLPALK-----------------HILPHGKLTT
KIRSIGVNNSNQ--RRAGVIQKQVGAAVFFERM--AVPNDWANVCLRVMLDAAQEAGVLFE-----------
------------------------------------------------------------------------
PIRQTNTELQLPSELIFLADKAIAQGKAVRLGQEPQAFTEEELYIIGKYTHCS-------------------
-------------ANWNIESDGNLWVDPTTGEIFIHRFGP--------------------------------
------------------------------------------------------------------------
-------------------------------------KGNKAFVFPNKPNDRWIRSVWYMDDQQRLNDNAVK
NTKVMMSGV---------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>PldB
-------------------------------------------------------------MSDLYKPQTLKLYA
QQAGSVRLTLDWFANKAFYPPR-----AGVHIKPLINGQA---AFDAVHAAMEAARHSIDIITWG-------
-------------FDPAMRFKRPDGPRIGELLQTKGREGVQARVLVWSNQLARLKENTIPGAGVGGSGGTWV
GSGVASGSAVDNEVLRLEQRR----------------------------------------------------
------------------------QHNLNLIARQQEALERSERLHREGRLPSFDPRGAAHARTRIAELEAEN
AEIQRTLDSSGAQGYGGKRGSGGTRQDPWGQIFTRDWFKAVRGGGLQNVEFRTRDFEQTARPVMNGEQVRLV
NGRLQSLIHLLRADGIDDLGIGQLLVLTQFASH----------------------------------------
-----------------------------------HQKMVLVDYGSPQ------------AIGFVMGHNMHR
NY-----------WDTSAHLFDDRAAGRDPG--FG-PWQD--------------------------------
-----------------------------------------------------------------ISMQVQ
GPVLADLSRNFSEAWDLETPWYKRW------------------------------FSTPSLTAERDALPLPK
IATP------ASNSVAQICRTQPQDDERSILEHYLKALGNATDYV---------------------YMENQY
FRYAGFAERLRK--TAQVRKARGVPGDLYLFVV--TNTPDSSDASKTTYDMMKGLGQEQLM-----------
-------------------------------------------------------------PQVQRDLAHD
LREKREQLKQVRENLHPDPYVRRGQENNIERLERKIEALEEKGVTPEVEQRLGDLGA---------------
-------------QEIPGLAKNTGEDDKPYQLVEVPGLKVVVATLATSDPAPGSPPPARLSAEAEAALGAPP
LKARYKHIYVHSKLLLVDDLYTLLSSANINVRSMHGDSE--------------------------------
-------------------------------------LGVAQPNPDLARAMREELWELHAQKVATTTEKNFK
LWNQKMDANWRQQRKDEPLVANLLRFWDVVTPYSPGLTVD--------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>6200_21
------------------------------------------------------------------------
-------NFKSVGKIKEERARR-------QTSSSAPYIKH---TMAKCKTQAQNISKKEAQYWDM-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------SKCES-----------------------------------------
------------------------------------------------------------------------
-----------------------------------NVAQVTAFRNRLE------------KEGLNKGYKVDL
GD------------NKGSHYYIY-DAGRNIG--FN---EG--------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------KETQYMRIEV
SSTN----------------------------EFHGHPISKQRY---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ESWQSKT----------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle1Bt
-------------------------------------MNFRFAPAERPDIGVVTKEEKDAILRRLHDDDGMSC
CKTLHIGIFFDGTRNNAERDKSGHKHSNVARLRDAFPQDR---YHKSIYVAGVGTPFSSEIGDYGIGLQAVA
GASAGWAGEGRINWALLQIHNAVHECAFRVGLSTALGVDDKNLVKLMSLDMNFKGIDLGGNAPQPGSTGDIK
SRSSPGIGALKLIAAEQYGAELTWDKDTNW----------------------------------------
------------------------SQLKDDLDSSKWAAAVRAWDGRRRKILGDRRAQLKARVGDMLVKGKPR
IQRIRLYVFGFS-RGAAEARTFSNWLVDALESDFSLCGVPVSYDFLGIFDTVASVGIAQSAAATLFDGHGGW
ARKELMAVPHYVRRCVHMVAAHEPRGSFPLDLIDCSLEGREEIVYPGVHSD--------------------
-----------------------------------VGGGYGPAEQGRG------------RGDADKLSQVPL
VD-----------MYRAARIAGVPLDIQGPG--ITSEAAD-------------------------------
-------------------------------------------------VFKISAGLKQAFTAYVKASEGYY
```

```
YAKEHGTAGLMRAHYGLYLRWRRMR--------------------------------LKDMSLQPSFKAAQA
NCPQ--------------DAMDIDSANKELRAEWEDLLEIEKEGG-------------------PSVAHYAK
KFGAKVARDNPK--IVASVSAVLLPGVIVFSTR--PEVIYGVRKAGDRVTELVRAQLQEKW-----------
------------------------------------------------------------------------
---------EQWQQVRSDWNMGPPEAPISALYDNYMHDSRAWFKPLGDDD----------------------
-------------DVWNYKQIQELKSKQASFEREHAAWRKRAETGAPGPWQIAQAMSAGASGLGPIAMQPEP
EPRSPLTAQQADLLKRYDAAMQSAKQARAAKDPNAPTDSAVLTDPKVTGG----------------------
-------------------------------------LALQTSGREFYFLWGFLRWRTVFVNGVRWDQPRVP
TVQEEMEGMRMQMQRQVDMKGIGVLFQ-----------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle3
-----------------------------------------------------------------MNDRVR
SRTIVSAQSITLPKGGDVHLVP-------PPPKPCVTIVV----HGVNDLAGCYERIERGLCQGL-------
-------------NERLDMPPTLPGGQANPGYLTPAGYSLPADDEGKAENPDVVYYRRKFASGAGGAAVRSV
VVPFYWGFREEEQYINKTAAHGEWLDRNGNRLDKSGTKEGGQFVNAT-------------------------
------------------------TNLPDMWGQGFNGKLFGFISLDWFGGTMTHPLFSAAGRKYMVLAAMRL
AMLIKIIRKRYPDDTINVVGHSQGTLLTLLAHAFLKDDGVAPADGVIMLNSPYGLFEPLNEKLQGWSSQQTR
EARLATLKGILEFICGRRHPVPALSS------------------------------------------------
-----------------------------------VALRNCQGYGAIG------------GPGWVGGQGCQT
TI---------------DGERLSFDERDNRG--SVYLYFT---------------------------------
-----------------------------------------------------------------PQDQTV
GLANVQGIGWRGIAEQVKGLPGRTG-------------------------------------LPQGFHQRIF
TVRK-------RNGEKEKIGGHAPPHVYPLLLAGEKTWEDTGLGG---------------------KDRFGR
ANFDQGDSVLLT--APRLPLPTEARFDFDGAVT--APGENSASGV---------------------------
------------------------------------------------------------------------
----------------------YQVRDTLDPIDAAIGVSNGGWKEKDSGHAVA-------------------
-------------QQVDAALAYRYGRDARSVERALNEGKELAQQTHVFSARELGTGMVLVTRAETPYEARLR
LQTAEGHLEPLSFHSAIPNNPEHNRRVLAYDLAIGAGDSVDDVVF---------------------------
-------------------------------------YQYLCRVADWRLDWKASDKGIFSQGDASVDLPDEE
VRALYRAEESKNSQLIDATVAYRKSGEFPVVVGNRLPSLVGTQTILDRYHEQAVRFGGTI------------
------------------------------------------------------------------------
---------------------------
```

```
>15A5_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>3027STDY5784958_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB07_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Ab4568_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>Ab4977_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>AC29_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AC30_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>AF-673_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0102_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AYP-A2_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>CBA7_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY--------------------------------------------
------------------------------------------------------------------------
---------------------------
>CMC-CR-MDR-Ab4_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY--------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>CMC-CR-MDR-Ab66_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>HRAB-85_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>JBA13_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB02_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>KAB04_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB05_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB06_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY----------------------------------------------
----------------------------------------------------------------------
---------------------------
>KAB07_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB08_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>SAA14_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>SSA12_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>SSMA17_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK----------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA-------------------------------
------------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>XH386_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
----------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV-----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
----------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY---------------------------------------------
----------------------------------------------------------------------
---------------------------
>XH856_18
-------------------------------------MSKIYIVKSGDTLWGISKKHHISVKELARINSLSG
RMIHNLRIGQKIYLQNDVNNTNNFETQLKIILMDLSFKPI---LKATIQLEFDGKKIIRNTKNSI-------
----------------FEDINIQDHSKGLKVFFKNLNGTFDLIADHKVLPLGRKVLKLTSRKMKVEGSHYAK
DGILNETVNQIMSNLKKVGKPIVESISTTSNKDELKNKQPPLKIPEEKIEQK--------------------
------------------------RTDNGNSTHIIAAQFTEDNFLLKPVNNKYRAYIVNAAKRHGFTPHSLA
AVIEAEAAKIKK-TGEWNTNSKANSSTAAGLTQFLDETWLAMCKDKSSLVG--QYVMNNPKL----TIQQKL
NLRFNAEMAIDAAAAYAISNFKSSGLPYQK------------------------------------------
-----------------------------------LTEPSSIAKFAYL----------LHHEGATGGKNFVL
NT-----------LSQERAKKLLFTQFGKNG--AK--QAA--------------------------------
----------------------------------------------------------------------
```

```
----DFLNRYKGDAKAAYGAWLRNY--------------------------------IDGHINIYQYVVDK
SKTS---------------GINLSTDETIKLLKGQTISTPAPKIS--------------------TTTNNQQ
VTNVSTIEKSES--KIRINTSQAPTNNVGGDNK----WHNPLADCKLRTAGLANAKGATFG-----------
------------------------------------------------------------------------
-----KVRNNGTKNHQGVDLQANPGTKIYAVCGGVIAFAGATGGAYGKV----------------------
-------------IVLKVDINDLPEKQKKYAQTKLTKNKYVYFFYAHLSVIDVD------------------
------------------------------------------------------------------------
-------------------------------------KGDPVDTGEVIGKTGATGNANKMTTISKGAHLHFE
ARSAPLLGVGLDGRFDPIPFINANLPY-------------------------------------------
------------------------------------------------------------------------
---------------------------
>3207_4
-------------------------------------MSNIHIVKKGDTLWGISNKYHIKLNELIEINGLYGR
KKNLLKIGQQIYLKKDNVKKYDTTLVIKIYDLKWEPITHG---KLLLEYDDKCHLATSNDKGVIE-------
------------------DIQIEDALKGIKISFYTLKNKFELIAHHKTLPLGKKILKLSSRAMMIKGNTYKV
EGIPRTNTKTIEKELKVNSKKVQHSSGASGASGASGASGASGASGASGASGASGASGASGASGASGASG
ASGASGASGASGASGASGASGASGASGAS-ETRIEGGLPAVTVAPVYSEENLYLHPDNEKYRKIIIDAAKKY
NLAPQALAAKINAEAGTKKGSQEWNPQAQASTSSAVGLTQFLSGTWYEICTVSTYKDTLLQQYVIKKKLISN
FKENMALKLISNTDKAKLKALGTDPTFSVDSAAAYARANIN------------------------------
-------------------------------------IVKKIYSKIDSLE------------PGDLAKVGYVAH
HD-----------GPTGFGKIVEATNDPSWS--KLQGQVC-------------------------------
-----------------------------------------------------------------------PK
NNPNCDTYLNYKERFSNGRDAYRWW-------------------------------------LCTEYTDSKI
NVNR----------------FTLSPKDGKKFKNARTMEEIIVFLG--------------------GKPLVRP
SRDFEKKGTTDN--SKLNDNINIVITSLVNNKV--QANISYFVKSKYGLKPHSTNVNGHEI-----------
-----------------------------------------------------------------IHA
KKGDKIEILFNDQVIASINAINDKEEFKINFPSKNITNASTEKQSSNSEQKLNF------------------
-------------NRWRNPLNGICQIRRFGYNSLPLKANASSYNEKNLEQATKIASRFNRTSYRASGIHQGV
DLEADNGVNIYPVCVGTIAKVIPAYPGYGKTIILECDV----------------------------------
-------------------------------------NDLPSSKKVLAKNLDTIYFIYAHLNSINVSEGDII
TTLDTVLGKTGNSGNAGSMTRIEDGSHLHFEVRSEIMKSMGKSGMSYRLDPFPWLDNCMTTENGVKVNR---
------------------------------------------------------------------------
---------------------------
```

```
>ATCC17978-mff_4
-------------------------------------MSNIHIVKKGDTLWGISNKYHIKLNELIEINGLYGR
KKNLLKIGQQIYLKKDNVKKYDTTLVIKIYDLKWEPITHG---KLLLEYDDKCHLATSNDKGVIE-------
------------------DIQIEDALKGIKISFYTLKNKFELIAHHKTLPLGKKILKLSSRAMMIKGNTYKV
EGIPRTNTKTIEKELKVNSKKVQHSSGASGASGASGASGASGASGASGASGASGASGASGASGAS-------
------------------------------ETRIEGGLPAVTVAPVYSEENLYLHPDNEKYRKIIIDAAKKY
NLAPQALAAKINAEAGTKKGSQEWNPQAQASTSSAVGLTQFLSGTWYEICTVSTYKDTLLQQYVIKKKLISN
FKENMALKLISNTDKAKLKALGTDPTFSVDSAAAYARANIN------------------------------
-----------------------------------IVKKIYSKIDSLE------------PGDLAKVGYVAH
HD-----------GPTGFGKIVEATNDPSWS--KLQGQVC--------------------------------
-----------------------------------------------------------------------PK
NNPNCDTYLNYKERFSNGRDAYRWW-------------------------------------LCTEYTDSKI
NVNR----------------FTLSPKDGKKFKNARTMEEIIVFLG--------------------GKPLVRP
SRDFEKKGTTDN--SKLNDNINIVITSLVNNKV--QANISYFVKSKYGLKPHSTNVNGHEI-----------
-----------------------------------------------------------------IHA
KKGDKIEILFNDQVIASINAINDKEEFKINFPSKNITNASTEKQSSNSEQKLNF------------------
-------------NRWRNPLNGICQIRRFGYNSLPLKANASSYNEKNLEQATKIASRFNRTSYRASGIHQGV
DLEADNGVNIYPVCVGTIAKVIPAYPGYGKTIILECDV----------------------------------
-------------------------------------NDLPSSKKVLAKNLDTIYFIYAHLNSINVSEGDSI
TTLDTVLGKTGNSGNAGSMTRIEDGSHLHFEVRSEIMKSMGKSGMSYRLDPFPWLDNCMTTENGVKVNR---
---------------------------------------------------------------------------
---------------------------
>Tde1
-----------------------------------------------------------------MSATT
TVAGAGGAIAGGWLGRVIGGLA-------GSLAGPGGTAVGA-WIGGQVGAMAGRAAASAIASYM-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------EDANVDADAKTKES
EQAKPCVDCGEI-DCFSPPEGATPKQVEEFRRQLKEQQDEINRM----------------------------
---------------------------------------------------------------------------
-----------------------------------EPDDLVRNIDKYR------------QQGRPTDDAANR
RQ-----------SREDYRTDRTRELEEKYL--SK--GRN--------------------------------
---------------------------------------------------------------------------
```

```
-------DYKEQAANDVAEEMKK----------------------------------------LAATHTLDLV
AGGD-------------------------GSISGLGDKSINSSLG----------------------SQWKG
RRSEQLRSHAKK--AAEQKKKMNAKLEECKPEG--GNDNSPDAET---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PDNGTGKGDGNPDVPVS----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>TseH
-------------------------------------------------------------MTDTVSSTPVADTT
PYEIFLSGNDDFLIPVVFPDYL-------ISVADEQSFEL---WGVKIKTPAVKAPYLGHAGVIL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----INGETGV-TRYYEYGRYKNPKSDIPGNVRKV-----------------------------------
------------------------------------------------------------------------
-----------------------------------GVSNVTIKSGLIT------------ESSLLKVLKEVS
LR-----------SGQEGRISGVVLRGKFFS--EA-----------------------------------
------------------------------------------------------------------------
-------DSWLRGKMDLNNSP----------------------------------------DKIPYDLDSH
NCMT-------------------------------------------------------------FVIDL
ADAMGLDPAWKP--PVVVPSAYIEQF-----------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------QLSEIDLDYDYKTNKLTVSE---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>KatN
------------------------------------------------------------------------MFR
HVKKLQYTVRVSEPNPGLANLLLEQFGGPQGELAAACRYF---TQGLSDEDAGRRDMLMDIATEE-------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LSHLEIIGSLVGMLN
KGAKGALAEGTE-NEAELYRSLTQNGNDSHITSLLYGGGPALTNSAGVPWTAAYVD----------------
------------------------------------------------------------------------
-----------------------------------TIGEVTADLRSNI--------------AAEARAKIIY
ER-----------LINVTDDPGVKDTLAFLM--TR-------------------------------------
------------------------------------------------------------------------
----------EAAHMLSFEKALHSI-------------------------------------RNTFPPGKLP
PLEK-------------------YKNVYYNMSEGEDVRGSWNSDE-------------------NFDYVSDP
VSAVDGGDGKAS--INLSTKQEAMIKAMATRLK-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------SHEDINPVTGAELAEGEPQTKINSKN--------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tge2
------------------------------------------------------------------------
------------------------------MGPGLLYNH---AAKTAVNGIDRSTEGTNVSARL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----CNNISAV-TFVSKYKAVCQPIAD-------------------------------------------
------------------------------------------------------------------------
-----------------------------------QLDLPVENLLGLA----------AQESQYGTGRIARE
LN-----------NYFSMHAPAPLQIGAEAP--LG--NAS------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IKVAKFDSFQ
KSAQ----------------------------SFASSFGTAVRGQ---------------------RDPMAF
AQALVRSGYNTG--NAKTGGRDGFARYLAD-----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------IIIAVRGRMAC------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Tke7
-------------------------------------------------------------------MSEA
RSFINPHAQSYESLKADTPMNANQRAKFDVLNAHVVNTVV---FPGELIIVGDPSTPSCTAHEAF-------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------------------------LMGKALGIHLDIELNGGGFDGFLLENFELLQSLLARASIGAGTASD
AWSKHLEAIK---KTLEEIEQLHRDYLLKGTLKARDEFYSKRTALFLKLE----------------------
------------------------------------------------------------------------
-----------------------------------AQLDSMATYGVGL----------RNGGKIKHALDIST
KR-----------FLHGGEIKGYAEKISGVA--KAANWIK-------------------------------
------------------------------------------------------------------------
----------KGTYLGMALD-----------------------------------------VASTELSIRN
ACVL----------------GREEECRKAEYVERTSLVASLGLGG---------------------MGGHVG
GLLGPIACVAVG--IPTGGTATFACAVLGGAAG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------GIAGGEFGEVLGESVGEILYEAVR------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>15A34_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-----------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>15A5_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>3027STDY5784958_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Ab4653_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Ab4977_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>ACICU_5
------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>AF-673_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0056_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AR_0102_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>BJAB07104_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>BJAB0868_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>CMC-CR-MDR-Ab4_5
------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>CMC-CR-MDR-Ab66_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CMC-MDR-Ab59_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
----------------------------
>HRAB-85_5
--------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
-------------DVAERYAAGKSVG---------------------------------------------
--------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
--------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
--------------------------------------------------------------------------
----------------------------
```

```
>KBN10P02143_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>MDR-TJ_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>MDR-ZJ06_5
------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>NCGM237_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>SMC_Paed_Ab_BL01_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>SSA6_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>TCDC-AB0715_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>TYTH-1_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>USA2_5
------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>WCHAB005133_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XDR-BJ83_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>XH386_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>XH856_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY---------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>YU-R612_5
------------------------------------------------------------------------
--------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG--------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPSTY-------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Ab4568_5
------------------------------------------------------------------------
---------------------------------ASTNSIG---SYGSVKSASDTYEKYATSKSLK-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DVAERYAAGKSVG----------------------------------------------
------------------------------------------------------------------------
-----------------------------------GSATAGVGVGIYA----------NYKGNGESTLT-ME
RK-----------VGLGYEYGVFERNYHYGE--RQ-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------VNRGYIEGCA
ATGE---------------------SKYCAGSHTDKISPYIYKDE-------------------------YK
SKSKARGITISQ--GKEMVGNPNGPSIIHGPG----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HSWDLGAHGFPST----------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>Tke10
------------------------------------------------------------------------
------------------------------MQRPSALRS---WPGPAAADDCNRAGCCLAGIAC-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------RLHLSRWPAMSSTADWLDQAVEKVADGFGWLRDLVLGEFAEERPLSVV
IADMLLSLVPGV-VIVLSARDLAAVCLRLGKRYAADGSQATPQPPEWQEWV--LLVACLMTL----IAP---
------------------------------------------------------------------------
-----------------------------------IIGAVVGAVGTPV------------GSMAGALVGQEA
AA-----------FLRGLCLLLIRESQVILQ--TVVAFLG--------------------------------
------------------------------------------------------------------------
--KFTRGSVEFWLHQVRFASYEKDL-------------------------------------LAYLNLFLTK
VLAA------------TAKLRSYLGNWPFNQAASHLLVRLQAMEA---------------------QFYAVQ
VHALREIPHALM--QLDARLAKVLEQASDLPAQ----VAQAGVHAQKPEPMAMSAGRVTSG-----------
------------------------------------------------------------------------
------IGMRPRYLERSEGALGPPVPTSPTIAAHGANVHVFDHATATRAQK---------------------
-------------GIYGEVVSDQYMLGKGHENLLSAARGPRSLEMKPTGRGLDGVYRNAHPPPPFIITETKY
RTGGTFSPGSLPVTKGSKGFP-----------------------------------------------
-------------------------------------SARQMSDAWIEPRLDLDLGKKQAEEIAFSGYERWL
MIVDESGVVTKIVKLDEHAKFVGNVIH-----------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tke6
-------------------------------------------------------------MRVSLDGLGQAV
DGDVTTTGAICIATGEGYLDEGRMVLRMGDPTTPCPLCGL---EGKVVEGVWHFISDGQPVAMDG-------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------ALVDCGCPEGSNRVVAPLG
EMPPPRLPVAVR-TSLTPAGPGSSSALAGASPAMVGGLPGQMQPGFYVVPR--SMSFP--------------
------------------------------------------------------------------------
-----------------------------------QILLELASHDSTL------------PISYLQRLNPTF
EQ-----------GFKAGEIFVIGDPDNGYA--CT-------------------------------------
------------------------------------------------------------------------
```

```
--------QEEGQLMAAAERARRSL--------------------------------AVLDFAESDFMMEY
QAEI----------------AGLLSDASLSMGVGKDMMDHGLRQL---------------------RSTLGN
IERLHQQEFLRH--GHLNSPSFFAERRLLLEQL--DGQLKATFLNKHLNLGAYERLKKSLN-----------
------------------------------------------------------------------------
--ISTKSLVHHWSKAGGPGQIPGYATYLDKVAKLSKYLRYGGHVGIGLGGTS--------------------
-------------SYLKVQEACRAGETEGCKKIRLSEAGA--------------------------------
------------------------------------------------------------------------
-------------------------------------FAGGLAGGIVGGKIAGITALAVCGVFSAGTAGFGA
PVCGIALVGGGAFAGSIAGAEGGEQMGELIYESHYD-----------------------------------
------------------------------------------------------------------------
----------------------------
>Tke2
------------------------------------------------------------------------
-------------------------------------------------------------ECWST-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------ARKNYWKAEAKAP------------TRAYSPTNLVRM
AE----------------------GKAPKMT--VE-----------------------------------
------------------------------------------------------------------------
--------VISRKTDKISIREYALE-----------------------------------LHHNDIPQRV
GGAG--------------------VHDSSNLLALTPWEHEAVDQF---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------RHVGSDLIRVIKGVDVW-----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>TecA
------------------------------------------------------------------------
----------------------------MQLTQLGGHVA---QSGIAERQKHAQALMFGMANID-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------EYVSRGVCYDAA-------------------------------------------
------------------------------------------------------------------------
-----------------------------------AYVRYLLRADALI------------APDALLDT----
-------------AGQSWRTRFNFETGDQWD--GR-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------ASIP
AGTA------------------------VGFARGGNVFHAAIAVG------------------------GTR
IRAINGGLLGAG-------------------------WMNPVDLA---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------RALQPDPAGGFTYDRTTIRVHLSRL----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tse1
------------------------------------------------------------------------
-----------------MDSLD-------QCIVNACKNSW---DKSYLAGTPNKDNCSGFVQSVA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------AELGVPMPRGNANAMVD------------------------------------
------------------------------------------------------------------------
-----------------------------------GLEQSWTKLASGA----------EAAQKAAQGFLVIA
GL-----------KGRTYGHVAVVISGPLYR--QK-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------YPMCWCGSIA
GAVG----------------------QSQGLKSVGQVWNRTDRDR---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LNYYVYSLASCSLPRAS------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tse3
-----------------------------------------------------------------MTATSDL
IESLISYSWDDWQVTRQEARRV------IAAIRNDNVPDA---TIAALDKSGSLIKLFQRVGPPE-------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------LARSLIASIAGRTTMQRYQARNALIRSLINNPLGTQT
DNWIYFPTITFF-DICADLADAAGRLGFAAAGATGVASQAIQGPFS-------------------------
------------------------------------------------------------------------
-----------------------------------GVGATGVNPTDLP------------SIAFGDQLKLLN
KD-----------PATVTKYSNPLGDLGAYL--SQ--LSP-------------------------------
------------------------------------------------------------------------
-------QDKLNQAQTLVGQPISTL-------------------------------------FPDAYPGNPP
SRAK-------------------------VMSAAARKYDLTPQLI---------------------GAIILA
EQRDQTRDEDAK--DYQAAVSIKSANTSIGLGQ--VVVSTAIKYE---------------------------
------------------------------------------------------------------------
---------------LFTDLLGQPVRRGLSRKAVATLLASDEFNIFATARYIRYVA----------------
-------------NLASQQDLRKLPKTRGAFPSIDLRAYAGNPRNWPRDNVRA-------------------
------------------------------------------------------------------------
-------------------------------------LASEYTSRPWDDNLSPGWPMFVDDAYATFLDPGMR
FP----------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Tse6
------------------------------------------------------------MDAQAAARLG
DEIAHGFGVAAMVAGAVAGALIGAAVVAATAATGGLAAVI---LAGSIAAGGLSMFQIVKGLTTI-------
----------------FELPEPTTGVLIRGSFNVYVNSRNAMRAGDDVSA----------------------
------------------------------------------------------------------------
------------------------TCSGLPLNHPLWPFPVLIAEGSATVYINGKPAARLQSKMVCGAHIKTG
SQNTFIGGPTERVAFVLDLEEWLHTGLEALGLAALAGGLLLAAMAGVAALV---------------------
------------------------------------------------------------------------
-----------------------------------GVVAIGGLMMGGM----------ALLGDLGDRLGPGY
RD-----------LFQGVAGMALLGFGPKLA--GR-------------------------------------
------------------------------------------------------------------------
----------RPAAVTSETAQRRAY-------------------------------------LNNKFGRSGN
LDHD------------------------INYRGNRETAAKFFKSK-----------------------DIDP
ADAESYMNGLDF--NHPVRVETLAPGKNLWQYQSPGAPQGNWYTL---------------------------
------------------------------------------------------------------------
-------SPRVQPTELGINPMGTNRAANTIEPKVLNSYRTTQKVEVLRSTAAPTD-----------------
-------------DFWSVKGQSYPAKGGAQQLFSNEKGSFGLLPREGS------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>TseM
------------------------------------------------------------------------
-----------------------------MRRRQRASRAG---VVARRATPGDAQANSGRAPAR--------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------------PFQSFV----------------SNGAMLMN
KQ-----------IVAGIVAGLVSMSSHAQ-----------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGQLFQSVKE
QVTQ----------------------------AATSQVNQGVRSA----------------------TDEAVQ
ATSSRTRKAINS--VRSPSSAAAATSTSPSAAE---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ETNDATLSEARK-------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>VgrG-5
--------------------------------MSSSHRHYADTALADVAALTDAASRADAAPLANARRFTFA
STAYDAATFDVVDIDGRDAISQPYRFEITLVSRSVRIDFA---KMLSCEATLAILPPFGEAGTTR----YAG
VLAEFEQKERFRDFTVYRAALVPRLWRLSLYKASDVYLNEQTIPDIVKRVLRAASFGKRNFRMRHRGVYRKR
SFVCQYDESHLDFVSRWMEKEGLYYYFEHDGRREKLEIVDDRRDQPGPADDLALRYLPATCLD---------
------------------------AGIESDRVQAFACRATPLPREVVLRDFNHRKAELSLEVREHVAHDGVG
ERVSSDEHFHTKDEGRRYAKLRAEALVCEGRRFAGESTAAGLRAGRFFALSGHYRKDFDGRYLVTAVTHRGS
QAHLLFPDLDAPFGATPGEPVYRAEFEAIAANLQYRPPRTTPKPRAA-------------------------
-----------------------------------GVVSAIVDGEGSG------------KRAELDEHGQYK
VR-----------FPFAHTAHPTNKASARIR--MATPYAG--------------------------------
-----------------------------DDRGMHLPLLKRTEVKIAFDGGDPDRPVIVGAVPNSSHRSVVT
RSNPDAHRILTEHNQLYMKDGSGAA--------------------------------TWLHAPNNHIGIGA
VGPG-----DGLALLTSGNKFDFSLGNAYSFSGGLKCSVSMGGNT---------------------DIYVGV
RNSLDVSANFLT--TLQGNLRWMLPGSRSFEIN--DSASTLLQTLHKQSATGAIRLSAGQD-----------
-----------------ASALLQKQLDKLKGTVRKFMIVSGLANAGAAATAAGLIKGGGALADLPWAGFGVS
AAQFAGATGFSTALMATSRTLLSKIAKLQEALPLVADLSLDKQGIALAAKNLTHATRMSLTVDGVSWSTHAK
GPGAAGAAMSVGKGRWGVEAAEHAHVHANDTLLFAVPADPTSKFDLKELIGLRRDLDECVKGIADLEADISE
NEVLSTDQNTFGVGALVPTPPSPANAVAAVAIKAKEAKLVELNAKRKLVA----------------------
-------------------------------------TKIDNLQQKLAKHAKNLSAARMSASDAEVGFKGNR
LVATAEGVTLAHAQGKAKLDVREAKIGVEAGKSSLELDESKLAAGCGGASLKLGSDGAIDVRATNVKLNGSA
SLKLDGQLIQLG--------------------------------------------------------------
----------------------------
```

```
>AB030_22
------------------------------------------------------------------------
------------------NSKK--------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV----------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AbH12O-A2_22
------------------------------------------------------------------------
------------------NSKK--------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV----------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AF-401_22
------------------------------------------------------------------------
------------------NSKK---------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AR_0063_22
------------------------------------------------------------------------
------------------NSKK--------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV----------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0101_22
------------------------------------------------------------------------
------------------NSKK--------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV----------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>IOMTU433_22
------------------------------------------------------------------------
------------------NSKK---------------------TPAQLTADRARFELGKTSGAAA-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------DLQVGNV------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------NITGISGRVGKNV------------HPQLKKALRDVP
KE----------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------EQAPWHGACA
EVDA---------------------------INKALKKGMNIEGA---------------------TIDVVN
INSNDKRHGTHK--PACSSCSNVLKQFGVKSNE--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------K----------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>Tse4
------------------------------------------------------------------------
--------------MSQLPIPL-----------PLNESRW---RYVTASGGGMTVAFLAGSGGSI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------TLLSPEGENVSFRYGGVGGGIGLG-----------------------------------
------------------------------------------------------------------------
-----------------------------------MRLPRFGKVNLNV------------KGKSVGGAGALE
-------------ALPSTGTVLVADGLVGRD--LS-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------RGDFTGPCM
YVEL-----------------------GAGVIAGGSGTAILFGLD---------------------PKLLAA
VALASASPLTAA--LGASMSRQLLQSSRGAL----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LMAGVNVGAQFGGGAAAYLGALF------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>VgrG2b
---------------------------------------------MRQRDLKFTFVVGEGKLAFDVVEFELEEA
LCEPFRLNLKLASDKNAIDFKQ-------VLDQPGTFTLWQDGRPARYVHGIVSHFTQGSSGFRR-------
---------------TRYELLLEPQLARLELCCNWRIFQEKSVPEILQALLKEHRVLDYEQRIYHEHLPREY
CVQAGDSDHYLHDRLAFEEGLVYYFRFDEHRHTLVCSDRLYVQERIAGGPVLF-------------------
------------------------SAQPEGDNPQPVLHSFRYSENVRTARQTQRDYSFKRPTYDQEHHLAGE
ALEHQGSSYERY-DYPGRYKRSGAGRPFTESRLRGHRRDARVASVSGDDPRLIPGHAFALEGHPRADFNAWW
RPVRVVHRGTQYAGQEEESADAPLGVSYDLRAELVPEDVEWRPAPLPRPRIDGPQ----------IATVVGP
AGEEIHCDEWGRVKVQFPWDREGRHDEFSTCWIRVAQNWAGADWGHMA------------IPRIGQEVIVDY
LDGDCDQPIVTGRTYRATNRPPYALPDHKILSTIKSKEYK-------------------------------
------------------------------------------------------------------------
```

```
-GSRANELRIDDTTAQISAALMSDH--------------------------------GASALHLGYLTHPR
PEGG-------KPRGEGFELRTDEHGAVRAAKGLLLSTEEQLRAG---------------------AGHLDR
GVVVQVLEAALE--LARELGDYAGEHQGVGHDAAPQQTLQEAVRDLGHGANDESGKSNGGKPAIALSGPAGI
AAATPASLTLAAGEHVDSVARQNQQVTAGQKVVINAGSDIGLFAQGGELRQITHQGPMLLQAQKNDIRLEAK
QSVEVSASQQHVLVTAKEHITLMCGGAYLTLKGGNIELGMPGNFVVKAAKHSHVGAASLEAEL---------
-------------PQFEVGETQRRFVLKQLDGQTAMPNVPYTITMANGEVIEGVTDAEGATQLLQKDAMNIA
KVDMKHTKSPASAVAGIAAAVGAAVAVGKLLGGPDAEAGRALSE----------------------------
-------------------------------------GEISLAKGVFGDSIDYSTVRLRDEDYVPWQGKDYV
MAPNGHIYFGEELRGVADWSLESLQRQGLFIHEMTHVWQHQHGVNVLLVGAYQQARQFLLGDQYAYRLEPGK
TLKDYNIEQQGDIVRDYFLEKNEFGEASANSRFAGVLKNFPTGY----------------------------
---------------------------
>AB031_26
-------------------------------------------------------------------QPVGG
KKSGLGIGFLFPNTMAGFAKNP----------EDARNLRA---LGAIRNNNLAAASVAGYGPYVV-------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------AGTAAAGSAAAPVVGRVAAPFIGTGAQLEGAGLTAG-----------------------
-------------------------------------------------------------------------
-----------------------------------TVGKAAVTSAGIG----------GGMDVISQGVKCKC
LK----------------DINLVRTGGVAAV--SA-------------------------------------
-------------------------------------------------------------------------
-----------------------------------------------------------VTSGWGATTS
AAAG--------------------------------FGQVGWKSI---------------------------A
LNAPNMGQFLKN--NASGMVIFANEQMIGQAGS-----------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------RAVKAATEKDKSSKK-------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
-------------------------------------------------------------------------
---------------------------
```

```
>VgrG1
-----------------------------------------MADSTGLQFTVKVGALPESTFVVAEFALDEG
LNRPFNLRLELASAQPDLDFGA-------VLDQPCELLVW---YNGELQRRVCGVVSDFAQGDSG-------
------------FRRTRYQLLVQPALWRLSLRQNSRIFQAQKPDEILSILLQEHGITDYAF--ALKNEHAKR
EYCVQYRETDLDFVNRLAAEEGMFYFHEFEAGKHRIVFADDAAALTAGPELFFNLGNRS-------------
------------------------LEQGPYVRQFHYREAVRPSDVELKDYSFKTPAYGLSRKKVGVELTHQR
DTYQHFDFPGRY-KEDPTGKAFAQHRLDALRNDAVAGSGKSNSAALLPGQT--FSLTEHPNG----SLNTDW
QVVHIRHTGLQPQALEEEGGSGPTVYHNEFSVVKASTTWRARIGSPEAPHKPMVDGP-------QIVTVVGP
DGEEIYCDEHGRVKLQFPWDRYGSSNDQSSCWVRVSQGWAGGQYGMMA------------IPRIGHEVIVSF
LEGDPDQPIITGRTFHATNRPPYELPANKTR--TVLRTET--------------------------------
-------------------------HQGEGFNELRFEDQAGKEEIYIHGQKDLNVLIENDAAWHIKHDEHRD
IDNERVTRIKANDHLTVEGEKRDQI--------------------------------KADYSLTVDASLHQK
LGQSLLMEAGSEVHHKAGMKIVMEAGAELTLKVGGSFVKLDASGV---------------------TLSGGS
IKMNSGGSPGSG--SGWGGKAPIQPGNVEVPTP---PPATLPAPAIHKSMESMAPLAKPCP-----------
-----------------------------------------------------------------AAPPPVPPP
PAGGPPAPPPAPPQLAGGPMMPPPPPPVAATGEGKKSAKKWATVEISKADEALRYYSAQGY-----------
-------------TLLNNYLRDRPYKQREAIDTLLSRSYLNDEPTSASEFDQAMKAYVADVEAGLAKLPASP
DLDFVYRGLALDKPELAALKDQFTGVGNIIVEPGFMSTSPDKAWVNDTL-----------------------
-------------------------------------LRIRLPAGHGGRLLGEAAHFKGEAEMLFPTQTRLR
VDRVVSSMSGDFDSLLNTIPTSDNASDNRSRIKRLIEVSVL------------------------------
-----------------------------------------------------------------------
---------------------------
>VgrG-1
-----------------------------------MATLAYSIEVEGLEDETLVVRGFHGQESLSNSVFLGQ
ACYGFRYEVQLASRVSNLTAEQ-------MVDKRAELKLY---RNSQLVQRVHGIVRAFSQGDIG-------
------------HHHTFYQLTLVPALERLSLRHNSRIFQKQTVPEILSILLQEMGINDYAF--ALKRDGVQR
EFCVQYRESDIDFLHRLAAEEGLVYSFVHEA-------------GKHTLYFSDASDSLSKLPEPIPYNALVG
G------------------------AIDTPYIHGLTYRTQAEVSEVQLKDYSFKKPAYSFLQTVQGTELDYQQ
TRYQHFDAPGRY-KDDVNGAAFSQIRLDYLRRHAHTATGQSNEPLLRAGYK--FDLQEHLDP----AMNRDW
VVVSINHQGEQPQALQEDGGSGATTYSNQFSLIPGHLHWRAEPQPKPQVDGPM------------IATVVGP
EGEEIFCDEHGRVKIHFPWDRYSNGNEQSSCWVRVSQGWAGSQYGFIA------------IPRIGHEVIVEF
LNGDPDQPIITGRTYHATNTPPYTLPEHKTK--TVLRTET--------------------------------
-------------------------HQGEGFNELSFEDQAGKEQIYLHAQKDFDGLIENDHTTVIRHDHHLT
```

```
VENDQFTQIKHNQHLTVEWESREAV-----------------------------TGEQVLSIEGSLHVKTG
KVWV--NEAGTEIHVKAGQKVVIEAGSEITVKAGGSFVKVDPAGV---------------------HLSGAL
VNLNSGGSAGSG--SGFGGAMPALPGGLEPAVA--LAPPQTISYQALLQAEQANVPAVKVCPLAAQEATPAV
NSITPPPPPPIAPPMAPPQPIMNPQPTANAQPNLGRSTKATPDFPTHFPKSSIGIENELAGLVVAMPANSAQ
KFGYVKSAQGDALFMLTKDMNQGSYQRPPSLQDGKNYQNWQTHTVELVSYPCEMDDKAAVETRKQAMLWLAT
HFTTHIDQSNHQ-PLAPIQSEDGRFVIEITNAKHVIAAGNGISAESQGQTITMTPSGQQATVGVAAKGFGTS
ATPELRLLESAPWYQKSLKSQFASLTSAENLDDKELAANVFAYLTSIYLKTAELA-----------------
-------------------------------------KKFGIYINEWDPMSEQITPNANGLTDPKVKNAWEI
LPRTKPSKIVEILSKSDAKAVMKHIKPQLQSRYSESLSKNVFQYFQDGGEVAGHGINNATVGDKHSPELAIL
FEFRTVPNELQSYLPKTESTTKSEVKLLDQFDPMKRKTVIQQVESLVQNSGDAFDKWYQSYRDSMNQPPVKN
AKKIASANQKAQWVKEHNPQEWQRIIA
>VgrG-3
-----------------------------------MARLQFQLKVDGLEDESLVVRGFEGQESLSDSVWRCE
PCYGFRYQVDLASALSNLTAEQ-------FVDQTAHLTIL---RDGQVVQQINGIVRQLSKGDTG-------
------------HRHTFYSLTLVPALERLSLRSNSRIFQQQSVPEIISILLQEMGIEDYAF--ALKRECAQR
EFCVQYRETDLQFLHRIAAEEGLVYSHLHEA-------------QKHTLLFTDSSDSQPKLAKPVPYNALAG
G-----------------------EINLPYVVDLQFKTTAQVSHTELKDYSFKKPAYGFTQRTQGKDIAYQQ
PNYEHFDAPGRY-KDDANGKAFSQIRLEYLRRDALLADAKSDEPLLLAGVR--FDLQDHLDH----AMNRDW
LVVQANHQGTQPQALQEEGGSGATTYSNQLKLIPAHITWRARPCAKPQVDGPM------------IATVVGP
QGEEIYCDNFGRVKVHFPWDRYSSSNEKSSCWVRVAQEWAGSQYGSMA------------IPRVGHE---VI
VS-----------FLNGDPDQPI-ITGRTYH--AT--NTAPYALPDHKTKTVLRTETHQGQG----------
------------------------------YNELSFEDQAGSEQILLHAQKDWDALIEHDHTEVIRHDQHLT
VDNDRFTRIQRNQHLTVEGEVRSKI--ALDSSHEVGASLQHKVGQRI-----------A---VEAGKEISLK
SGAK----------------IVVEAGAELTLKAGGSFVKVDAGGV---------------------HLVGPA
INLNAGGSAGSG--SAYGGQLAAAPRMLAQAKP----VAELVQPDIAASMQSGAARVIDVA-----------
-------------------------------------------------------------SLPTMMPS
SANNTANDEPVAEEKTPERILKSDLLKPSDELEKLAKRQASAYRQGNHSDEVKLLQEALIKLGF--------
-------------DLGKAGADGDFGSKTKTAIEQFQKSYQPSHQTHPSYSIGAVDGIVGKGTLLALDEALMD
GWVYENNIYQIWPLGKTSEKYESAGRGPGVISTGNGDYGGASYGCYQMSSNLGVVQKYIQSSKFKEFFSGLN
PATKEFNVVWQDIASRYPQEFREEQHQFIKRTHYDIQIGHLRGKGLLFEHNRAAVHDLIWSTSVQFGGRTNL
IFNALNGQNMESMTDKDIIILVQDYKLVNTERLFKSSPSWWSDLKKRAVSEKKALLELEIDGLEVDIK----
---------------------------------------------------------------------
---------------------------
```

```
>AR_0078_29
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------EVKNQRTGQVI---AAGTTNSSGCIVEISRDKGTAL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLNLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRVLERLNKIDDPNKISIGQVIKLPVHIPASG------------------------
------------------------NHSHQDKPKHKHSAQSTNKPTASSTKTTPAPAAKRPANPASQTKQENG
LPEKAHQLYEDT-KKALNEAASSVSKILTIDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC-------------------------------------------------------
-----------------------------------IRQFQRDYMGVPD------------TGKICGSVLVAL
DQ-----------FYDEYPISSFMGKAACNC--GKCSGFG-------------------------------
-------------------------------------------------------------NGKMGVQSGINTA
NEYPGIHRSLIWILKSLNFYLK---NEF--KDKK----------------------------INVAYIESGY
RCIE------------NNKKHERTSVNHMGLALDIHFHKNGVRTR--------------------ELSDMEF
IRKNIMAKKMGASEQRIRDKIYLEPKVFRSGEAGATSWVHFDITM---------------------------
-----------------------------------------------------------------------
-----FLAKYFNNNMFKTKVSDLNGVKLVNLAASSRILSCGGIVALPKSQNNITDEL---------------
-------------VLSNEDIIDIMKVTETEVIKFKTEKYFLEQAAGVVDTIMNRTKSGVWGNSVRKVVNADR
QFSKITGPKSLDPYGSVENMPMSHVSRKVRNFVNSYLL----------------------------------
--------------------------------------ERANGKKSIIGENLNYANKYYSDEKNRKAWVDKFH
NEAVKNGMILGTGKAIHAHGTVRELRDKMPKPFKIVLPKDFKGI----------------------------
-----------------------------------------------------------------------
---------------------------
>AR_0088_14
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------VVKNQRTGKVI---AAGPTNSSGCIVEISQDKGTTL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLDLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRALERLNKIDDPNKISVGQVIKLPVHIPASG------------------------
------------------------NHSHQDKPKHKHSAQSTNKPTASSAKTTPAPAAKRPANPASQTKQENG
LPEKAHQLYEDT-KKALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC-------------------------------------------------------
-----------------------------------IKQFQRDYMGVPD------------TGKICGSVLAAL
DR-----------FRDEYGIASYFESMKCPC--GECSGFG-------------------------------
----------------------------------------------RSRSGNFRFEMYNKTTRQYVEVYRDA
```

```
KEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIVKISSGYRC--------------------IDNNWKNRRP
TTNH---MGCALDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTS-----------------LGWSPDKFGL
ERISDGAKTWVHLDVREFNKKYKIDKLFSTSKD--GLNGDYLINLFKADEKANKILGCSGI-----------
------------------------------------------------------------------------
---VVSPNKNPNLNDSSLEDLIRQLGSVISHGEGNYESYNTGTKNVKGDKVGYSFKNPGKGTVTS-------
-------------KRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFTGSEVYDANMQEQVFR
EFLISKRTKLSQFVRKGIGSLRDAQYDAAQEWASVAVP----------------------------------
-------------------------------------KGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVL
EILEKIHRFHKDGK----------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CIP70.10_14
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------VVKNQRTGKVI---AAGPTNSSGCIVEISQDKGTTL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLDLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRALERLNKIDDPNKISVGQVIKLPVHIPASG------------------------
------------------------NHSHQDKPKHKHSAQSTNKPTASSAKTTPAPAAKRPANPASQTKQENG
LPEKAHQLYEDT-KKALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC--------------------------------------------------------
-----------------------------------IKQFQRDYMGVPD------------TGKICGSVLAAL
DR-----------FRDEYGIASYFESMKCPC--GECSGFG--------------------------------
-----------------------------------------------RSRSGNFRFEMYNKTTRQYVEVYRDA
KEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIVKISSGYRC--------------------IDNNWKNRRP
TTNH---MGCALDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTS-----------------LGWSPDKFGL
ERISDGAKTWVHLDVREFNKKYKIDKLFSTSKD--GLNGDYLINLFKADEKANKILGCSGI-----------
------------------------------------------------------------------------
---VVSPNKNPNLNDSSLEDLIRQLGSVISHGEGNYESYNTGTKNVKGDKVGYSFKNPGKGTVTS-------
-------------KRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFTGSEVYDANMQEQVFR
EFLISKRTKLSQFVRKGIGSLRDAQYDAAQEWASVAVP----------------------------------
-------------------------------------KGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVL
EILEKIHRFHKDGK----------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>HWBA8_14
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------VVKNQRTGKVI---AAGPTNSSGCIVEISQDKGTTL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLDLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRALERLNKIDDPNKISVGQVIKLPVHIPASG------------------------
------------------------NHSHQDKPKHKHSAQSTNKPTASSAKTTPAPAAKRPANPASQTKQENG
LPEKAHQLYEDT-KKALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC-------------------------------------------------------
-----------------------------------IKQFQRDYMGVPD------------TGKICGSVLAAL
DR-----------FRDEYGIASYFESMKCPC--GECSGFG--------------------------------
----------------------------------------------RSRSGNFRFEMYNKTTRQYVEVYRDA
KEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIVKISSGYRC---------------------IDNNWKNRRP
TTNH---MGCALDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTS-----------------LGWSPDKFGL
ERISDGAKTWVHLDVREFNKKYKIDKLFSTSKD--GLNGDYLINLFKADEKANKILGCSGI-----------
-----------------------------------------------------------------------
---VVSPNKNPNLNDSSLEDLIRQLGSVISHGEGNYESYNTGTKNVKGDKVGYSFKNPGKGTVTS-------
-------------KRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFTGSEVYDANMQEQVFR
EFLISKRTKLSQFVRKGIGSLRDAQYDAAQEWASVAVP----------------------------------
-------------------------------------KGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVL
EILEKIHRFHKDGK----------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
>R2091_14
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------VVKNQRTGKVI---AAGPTNSSGCIVEISQDKGTTL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLDLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRALERLNKIDDPNKISVGQVIKLPVHIPASG------------------------
------------------------NHSHQDKPKHKHSAQSTNKPTASSAKTTPAPAAKRPANPASQTKQENG
LPEKAHQLYEDT-KKALNEAASSVSKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC-------------------------------------------------------
-----------------------------------IKQFQRDYMGVPD------------TGKICGSVLAAL
DR-----------FRDEYGIASYFESMKCPC--GECSGFG--------------------------------
----------------------------------------------RSRSGNFRFEMYNKTTRQYVEVYRDA
```

```
KEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIVKISSGYRC--------------------IDNNWKNRRP
TTNH---MGCALDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTS-----------------LGWSPDKFGL
ERISDGAKTWVHLDVREFNKKYKIDKLFSTSKD--GLNGDYLINLFKADEKANKILGCSGI-----------
------------------------------------------------------------------------
---VVSPNKNPNLNDSSLEDLIRQLGSVISHGEGNYESYNTGTKNVKGDKVGYSFKNPGKGTVTS-------
-------------KRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFTGSEVYDANMQEQVFR
EFLISKRTKLSQFVRKGIGSLRDAQYDAAQEWASVAVP----------------------------------
-------------------------------------KGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVL
EILEKIHRFHKDGK------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>TYTH-1_14
-----------------------------------------------------------------------MN
KKSLVTIQILDLFGSPISKAQY-------EVKNQRTGQVI---AAGTTNSSGCIVEISRDKGTAL-------
---------------DVYIKSMFKGSMVKVQSFVMSKDRMVVKITSPKVLLNLKTLTNQGNNGQYKRKTHIV
KKGDTLFEIAQKNHTTVRALERLNKIDDPNKISIGQVIKLPVHIPASG------------------------
------------------------NHSHQDKSKHKHSAQPVNKPTASSTKTTPAAAAKRPANPTSQTKQENG
LPEKVHQLYEDT-KKALNEAASSASKILTVDDRSQDGGTPKANTTNICKTNPQCISSGKSELIREVNIRLAG
FGGALPTDEFTELTATC---------------------------------------------------------
------------------------------------IKQFQRDYMGVPD------------TGKICGSVLAAL
DR-----------FRDEYGIASYFESMKCPC--GECSGFG--------------------------------
-----------------------------------------------RSRSGNFRFEMYNKTTRQYVEVYRDA
KEYNGMHRSLIWALKAMLFYFKKMPNSAGYKIVKISSGYRC--------------------IDNNWKNRRP
TTNH---MGCALDIVVHNKNNQVVSMSELENQVRIKWFGKYLNTS-----------------LGWSPDKFGL
ERISDGAKTWVHLDVREFNKKYKIDKLFSTSKD--GLNGDYLINLFKADEKANKILGCSGI-----------
------------------------------------------------------------------------
---VVSPNKNPNLNDSSLEDLIRQLGSVISHGEGNYESYNTGTKNVKGDKVGYSFKNPGKGTVTS-------
-------------KRIQQIIDNAEAKDGNDKNRLFATGKYQTTYYTLQEGIKQGYFTGSEVYDANMQEQVFR
EFLISKRTKLSQFVRKGIGSLRDAQYDAAQEWASVAVP----------------------------------
-------------------------------------KGLPLKNGKISDGNKSYYEKPGQNSSSPESTKMVL
EILEKIHRFHKDGK------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>6200_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA--------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>A1_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA--------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>A388_15
------------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA------------------------------
------------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>A85_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB0057_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>AB030_15
----------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
----------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA------------------------------
----------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
```

```
>AB307-0294_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB5075-UW_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>AbH12O-A2_15
----------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
----------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ----------WTGEYYISGSKDSLLIPV--AK--SVA--------------------------------
----------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
```

```
>AF-401_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0063_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>AR_0078_15
----------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
----------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA------------------------------
----------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK---------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
```

```
>AR_0083_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0101_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>D36_15
------------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA------------------------------
------------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>IOMTU433_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>USA15_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA-------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>WCHAB005078_15
------------------------------------------------------------------------
---------------NSFNYGE---------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ----------WTGEYYISGSKDSLLIPV--AK--SVA--------------------------------
------------------------------------------------------------------------
------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMTMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT-------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>SDF_15
------------------------------------------------------------------------
---------------NSFNYGE--------------------MFGIPASAQSGLAYQGQRNY---------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------ECYAETGELCKI-------------------------------------------
------------------------------------------------------------------------
-----------------------------------KVPPLFDYVACSG-------------GGLGIGVGFVK
NQ-----------WTGEYYISGSKDSLLIPV--AK--SVA--------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------QNKQFSAKDL
AGAS-------------------CVGGNIHNIPSYTKTTMAMGEI---------------------TNEFVS
GASVTVGGGAYG--AVANVVVPLVSKSSPVKGT----WASELGVGT--------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------PGFNVGVSGTVSVDTILDAVKPSKK----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle5
MLQKKPYNGLHEKELNQINQQDGSPCVAISAPGCFIKGSNLFSEKRAGNRVRFFTTGRDYFSDLASALDSAS
SSIFITGWQVNYDVLLDGRRSLWQCLRQALERSPALKVYV---MPWLSPSGSLGTYDFETMLAVF-------
----QLNAGLEGGARAFCTPAIQQSDMQGLGVAFSHHQKSVVIDNRIGYVGGIDLAYGRRDDNDFSLDASGR
RGNDAYNPGLPHLGWMAEDEHVSSMGLMMATLFDLSRPLASLTLHAPTLRLSPFPHIAASDEPLLSIPLAPS
RARALNGAAY--------------LSDLFRSPMLPSLQWLGRAYNSSKEGLDEGFERLDALRRQMVASSIRA
IANLIADNLDAL-PIEPELERRLRAWLEELRTAALNLPEALRIKSLLLINQWMSETELGQVLTLISGKGFED
IPQNLSGKAGELAGSLFWTLHRLMQARAGGHQQPYRYLDEAPQPLASPDNARLAADQPRMPWQDVHCRIEGP
SVYDLAR----------------------------NFIDRWNGQQAYL------------AKTPALQDTALV
RSALEAVMKWLNSLAAAAGLENYLDEKRNLR--LELDPPTPCWINAPEQLPQEPEVRRGGMTVQVLRSAAAR
MLEQEQAGRLGAGVNLPLQVGVSTEGVQSNCKDAMLLAISGAQQFIYIENQFFQSEFGKEGEVFKDLPLSGP
```

```
MASLRDVGSLRRDFVVRIRLEEALE--------------------------------QRDLWLLDWAEVEK
IAQE-PGTEARQFLKSMLAMWGVNAQGWLTHKLGEAQHGLLNEIG-------EALARRIERAIQREHPFHVY
LVLPVHPEGALN--VPNIMHQVHLTQQSLVFGE--QSLVKRIQRQMALKALEGKSDPAQAR-----------
-------------------------------------------------------EIIERKDARGRPVYEQQD
WSRYLTLLNLRTWAVLGGRVVTEQIYVHSKLLIADDRVAILGSANINDRSLQGERDSELAVMVRDSEPLTVR
LDGKNDAIVGKAIHQLRVNLWKKHFGLSQGPGGFVKPASELSAYLSIPAAQEAWEAIQTLAKENTRAYERTF
NFIPQNISQTQLQLTPEPPKGFEDGFPASIWPTWAYRKPGELRA----------------------------
-------------------------------------GGQLMEPMPYQEIFWRSSNLTSVKTFPPPNGVSGF
ITALPTSWTRGERNDSGLNLSILAHQDSRSLPTQVAMNGDSSAQGKHRT-----------------------
----------------------------------------------------------------------
----------------------------
>6200_17
-----------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVISSKILLDNIILAKS-------------
----------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSSISHRFNCKTSEIVHLNKLKNPDHIDV
GQIIKIPYKGES-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
----------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
----------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
----------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NQTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM---------------------------
----------------------------------------------------------------------
----------------------------
```

```
>ZW85-1_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVISSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSSISHRFNCKTSEIVHLNKLKNPDHIDV
GQIIKIPYKGES-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM--------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NQTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT---------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>A1_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
```

```
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>A388_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
```

```
>A85_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ--------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT---------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>AB307-0294_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ--------------------------------
------------------------------------------------------------------------
```

```
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>AB5075-UW_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AR_0083_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM--------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT---------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>AYE_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
```

```
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
>D36_17
------------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
------------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
------------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
------------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM---------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
------------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT----------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
------------------------------------------------------------------------
---------------------------
```

```
>WCHAB005078_17
-----------------------------------------------------------------------MN
KKGLIQFRFVELFTGNNIPNLY-------HVIKNEKGTTI---ASGMTNSNGLTVMISRDVGDTL-------
---------------YVYLKNIITGDLKEKVRHTVIYKKEIVRVTSSKILLDNIILAKS-------------
-----------------------------------------------------------------------
------------------------TNKPGNYRYLTHKVKKGENLSLISHRFNCKISEIVHLNKLKNPDHIDV
GQIIKIPYKGGS-SDSKKSPDNKQSKHENNKSSSTQKVNSHENNNKNTSDK--PQKRIESKD----------
-----------------------------------------------------------------------
-----------------------------------ITDEYTKESGKPM------------KVATNATSPCIC
KQ-----------YNLAWGSKVS-CEFRKRV--IK--IAQ-------------------------------
-----------------------------------------------------------------------
-------NLWPNDSENMASQLMAVM--------------------------------H---LESAGTFSPK
IGTF-----------ISKKLTDDAKGGYVGLIQFGKFASIDLKVK---------------------RSDLAK
MSAVQQLDYVEK--YYKLNSAHTKIKNLTGLYL----WVNYPKNV--------KENRLEDE-----------
-----------------------------------------------------------------------
---DIVYAAPKDAEVTSKKFLESPYHQNPSFMKENEEYKRDGKKVIRQGFKNGST-----------------
-------------KVWEVEQEIKKHLTEGIKSQNLEKNYNCAYI-------------------NHTEIKNTQ
KINLEKFAEILRKRAKEKSQHQCAKYVRIALEAGGADT---------------------------------
-------------------------------------SGHPVAASDWGPTLKKIGYKEIPEEFNKPQLGDIY
IITKTDKHQYGHIAGYDGSQWISDFKQKGHRIYSDHVNYRYFRM----------------------------
-----------------------------------------------------------------------
---------------------------
>TseT
-----------------------------------------------------------------------M
SGIGALFRPLPRMGPRLPFELPAPPRPHLPMPAPRPLPRP---APGALPRPVPRPMPVPQTLPRT-------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------ETGTLSRDRTREAERDCSKSQGRDK-----------------------------
-----------------------------------------------------------------------
-----------------------------------DCVECPPSRGEMA----------IANNGKGHSMSDLS
AR-----------YQQWVTNFPFPHEWFWSG--TW--WDG-------------------------------
-----------------------------------------------------------------------
```

```
--FDEPRCTLLEAKANYAFLFVPLL--------------------------------G---VPRPWARAKV
KSDL-------------------LQKAEVHSDKARPTPPVFVEWH--------------------------F
LQRIVYEYCAAE--YLRMGLANLKAFWNPMPGT--DEHDDYQETR---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------AKEQEEMKRFCEENPGYCA----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB031_27
------------------------------------------------------------------------
------------------------------NNNPLVGIDL---SNKSRSEIENILSNSSEVSYKG-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------------GSPDKK--------------------------------------------
------------------------------------------------------------------------
-----------------------------------FMQWKWNDNGQTA------------------------
-------------VRLDPPDKVT-----------------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LYDHAHLYDK
NGNP--------------------------LDKDGNIVPRESPDA---------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------HIPIGDCK-------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>A1296_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKN-----------------------------------TPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTPTPTPTPTPTP-
----------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI-----------------------------------------------
----------------------------------------------------------------------
---------------------------
>1656-2_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP-----TPTPTPTPTPTPTPTPTPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
```

```
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTP-----------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI----------------------------------------------
------------------------------------------------------------------------
---------------------------
>ACICU_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP-------------------------TPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ---------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
------------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTP-------------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI----------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AR_0056_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP---------------------------TPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTPTPTP-------
----------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
----------------------------------------------------------------------
---------------------------
>D1279779_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP---------------------TPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
```

```
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTP-------------------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
------------------------------------------------------------------------
---------------------------
>DU202_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP-----TPTPTPTPTPTPTPTPTPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ-----------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
------------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTPTPTP-------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB03_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP--------------TPTPTPTPTPTP-TPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTPTPTP-------
----------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI-----------------------------------------------
----------------------------------------------------------------------
---------------------------
>NCGM237_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP---------------TPTPTPTPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
```

```
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTP---------------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
------------------------------------------------------------------------
---------------------------
>R2090_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP-------------------TPTPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFETKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ-----------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
------------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTPTPTPTP-----------
------------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AbPK1_8
----------------------------------------MYIVKKGDTLTSIANKNGCTVEQIIKLNSIKN
KNLIFVGQKLKLKNTPTPTPTP-------------------TPTPTPTPTPTPIQNLGGKVGIAI-------
---------------VNKKGEPISNFKLKIQVGNNIYSNQLTNARGVVTLPRQKSGENIIIQGWSKTNNSYK
LISNRFITENRNLGIGISLDTIKFEAKTDNHK------------KPINNNVNNNGQST--------------
------------------------TTNGSNSQNNPIARTSVEGCSNCTKITENELKQIFTQANSNDIKKIID
VYTNFSEKFGMN-NCLSKAHFFAQVLEEVGKKIEVKDGESLNYHSDILFLS--YTKIKRKEYIIEKGKRVEK
MTHGGPFSAFRGNRQ------------------------------------------------------
-----------------------------------LCDKYGRNDNHPADQVMIANIAYANRNGNGDIQSGDG
WK-----------YRGRGIIQ---ITGKDKYDKIN-------------------------------------
----------------------------------------------------------------------
-------KAIKDNYPNVGISIDANN-------------------------------------INNIYEGTLA
SMAY---------------------WKSFGLSKLATQKQVDIRTQ---------------------LEVVDS
LIDIINRDTASR--SDRKKNFEYITAKVFKLNE----CKNSIVEANLLSKSTPTP-----------------
----------------------------------------------------------------------
---------------TPTPTLSNVLKEIKQLVDRNIPYSQTGARGAGSNKNATSV-----------------
-------------ITANDLKGLDCSETVAIYLLKLGVTDKFYSI-------------------HTGVMLTEN
DFRKAIRSNKIEYVVGSKDLNFIPQIGDIFVWRNGGGHCGIVYDVDRQNDT---------------------
-------------------------------------VTILEAIGDVGSADENFNINNGGEKKVGCTRTAVY
RRSGKALAQHRGWVGYFRPIISGKKI------------------------------------------------
----------------------------------------------------------------------
---------------------------
>Tde2
-------------------------------------------------------------------MSIPRD
NYIGEPQYPDTWTTKTPREGLRDIDEARIVSLAPDVCLTPV--GSSVVPIPYPVVDFCGHDKNYT-------
---------------PSVRFTGKKAMVMRSCTTHVHGDAPGVRKGVKSGTVESVCEPIGHADQVRAEGSHVI
RHLDRFHMNSKNTE------------------------------------------------------------
------------------------GEAIFVRSTQTYNSPKDDDPVRGSLRAIEVADASEEQNRSSDAAPSGG
AALGFLVTPGFA-PLVQGAGGAAAGGASTAAGAATSGAGGAAAAAGGV------------------------
----------------------------------------------------------------------
-----------------------------------SLGTILAGIGIFA------------AGVLIPTNKMNF
SD---------TVPQDDFEQKLLLDAQRRMN--ELPFWDS--------------------------------
----------------------------------------------------------------------
```

```
-----GADIRTETFAKIQEHRKKNK---------------------------------PTQDPEPTPVPVPP
PGSN---------VRIDEDENRRCRLLIICFMPTKSTIDIDEFKR---------------------------
-QMELQEQGLNN--MSPQQMLANQAKYLANPAG--MRALSEPLQA---------------------------
------------------------------------------------------------------------
-----------------------KARQEYRNDPRIQKKYVDQYGPIQGPIKLGEY-----------------
-------------LDSAAALHNPDMIAGGKYNSVVDQTLPIENR----------------------------
------------------------------------------------------------------------
-------------------------------------IGGLSENSSMGSQWINPNRNGHTRASRLTEHAKRQ
AANNCPSVQVDLRLCPSNPSRPGEPLTGT-----------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle4
----------------------------------------MSSEPLEPNQDVIIPRSRDSLGRPVYKAQLTR
TDNQSEKVALIRQTAPLPVIFIPGIMGTNLRNKADKSEVW---RPPNGLWPMDDLFASIGALWTW-------
------------------------AWRGPKARQELLKAEQVEVDDQGTIDVGQSGLSEEAARLRGWGKVMRS
AYNPVMGLMERRLDNIVSRRELQAWWNDEA----------------------------------------
------------------------LSPPGDQGEEQGKVGPIDEEELLRASRYQFDVWCAGYNWLQSNRQSAL
DVRDYIENTVLP-FYQKECGLDPEQMRRMKVILVTHSMGGLVARALTQLHG--YERVLGVVH----GVQPAT
GSSTIYHHMRCGYEGIAQV----------------------------------------------------
-----------------------------------VLGRNAGEVTAIV------------ANSAGALELAPS
AE-----------YREGRPWLFLCDAQGQVL--KD--IDG------------------------------
------------------------------------------------------------------------
---------KPRAYPQNQDPYEEIY-------------------------------------KNTTWYGLVP
EQNS---------------QYLDMSDKKEGLRVGPRDNFEDLIDS--------------------IANFHGE
LSAAGYHSETYA--HYGADDSRHSWRDLIWKGD--PTPLETPGAT--------------------------
------------------------------------------------------------------------
----LNDDENGTYNSWFRRGLPTIVQGPLETGNPLDASGSGGDETVPTDSGQA-------------------
-------------PALAGVKASFRHGSKGKGQANTKRGYEHQ------------------------------
------------------------------------------------------------------------
-------------------------------------ESYNDARAQWAALYGVIKITQLADWHPNDKGGT--
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>Rhs2
------------------------------------------------------------------------
--------------------------------SNCSTLDR---IIGDANKVASRGGAITAKQAQI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------------------LRDNLPVVQRRSV------------------------
-------------FQNQMARKEFVRDQHYLM--SQ--WEA--------------------------------
------------------------------------------------------------------------
-------------------------------------------------------N---TGRTWPTGAT
PHHI----------------------IPLESGGANKWWNLMPTHG---------------------------
TLPNHSLPGVPG--PHAAGG--------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------VLRTTVQQSRKALPPGTITDLRL-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Tle2
-----------------------------------------------------------------------M
DSFNYCVQCNPEENWLELEFRS-------ENDEPIDGLLV---TITNQSAPSNTYTQTTSSGKVL-------
---------------FGKIAAGEWRASVSQASLLTEVEKYASRKEGQESPVKKRAAAELDAADKDTKQYRFT
TIGDFWDEAPKDEFLQKQHKGIDVNASAEKAG--------------------------------------
------------------------FRLSHNQTYVFEIKALRSYMPVIIDTDEFNLVNSYTFALLSKLAYATN
DFNRDDGKTIDNQGAISTVISQLKRKERPTYSGDLQAKWLLEEIPYSKALSAQYYAEDDVGSEGYIIFNDEL
AIIGVRGTEPYFQSKKPPVDNTKFKIIKAASGMAAV----------------------------------
-----------------------------------IADKIESATDSPG-----------MKDLIITDLDAAQ
IAPEEFGGTYVHRGFYQYTMALLSLMEKDLG--LH-----------------------------------
-----------------------------------------------------------------KIK
```

```
KFYCCGHSLGGAGALLISALIKDSY--------------------------------HPPVLRLYTYGMPR
VGTR-------------------SFVERYQNILHYRHVNNHDLVP---------------------QIPTVW
MNTDVSEGFHVL--DVFKSRVDLMRKMLTDDDD-----DNYQHHGHLSQLLTYNSNNQVLL-----------
------------------------------------------------------------------------
-----TPKQTQVTMLDLANLATNDSVAMVDGLSDASIVEHGMEQYIPNLFEQLT------------------
-------------ALSDESLMVHYQRAISALEQEIATLQQSYLTVKQAWIES--------------------
------------------------------------------------------------------------
-------------------------------------IGNGTPTMNIGRLMSEMHSINKLIENRNKIRGELR
QIVSDPQRMPATKFLISQQTLPDEIKVQIR----------------------------------------
------------------------------------------------------------------------
---------------------------
>EvpP
------------------------------------------------------------------------
----------------------------MSILNSELDWSH---VGSISTGPGTVVSDAFNISYGL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------PTKE-LLPAGTALYKFNGFSSLARPPITGDT--------------------------------
------------------------------------------------------------------------
-----------------------------------PLSPWWSPVQPFR------------HDGGLQQRMLVA
KL-----------------NGVSMREWGRLT--SV-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------IKENWSSLDH
LLEI------------------------VLKVPVYAWFGGFKGMS-----------------------RIDN
GMPSKRNITLEQ--KGRGSNLPGGATQFYIPNL---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------TVGHISSHNFSALK----------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>15A34_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>15A5_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>1656-2_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>3027STDY5784958_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AB07_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AB34299_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>Ab4568_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Ab4653_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>Ab4977_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>AbPK1_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AC29_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
>AC30_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------------------------
```

```
>ACICU_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AF-673_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>AR_0056_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>AYP-A2_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>BJAB07104_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>BJAB0868_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>CBA7_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CMC-CR-MDR-Ab4_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>CMC-CR-MDR-Ab66_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>CMC-MDR-Ab59_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>DU202_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>HRAB-85_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>JBA13_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB01_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB02_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB03_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB04_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB05_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KAB06_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB07_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>KAB08_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>KBN10P02143_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>MDR-TJ_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>MDR-ZJ06_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>NCGM237_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>SAA14_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>SMC_Paed_Ab_BL01_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>SSA12_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>SSA6_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>TCDC-AB0715_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>TYTH-1_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>USA2_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>WCHAB005133_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>XDR-BJ83_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XH386_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XH856_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>XH857_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR---------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XH859_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>XH860_6
------------------------------------------------------------------------
--------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-----------------------------------
------------------------------------------------------------------------
------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR--------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
```

```
>YU-R612_6
------------------------------------------------------------------------
-------------------------------APCSLVRY---KPDKVTPQAGSRQDAIDRAWSL-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
----------EK-QLIQTTGTG-----------------------------------------------
------------------------------------------------------------------------
-----------------------------------TRDWSKAELDTIL------------RTPSGSGKGHLS
S------------VMSNLGYTGHHINSVKNN--GA-------------------------------------
------------------------------------------------------------------------
-------------------------------------------------------------LGESWKGDPR
NIVF-------------------------------------------------------------LENPKH
PNSSPMPNAYNE--HFHSKQGHRGSTTNVSRGR----------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------------LIDRQAMINQFNKGCSI------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------------------
>Rhs1
------------------------------------------------------------------------
-------KPRCAATKANDHNQA--------------------AFGRQW-QGRGIYKGRDSWSNI-------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-------MLKEG-DIVYGGAPGQSGFYFNKATLDAAGG---------------------------------
------------------------------------------------------------------------
-----------------------------------SRAKLWESLQVL-------------------------
-------------PHEKFGYRSKIQAYRVKR--ET-------------------------------------
------------------------------------------------------------------------
```

```
------------------------------------------------------------IAGTGKAISQ
DPTR------------------------------------------------------------------
--------------FGEGGGTQFFLSNYKTVLE---------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
-------------PIDKPFEIGL-------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
----------------------------------------------------------------------
---------------------------
>AB042_3
---------------------------------MNPYTIFEYTIVFYNQRNKELPNVKYSIIFFCEDGTKKT
YEGATNPKGQTKPIPLNQNGKL-------HIFVEGHETIF---SPKKTIKPILAEGSNIVEVNDIRLKSNTS
FLTKAQYELMQKKTSKDLEELRKNAKAVKQKNFFNLSKIRPTFPLDLAEELNERINMSYEEYRKKNTHIVKK
TKYLKFKNYALYRFVDSAGNGIPIVDYQIFAQGQSRPLINARPGPPDKKGYTQLVYTHLKSRVTYTLGSARK
NSEWYEPITCVDK-----------QTIYQIIFPTSIAVTQPDINHKENMEARQKPPIVINPTTNEVLILPSA
VYAEFDKKTKILSDAVREVHKSNANLIKAIQSRDLDEIKELEKRLNINQEK--AIEKINGEFKQTADLREVW
VVETTGKTNEKISKYNLKRRYLKVTEYEELKAKRRNPQTEVDVTANQYTVQQPAQ-----------------
-----------------------------------IRSSFEKLSQQLL----------TVKGNAGSDEKAVY
NLIGGLGGEIAEEYKNSRDVTVTQEAQWMRM--VAGASGE-------------------------------
------------------------------------------------------------GSISAAPKGV
SIKTSGDMSAKWTLFEGVKEWRKFYP-----------------------------------CETGWKLEYD
NYDLGTIRFLIGAEISGFSGANLGIAGNLSVDISHQGAAQVIKAV----------VRPPERSMSQMVDRNKK
PMFQPAQGSLKI--IGNNNQENAQNQGNISINAFAGVQIQGLLKGAVEWFKPKGDGSGEGE-----------
--------------------------------------FVAIASAAAGGGVSAGVGAQGQFQIGYDQTSGNF
KILVAAHLCWGMGAKGVASFVVGTEHLLSYLGFIKSQVAHAGFKTLLYINEAAFLLAAQVLAYCIGE-----
-------------NHPVISDINRIAASYGDWIRRLDIDQGRYKTAQNINSSSGKKELLYATPETKGILLYAV
THWTDRTAPIFDMNVKFSDMKIEFFPTRKTAVINI-------------------------------------
-------------------------------------FKTCISTEEWENTIQHIHPRGNKLTQTQLGKVEGD
IIRFLNYGNDEKYAEDIIRCLNSGIEYKGTQINAWLQDYLKYRKGAKKIAGSLNYMLVKNQDDNRFKQLEIQ
QGVWGDSEEITLIASNLNVLSPFDQDDTDKYETYNV------------------------------------
---------------------------
```

```
>ATCC17978-mff_3
---------------------------------MNPYTIFEYTIVFYNQRNKELPNVKYSIIFFCEDGTKKT
YEGATNPKGQTKPIPLNQNGKL-------HIFVEGHETIF---SPKKTIKPILAEGSNIVEVNDIRLKSNTS
FLTKAQYELMQKKTSKDLEELRKNAKAVKQKNFFNLSKIRPTFPLDLAEELNERINMSYEEYRKKNTHIVKK
TKYLKFKNYALYRFVDSAGNGIPIVDYQIFAQGQSRPLINARPGPPDKKGYTQLVYTHLKSRVTYTLGSARK
NSEWYEPITCVDK-----------QTIYQIIFPTSIAVTQPDINHKENMEARQKPPIVINPTTNEVLILPSA
VYAEFDKKTKILSDAVREVHKSNANLIKAIQSRDLDEIKELEKRLNINQEK--AIEKINGEFKQTADLREVW
VVETTGKTNEKISKYNLKRRYLKVTEYEELKAKRRNPQTEVDVTANQYTVQQPAQ-----------------
-----------------------------------IRSSFEKLSQQLL----------TVKGNAGSDEKAVY
NLIGGLGGEIAEEYKNSRDVTVTQEAQWMRM--VAGASGE-------------------------------
-------------------------------------------------------------GSISAAPKGV
SIKTSGDMSAKWTLFEGVKEWRKFYP-----------------------------------CETGWKLEYD
NYDLGTIRFLIGAEISGFSGANLGIAGNLSVDISHQGAAQVIKAV----------VRPPERSMSQMVDRNKK
PMFQPAQGSLKI--IGNNNQENAQNQGNISINAFAGVQIQGLLKGAVEWFKPKGDGSGEGE-----------
---------------------------------------FVAIASAAAGGGVSAGVGAQGQFQIGYDQTSGNF
KILVAAHLCWGMGAKGVASFVVGTEHLLSYLGFIKSQVAHAGFKTLLYINEAAFLLAAQVLAYCIGE-----
-------------NHPVISDINRIAASYGDWIRRLDIDQGRYKTAQNINSSSGKKELLYATPETKGILLYAV
THWTDRTAPIFDMNVKFSDMKIEFFPTRKTAVINI-------------------------------------
--------------------------------------FKTCISTEEWENTIQHIHPRGNKLTQTQLGKVEGD
IIRFLNYGNDEKYAEDIIRCLNSGIEYKGTQINAWLQDYLKYRKGAKKIAGSLNYMLVKNQDDNRFKQLEIQ
QGVWGDSEEITLIASNLNVLSPFDQDDTDKYETYNV-------------------------------------
---------------------------
>YezP
---------------------------------------------------------------------------
------------------------------MLDPKNIQNV-----LKSSTDLGQQSQSDLQKPFV-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------KGMQNMEMSGADAARSIMQSVNQ-------------------------------------
---------------------------------------------------------------------------
------------------------------------SCETMMSDMNKIL--------------GGLQDNVDAH
QK-----------MQSEERPKDFERAMSDLR--ST-------------------------------------
---------------------------------------------------------------------------
```

```
------------------------------------------------------------LSNGFPEEMK
SMFD-----------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-------------KLPKM-----------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------
```

Supplementary file S4c

```
>AR_0078_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIFRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
```

```
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>A1_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>A388_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
```

VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
----------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS----------TKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI----------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G-----LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------HRKYHYDKNYLLSQV--
----------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP----------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK----------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>A85_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-

```
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AB0057_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
```

```
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AB307-0294_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
```

```
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AR_0083_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>D36_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
```

```
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>USA15_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
```

```
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>WCHAB005078_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
```

```
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AB5075-UW_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK---------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIREYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPVSIIFETYEVP-YEGWIIKPLKN---------GELI-----LDFGGEWRS----HFQSFDGGKNYYL-
-VKKMNETSQEEILLEYLLLDHI-----AYLKVINFKLKQAEY-ELKFAF--------NEQVKIIAVFLDDK
A------EPL-------ARYEYDTQGNLIKAIDQNG-HTRTYEYNQFHQLTRYTDRTGRGQNIRYEST----
-----------------------EAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLD
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NKQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFQIRRPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDLYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------ESVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
```

YYDRETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AB031_26
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPSNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSAATLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPINQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFEQSMVGARWMMPFSNMIQQT----------AQGYLFIDSKGRK
HQLPASITLETYEVP-YEGITIQPLKN---------GDLI-----LNFGGDWSF----QFHQFSVGQPYQL-
-IQQFNEETKEKIDLSYLIFEKV-----AYLQHVDFQLEHAKH-QLKFAF--------SEQIKIIAVFLDDN
A------EPL-------ARYDYDTQGNLIKAIDQNG-HTRTYEYNDFHQLTRYIDRTGRGQNIRYEST----
----------DAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFDGRETQQEYNDQDQLVKIVQPNGGIIRFAY-NEQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
SIWEYDEDGVLTAEQTANNKVVQYFYS----------TKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSIAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFKIRQPNI----------VTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLIREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------HRHYQYDQNYLLSQV--
----------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP----------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN----------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNTRGECVWEILQDT-WGTALEIKV----VNQDNPFEQNNLRFQGQ
YYDSETELHYNRYRYYEPHSARYMSKDPIGLEGGLNTSAYVNN-PTHWIDPMGL
>AB030_15
MAKENTQQKEIKKQPTVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS

VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTHYYF---DLN
GFTYRTRLADGRESWYSRDGQKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIHFAY-NEQGNLVEIKD
PEGSIWKREYDENGNLSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAQQTANNKVVQYFYS----------TKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLILEQAFDGEEKHYSYNE-NGRLFQIRQPNI----------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLVREHQHYKIPELKSLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------HRHYQYDQNYLLSQV--
----------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP----------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN----------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTDIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AbH12O-A2_15
MAKENTQQKEIKKQPTVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYL-PKIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTHYYF---DLN
GFTYRTRLADGRESWYSRDGQKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIHFAY-NEQGNLVEIKD

```
PEGSIWKREYDENGNLSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAQQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLILEQAFDGEEKHYSYNE-NGRLFQIRQPNI-------------------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKSLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------------HRHYQYDQNYLLSQV--
--------------------------------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTDIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AF-401_15
MAKENTQQKEIKKQPTVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTHYYF---DLN
GFTYRTRLADGRESWYSRDGQKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIHFAY-NEQGNLVEIKD
PEGSIWKREYDENGNLSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAQQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLILEQAFDGEEKHYSYNE-NGRLFQIRQPNI-------------------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKSLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------------HRHYQYDQNYLLSQV--
```

```
--------------------------------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTDIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AR_0063_15
MAKENTQQKEIKKQPTVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTHYYF---DLN
GFTYRTRLADGRESWYSRDGQKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIHFAY-NEQGNLVEIKD
PEGSIWKREYDENGNLSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAQQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLILEQAFDGEEKHYSYNE-NGRLFQIRQPNI-------------------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKSLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------------HRHYQYDQNYLLSQV--
--------------------------------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTDIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AR_0101_15
```

```
MAKENTQQKEIKKQPTVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTHYYF---DLN
GFTYRTRLADGRESWYSRDGQKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIHFAY-NEQGNLVEIKD
PEGSIWKREYDENGNLSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGALTAQQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLILEQAFDGEEKHYSYNE-NGRLFQIRQPNI-------------------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKSLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVASFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------------HRHYQYDQNYLLSQV--
--------------------------------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPNS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTDIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>15A34_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
```

HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAVQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>SSA6_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAVQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK

```
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>USA2_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAVQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
```

```
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>AF-673_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK---------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS--------------IKGRDKGQL--------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQILQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>CMC-CR-MDR-Ab4_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
```

```
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQILQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>CMC-CR-MDR-Ab66_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
```

```
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQILQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>CMC-MDR-Ab59_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQILQPNI-------------------LTQFDYYADGQIASKSFTHL
```

```
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>BJAB0868_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAGFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
```

```
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>15A5_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>3027STDY5784958_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
```

```
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>Ab4568_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
```

```
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>Ab4653_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
```

```
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>Ab4977_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI--------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
```

```
>ACICU_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>AR_0056_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
```

```
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>AR_0102_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
```

```
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>BJAB07104_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
```

```
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>HRAB-85_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>KBN10P02143_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
```

```
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G-----LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
---------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>MDR-TJ_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
```

```
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>MDR-ZJ06_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
```

```
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>NCGM237_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
```

```
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>SMC_Paed_Ab_BL01_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
---------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>TCDC-0715_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
```

```
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>TYTH-1_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
```

```
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>WCHAB005133_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
```

```
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>XDR-BJ83_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------IKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
```

YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>XH386_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS----------IKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI----------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------HRKYHYDKNYLLSQV--
----------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP----------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK----------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>XH856_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS

VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS----------IKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI----------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------HRKYHYDKNYLLSQV--
----------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP----------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK----------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>YU-R612_5
MAKENTQQKEIKKQPAVELAVFNLNSVTDVADLQMVA--------SQVQRYLQVCGNTSLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLTSATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFTRQYNSQMDEFDQSMVGARWMMPFSNMIQQN----------AKGYLFIDSKGRK
HQLPASITFETYEVP-YEGITIQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQYVVFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDK
A------EPL-------ARYEYDIQGNLIKAIDQNG-YTRTYEYNNFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAVEEWADDGSFHTKLKWHPRLRQVAVYNAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD

PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS----------IKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI----------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------HRKYHYDKNYLLSQV--
----------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP----------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK----------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLSGGINTSAYVSD-PTQWIDPRGL
>SDF_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGSTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------ETDIKRLGLHFNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ----------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC----------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQRT----------AQGYLFIDSKGRK
HQLPASIIFETYEVP-YEGIIVQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQCVNFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDN
A------EPL-------AHYDYDTQGNLIKAIDQNG-HTRTYEYNYFHQLTRYTDRTGRGQNIRYEST----
----------DAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIRFEY-NEQGNLVEIKD
PEGSIWKREYDENRNVSKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
SIWEYDEDGVLTAEQTAKNKVVQYFYS----------TKGRDKGQL----------QSIIYPDGLK
EYFEHDEEGRLLKHIDTKGLVTEYKYNQVGLLEQRIDANRHSVTYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRLFKIRQPNT----------LTEFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS----------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------HRKYHYDKNYLLSQV--

```
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQTGYKDLIQLIETPDYQEYQTKPYSIYKDPVWNS
TTRKKRADLEQITFYHCDQVGIPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>6200_15
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGISTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALSQTLQQQ---------------------------ANAGQKYTLAWLLQEALKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQRT----------------AQGYLFIDSKGRK
HQLPASITFETYEVP-YEGIIVQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQCVNFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDN
A------EPL-------ARYDYDTQGNLIKAIDQNG-HTRTYEYNYFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGVIRFAY-DEQDNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LIQTKQYNDVGLLSSQLIQPEQETQDYLQYQA----------------HRHYQYDQNYLLSQV--
--------------------------------EDSRLGRLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDAQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTTN-------------ELTL
FGWDGDLM--IWESVKSAQMSYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>IOMTU433_15
```

```
MAKENTQQKEIKRQPAVELAVFNLNSVTDVADLQMIA--------SQVQLYLQVCGNTTLEQ-IKSKANITT
VANIFALTGSVLDLMLYATDKKTGDAAVQRGALLAANLIGLFS----EPNNEAHARMALRPMFGLMAECLYR
ENGKIK----------------------ETDIKRLGLHLNAMIAGDLENFLKETQAKLSSLLISATTLGVTI
LQSMATPATGI----NAGITTAAGASAEKRDPKLKFTNWAVPLIDLLGKPSQANLTPKIQPNITSRLQQEAT
QAIAALGQALQQQ---------------------------ANAGQKYTLAWLLQETLKAIQALENKG--NAS
VPVNQTGEYERHTKGDTLEFVSLQADAL-NAPPC------------EGADSQSGKSISYSIGAERV---QHA
DFYLP-KIGFSFIRQYNSQMDEFDQSMVGARWMMPFSNMIQRT----------------AQGYLFIDSKGRK
HQLPASIIFETYEVP-YEGIIVQPLKN---------GDLV-----LNFGGDWTF----QFHQFSVGQPYQL-
-IQQFNEKTQEKIDLSYLIFEKV-----AYLQCVNFQLEHAKH-QLKFAF--------NEQVKIMAVFLDDN
A------EPL-------ARYDYDTQGNLIKAIDQNG-HTRTYEYNYFHQLTRYTDRTGRGQNIRYEST----
-----------------------DAKAKAIEEWADDGSFHTKLKWHPRLRQVAVYDAYDVPTYYYF---DLN
GFTYRTRLADGRESWYSRDGKKRITRQIDFEGRETQQEYNDQDQLVKIVQPNGGIIRFEY-NEQGNLVEIKD
PEGSIWKREYDENGNLNKEINPLGHITQYKYNN---DNQLVEVIDAKGGVKKIQYNELGQMISYTDCSGK-S
STWEYDEDGVLTAEQTANNKVVQYFYS-------------TKGRDKGQL-------------QSIIYPDGLK
EYFEHDEEGRLLKHTDTKGLVTEYKYNQVGLLEQRIDANRHSVAYQWDKQG-RIQKLINQNQAEYLFGYNPY
GYLIREQAFDGEEKHYSYNE-NGRIFQIRQPNI-------------------LTQFDYYADGQIASKSFTHL
HT----GQKQTEQFDYNLNSQLSRAS------------NEVSQIDFYRNALGQLVREHQHYKIPELKPLTAV
LHYEYDELGNLIKTIRP-DGH---------TLNHLVY--GSGHIYAIGLNNQEVVSFQRDDLHRETTRLLAN
G------LMQTKQYNDVGLLSSQFIQPEQETQDYLQYQA----------------HRKYHYDKNYLLSQV--
--------------------------------EDSRLGKLNYQYDPIGRLI------AAQSLHKTESFNFDP
AGNLIDS------DSVLSP-------------------------AQIKNNLIKSYKGKHYQYDVQGNVTEII
QAGKNL-----KLTWDNQNRLIR-------SDNNGLVTEYGYDVFGRRLYKKTAK-------------ELTL
FGWDGDLM--IWESFKSAQTNYTKHYIYEPDS-FVPLLQAGYKDFIQLIETPDYQEYQTKPYSIYKDPVWNR
NLGKERTALEQFTFYHCDQVGTPQTMTNIRGECVWEILQDT-WGAVSQIKA----LNQDNPFEQNNLRFQGQ
YYDQETELHYNRYRYYEPHSARYVSKDPIGLEGGMNTSSYVSD-PNQWIDPKGL
>AB030_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLIRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
```

```
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTILQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLYYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHIDQKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
--------------------------------NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETVYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTSGEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>AbH12O-A2_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLIRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTILQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLYYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPIIKGLPLNAFGQL-------------EKIKHADGTE
```

```
EHFIHDAEGRLLAHIDQKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
--------------------------------NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETVYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTSGEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>AF-401_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLIRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTILQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLYYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHIDQKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
--------------------------------NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETVYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
```

STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTSGEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>AR_0063_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-----DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLIRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----EPTSKAYHEWADDGSSDTILQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLYYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPIIKGLPLNAFGQL----------EKIKHADGTE
EHFIHDAEGRLLAHIDQKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK----------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
-----NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV----------QSHSQKLDETVYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTSGEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>AR_0101_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG

```
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLIRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTILQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLYYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHIDQKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
--------------------------------NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETVYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTSGEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>IOMTU433_22
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSISGTKRNITFALGTECL---THQ
DAYVSSILSFVLTRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIVIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
```

```
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTTLQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDKHGNIVSMTQPDGSLLHYAY-DENRQLIGMVD
AEEGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPVIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVILEHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVSQTQNNAIQETQQLIQRLYQYDKTGQLTGI--
---------------------------------NDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKA-----------QSHSQKLDETGYGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTGDEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQRDPLWKV
TKTPK--DFKEFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAEKAKSNFFEDSEIISN-NIRFQGQ
YFDQETGLHYNRYRYYSPYVGRFISKDPIGLLGGDNVYAYAPN-PVEWVDPLGL
>AB031_27
MPTAPKTISQAKAKPSVRTNTGQVAVVPL--NKLYAADVKAGMNKIDSWLKTNTKGYVDLNTIKSTLGTLPV
IGNAIALVDAIYDVIDISKK---PSPAFTDWLNLGLDVIGIIP----APPTMATMRMSLRPTLNLVRQKAKG
TIS-------------------------DTILVILSDHLNERIAGELDQFAKNAQPLVNQMLQNCGTKITAI
SNDFANGIQKV----LNGKVYSSAGNLKNAQK--QLNKVNLNNLQRNPKATISNAVDGLVNIWKAGVKE-QI
NTVAKGVSAVVPASATQPIQNAITSIRVFGRKAPSYLMALADPAKAMSIAWLLNVLLKAVQKFKLKGTKTAN
IKPTQVTEKRRQKPNGELEKANVQAKSKGNPSETVCALNLRGGKSKPKSTSGTKRNITFALGTECL---THQ
DAYVSSILSFVLTRKYASNLYQLDHGEFGARWITPFTTRIVPQSEYIEETEERAGYLKHLSGFEFIGADARP
VKLPNLKVGESFHNK-TEDFYYSVISE---------KVQM-----ISYQKEEKH--------LFEKYQDGY-
RLSAIEYKNGLTLA---VRYDHHFEGL-SFISDIIIKEKQKQLIHVAFQV--------NASGRIEDVWLVEN
G---QLARPL-------ASYNYNEKGDLVEAITENG-ASYHYQY-DHHLLTRYTDLTGRGMNLEYDGV----
-----------------------EPTSKAYHEWADDGSSDTTLQWDENIRLTYVTDAYGAETWYYY---DIE
GYTYRIIYPDGLEEWFFRDDFGRVTKHVDTDAAVTIYDYDEHGNIVSMTQPDGSLLHYAY-DENRQLIGMVD
AEGGRWFKEYDAAGNITKETDPLKRETQYSYNG---LGLLTSIKDPKGGTKTLSYDDQGNLISYIDCSGK-E
TKWTYDKKGRVVAIENALKQKVEYFYSDLTIEQREPVIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHIDPKQNITRYEYDAAGLIASRTDALNHKLKYEWDKLN-RLKRLINENGASYQFFYDVA
SRLVKEIDFDGKETIYNYDETDGNLVSSVEVASMHGQDLRDRIAPKDR----IQKFLFDSMGRLEQRTAGYG
```

```
YVEHDLEQQLVEEFAYDSNGNLIQAK------------NAESNLQWYYDAVGNVIREHHQ---DYKTKKTGV
WKHSYDEINDRIKTVRP-DGQ---------KIDWLTY--GSGHVHSLIVNGQDVVSFERDDLHREIARHYAN
G------ISQEQHYDTMGRLTQQNIVNGHE-FGYPSNEQVS--QNNAIQETQQLIQRLYQYDKTGQLTGI--
--------------------------------KDTRRGNINYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLEETGFGYNRLVNNVVKEYLDQQYQYDVYGQLVCQK
STKGNL-----YLEWDACGRLIK-------SRNAEYTAEYRYDALGRRIQKRSKH-------HHTGDEHNII
YGWDGNTL--AYES----NEQITKHYIYEKDS-FVPLAQAVYAEEIELHQTPDWAD---KPYSLQCDPLWKV
TKTAK--DFKDFWFYHCDHLGTPQEMTDHTGAVIWKAEYKA-WGECKAERAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNGYVYAPN-PIGWVDPYGL
>A1_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
```

```
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>A388_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>AB0057_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
```

```
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>AB307-0294_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
```

```
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>AB5075-UW_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
```

```
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>AR_0083_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
```

>D36_16
---MSQN-SVVAPLNTFSPKDLTAKKAE----------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC----------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
----------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL----------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK----------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
----------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>USA15_16
---MSQN-SVVAPLNTFSPKDLTAKKAE----------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC----------KNCMGGTGGSITFAMGTEFF---THV

```
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
---------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>WCHAB005078_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEK
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
```

```
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>A85_16
---MSQN-SVVAPLNTFSPKDLTAKKAE-----------------VDKWFREYTNGVVTVDRLETICRSVPV
LGSAFAIGDIIIDIISMINKGGLDKVEIFDWLNLGIDVIGLVP----MGPVGPSVRSAARPALFYVKNESEI
IIKAQAKKLGKKTLTSQEVKKALSTGFKDSASVFLTTIIAENVAGTLENFAKKGQSLLNQILKEVGNWIVLL
TKTIDDGFKKLVSGSLNGLPNLKRAGQQSLGV--------IKGIFELDGTRIVNNAKYATENVAKTVGK---
-GYVNLANLAVSDEARAKVLALGAKIRSIGQVAQAKVNGLSDPNTLWTIGWLFSIMGMVAAKHRQKR---AQ
IKAKETTKANASHPSTATDKSNKQAHAENNANQC------------KNCMGGTGGSITFAMGTEFF---THV
DAQLGGIIQDSISRTYVSNLYQMDDAIFGARWVTPFTTKISRKFKYTSKKKDHKDY---LNGLEYICLDGRA
IDLPDLKKGQSIYDP-IEQYTYTVLSD---------QLHL-----IAYGEDEKR--------YYEKYGEDY-
RLSYIERKNGFKVA---LRYDHVSTDNKTILSDILFKQDDNLLAHLALQL--------TPQGLVSDIWTIKN
G---QLDRVL-------ASYDYDQQGDLVQATNEFA-ASYYYQY-THHLITRYTDLTHRGMNLKWDGI----
-----------------------LPTSKAIEEWADNASRASKLEWDKNIRKTTVLDVEGNSTEHYY---DID
GYTYRIVYPDNFEEWFFRDDAKNITLHIAKDGSKTSYTYDERGNVLTTTQDDGATSYFEY-DEKNQLTGMVD
AEQGRWFKQYDGSGNLIKEIDPLKHETAYVYNA---MGLVTSITDAKGGSKSLKYDDQGNLISYTDCSGK-E
TKWQYDERGRVISIENALNQKVEYFYTELTLENREPIIKGLPLNAFGQL-------------EKIKHADGTE
EHFIHDAEGRLLAHVDPKQNITRYEYDEAGLILSRTDALNHKLKYKWDRLG-RLTRLINENGASYQFFYDVA
SRLVKEIDFDGKETVYHYDEKSGQLATSIEVASAYGQDLKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
HYGLELEEKQTEEFAYDYMGRIIQAK------------NAQSNLQWFYDAAGNLVQEHQQ---DYKINKTAV
WKHQYDEINDRIKTTRP-DGQ---------VIDWLTY--GSGHVQSLIVNGQDFVSFERDDLHREIARHYAN
G------VSQEQQYDLAGRLKSQMMLSEHE-NGYQNQYK---RHNNALEQTSQLVQRLYQYDKTGELTAI--
--------------------------------RDTRRGNIAYKYDPVGRLL------EASSKLGKETFSFDP
```

```
ASNILDS------YHSQKV-----------QSHSQKLDETSYGYNRLVNNVVKEYLDQQYQYDAYGQLIRQK
TSQGDL-----NLEWDVYGRMVK-------SRNSQYTAEYRYDALGRRIQKWSKH-------HHTGQEQNII
YGWDGDTL--AYES----TEELTKHYIYEKDS-FVPMLQAVYLSPIELHQTPDWSD---RPYNIHRDPLWKT
EKEGK--EFDDVWFYHCDHLGTPQEMTDHTGAIIWKAEYKA-WGECKAEEAKSNFFENSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFVSKDPIGLLGGNNVYVYAKN-PITWIDSKGL
>15A34_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>15A5_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
```

```
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>1656-2_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
```

```
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>3027STDY5784958_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
```

```
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AB07_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
```

```
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AB34299_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>Ab4568_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
```

```
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>Ab4653_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
```

```
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>Ab4977_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
```

```
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AbPK1_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
```

```
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AC29_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AC30_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
```

```
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>ACICU_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG----------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
```

```
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AF-673_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
```

```
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AR_0056_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>AYP-A2_6
```

```
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
------------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>BJAB07104_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
```

```
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>BJAB0868_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
```

```
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>CBA7_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
```

```
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>CMC-CR-MDR-Ab4_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG--------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>CMC-CR-MDR-Ab66_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
```

```
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>CMC-MDR-Ab59_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
```

```
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>DU202_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
```

```
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>HRAB-85_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
------------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
```

```
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>JBA13_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB01_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
```

```
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB02_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
```

```
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB03_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
```

```
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB04_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
```

```
>KAB05_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB06_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
```

```
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB07_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
```

```
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KAB08_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
```

```
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>KBN10P02143_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>MDR-TJ_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
```

```
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>MDR-ZJ06_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
```

```
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>NCGM237_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
```

```
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>SAA14_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
```

```
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>SMC_Paed_Ab_BL01_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>SSA12_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
```

```
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>SSA6_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
```

```
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>TCDC-0715_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
```

```
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>TYTH-1_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
```

```
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>USA2_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>WCHAB005133_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
```

```
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XDR-BJ83_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
```

```
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XH386_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
```

```
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XH856_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XH857_6
```

```
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
------------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XH859_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
```

```
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>XH860_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
```

```
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>YU-R612_6
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLQSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG---------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHI
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAAWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDRGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRTDPLNQTLKYQWDRLS-RLKRLINENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDVVSFERDDLHRETLRHYAN
G------LSQQQSYDEVGRLTQQLMLSGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILER------YNSTKE-----------QSSQHISDEKGYGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
```

```
SSQGDL-----NLEWDVFGRLVR-------SRNNQYTAEYRYDALGRRIQKRSKH-------HHTGQEQNIS
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHPIELHQTQDWSD---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSDQTGAIIWKAEYKA-WGECKLEQTNSDFFEKSEIISN-NIRFQGQ
YFDEETGLHYNRYRYYSPYVGRFISKDPIGLLGGFNVYAYTAN-PVQWVDPYGL
>6200_21
---MSGKTEVVKPLTEVAIKDVSHSKQK-----------------IDSWLKSHTHQIVTLDLVASVMGTVPI
IGNVMAAIDVV-SDICYIYDKGFQNADIMDWTTMGIDLIGVAP-----IPGTTAIRTSARPALFLVRQEVKR
VGKAALG--------------------EAVIVVISNHLNDQVAGDIEKFCKTGLNKLNSILATCGATVQNA
TTQINGGIVRV---VTKGQIFTNAGSNASRAQ--QQAAGVIKGIKSGDLTRAGKNLVYMTENWGKALIKTGA
NSNAKVASSLVPAHLKQPILNVGATINKIGITANTKIKGLGNTAQPQTIGWLFDVLRMSASKFRKKK--SAQ
VKPTQTTQVKHDKKNNKLEKSNDEHAATHNANAC------------KNCKGGTTHSITFALGTEFL---NHT
DAQIHPLLIEQFSRTYVSNLYQYDQSIFGARWITPFTTKIVRCSSYNVHHPKEPIE---QDGWEYIGSDGRP
VRLPELKVGQSYYDE-VETFTYTVISP---------EIRA-----ISYGVSETR--------FYQKYKNEF-
RLASIERQNGFSIG---LRYDHELENSDSYLSDIIFKQQQQILAHVALQI--------NDAQKVVAVWLVEE
G---QLIRQL-------SAYQYNEQDDLIKATNEFA-ASYEYQY-QAHLLTRYTDLTHRGMNLKWDGV----
-----------------------LPSSKAIEEWADDYSSATKLDWDENVRVTSVMDIDGNVTEYYY---GIT
GYTYRIIYPDNLQEWFFRDQAKNITSHIATDGTETSYTYDERGNVLSMVQADGSTFYYEY-DEKDNLIGFVD
AEQGRWFKEYDASGNIIKEIDPLKRETVYAYNA---MGLVTSITDAKGGKKTLKYDDQGNLISYTDCSGK-E
TKWHYDDRGRVKFIENALKQKVEYFYTELTTELRQPIAKGLPLNAFGQL-------------EKIKHADGAE
EHFIHDAEGRLLVHIDPKGQQTRYEYDAAGLITKRIDPLNQTLKYQWDRLS-RLKRLTNENGASYEFVYDAA
GRLVKEIDFDGKETVYAYDEYNGRLTTSIEVASTYGQDFKDRAAPKDR----IQQFIFDSMGRLEQRTAGYG
YQGQELEEKQTEEFSYDGLGNLVQAK------------NAETNLQWFYDAAGNLIKEHHQ---DVVTQKTAV
WKHVYDELNNRTTTIRP-DGQ---------KIDWLSY--GSGHVYGMALNGEDIVSFERDDLHRETLRHYAN
G------LSQQQRYDEVGRLTQQLMLNGHD-KGYQAQTQ-----NNAIQHTNQLIERLYHYDKTGELTLI--
--------------------------------KDTRRGAIHYKYDPVGRLL------EATSKLGKETFNFDP
ASNILDR------YNSTKE-----------QSSQHTATEKGLGYNRLVNNIVQEYLDQQYQYDAFGQLIRQK
SSQGDL-----NLEWDVLGRLVR-------SRNNQYTADYRYDALGRRIQKRSKH-------HHTGQEQNII
YGWDGDTL--AYES----SADLTKHYFYEKDS-FVPLLQAAYHHSIELHQTQDWTE---KTYSIYKDPLWNT
VKQSQ--GFDDVWFYHCDHLGTPQEMSNKTGAIVWKAQYKA-WGECKVEQAKSDFFENSEIISN-NIRFQGQ
YFDGETGLHYNRYRYYSPYIGRFISKDPIGLLGGYNHYQYGPN-PISWVDPTGL
>RhsB
---MLNDILSRVARVGAMHAGNRPNPPADRPQPCQGKPPTSPGKTIKHKSFLGALAGAVAGALVAAAVAAAA
VFLVGVTGGLAVAAVGALAVFAAGDLISAVTNKVSAVVDSASPAFGPVASGSGNVFVEKQPVARA-------
```

```
------------------------------------------------------------TKDTVACTKHNSPQ
L--IAQGSESV---FVNDAPAARIDDKTVCGA--TLKEG-ASTVFFGSGQGTYLEIADEFSWW---EKA---
----------------------------------------LLIAVEFLVPPSRGMLKGLGKLFTRNG--LKS
VLKGAKAGALFIT--KVPGKMGCAARAFKANKGM--------ARFKEAAKAFKKDPVYLASGEVIE---SRT
DIELGQTLPLVFERTYRSAS-AHT-GLLGRGWHDSWSE-VATVTHDGL-----------NTHVVITLAQGYD
IDFTFHQDVQAVYCPHYPEFTLHRRGD---------GFS------LWHRDQQTW------RDFSVVQGERR-
LLSAIHDSHDNRIE---LVRDPK-----GYLRQLRHSDGVTLL--LVWQG--------EYLHQIQRI---DG
G------QKT-----LLAEYRQDEQGRLVEANATHA-YHLYYEYNTAHRLTRWHDNDQTWARYEY-------
-----------------------DAQGRCV-YTTCADGFLT-ARFDYLPDRVVMTDGLGQRSEFGF------
----------NDLHLMSWEQS--------PLGHITRYEYDEVGNLLREISPAGRVVEFTYLDDTGRVSTFTD
GSGHQWQYDYDDAQRLCGVTDPLGREWGWVYDA---EGNPERLTGPDASEVRFTWNRYGLLTQVSDAAGEVQ
ARLQYDHRQRLLSATDAESRTRQLRYD------RQDRVVQWQRADGARFRL-GYRRASWTLPEQLIRPDDKE
EQRQYDRHNNLLSYVDGNGALWRQTFGPFDLLTARTDAEGRTWRYEYDRESQQLIAVTAPDGSRWQWWLDAD
GRVIRERDMTGTETHYGYDE-DGLCIRVRN---------GEGD---------TRHFLYDARGLLLRETAPDD
TL----------HYRYDAAGRLTEVS------------SATAHVQLDYDLRDRVVREWHN---------GTL
LTRQYDDAARTVTRTLTWDGDADDTTGTLAPLTSLFHYTRTGELRQVQLPDGADLTLTHDAAGRESLRTGGS
G------FVQQREYDVMGWLTREQSGAQHD-GRLQPAQT-----------------REYRYDGAGNLTGV--
---------------------------------RHNRDAEGYRLDATGRVQEMLSGGAGKPVDTTARFHYTR
TG--LPQ------EAGRLT--------------------------EWQAGRLVQHDDTHYQYDRAGRLIRKQ
VVQPGYRPQVWQYRWDSRNQLRVV------DTPNGERWLYRYDPFGRRVGKRCDQ----------KAEE-TR
YLWDGDQIAEIRHY-RHGQLIQRRHWVYNG---WELVVQ------QRQHTGGDW------------------
----------ETDFVTSSQNGTPQALFTPDGTLRWQVPKATLWGQRQTEKS--------ESPDP-GLAFAGQ
LRDSESGLCYNRFRYYDPAGGCYVSPDPIGIAGGESNYGYVQN-PNTRVDPLGL
>RhsA
---MLNDILSRVARVGAMHAGNRPNPPDDRPQPCRGKPPTSPGKTIKHKSFLGALAGAVAGALVAAAVAAAA
VFLVGVTGGLAVAAVGALAVFAAGDLISAVTNKVSAMVDSASPAFGPVASGSGNVFVEKQPVARA-------
------------------------------------------------------------TKDTVACTKHNSPQ
L--IAQGSESV---FVNDAPAARIDDKTVCGA--TVKEG-ASTVFFGSGQGTYLDIADEFSWW---EKA---
----------------------------------------LLIAVEFLVPPSRGMLKGLGKLFIR-G--PKA
VLRGSRAGA-KWIAGRLADKSSCASKAFKASSGL--------TRAKAAVKAFLKDPVYIASGEVIE---SRT
DIELGQTLPLAFERTYRSAS-VHI-GLLGRGWHDSWSE-VATVTRDGL-----------NTHVVITLAQGYD
IDFTFHQDVQAVYCPHYPEFTLHRRGD---------GFS------LWHRDQQTW------RDFSVVQGERR-
LLSAIHDSHDNRIE---LVRDPK-----GYLRQVRHSDGVTLL--LVWQG--------EFLHQIQRI---DG
```

```
G------QKT-----LLAEYRQDEQGRLVEANATQA-YHLYYDYDAAHRLTRWHDNDQTWARYEY-------
-----------------------DAQGRCV-YTTCADGFLT-ARFDYLPDRVVMTDGLGQCSEFGF------
----------NDLFLMSWEKS--------PLGHVTRYEYDDYGNLLREISPAGRVVEFTYLDDTGRVSTFTD
ASGHQWQYDYDAAQRLCGVTDPLGREWGWMYDA---EGNPERLTGPDASEVRFTWNRYGLLTQVSDAAGEVQ
ARLQYDHRQRLLSATDAESRTRQLRYD------GQDRVVQWQRADGARF-RLGYRRASWTLPEQLIRPDDKE
EQRQYDRHNNLLSYVDGNGALWRQTFGPFDLLTARTDAEGRTWHYAYDKESQQLTTVIAPDGSHWQWWLDAD
GRVIRERDMTGTETHYDYDE-DGLCIRVRN---------GEGD---------TRHFLYDARGLLLRETAPDD
TL----------HYRYDAVGRLTEVS------------SSTAHVQLEYDLRDRMVREWHN---------GTL
LTRQVDDAARTVTRTLTWDGDADDTINALAPLTSLFHYTRTGELRQVQLPDGADLTLTHDAAGRESHRTGGS
G------FVQQREYDVMGWLTREMSGAQHD-GHLLATQT-----------------REYRYDGAGNLTGV--
---------------------------------RHNRDAEGYRLDATGRVQEILSGGAGKPVDTTARFLYTR
TG--LPQ------EAGRLT-------------------------EWQAGRLVQHDDTHYQYDRAGRLIRKQ
VVQPGYRPQVWQYRWDSRNQLRVV------DTPNGERWLYRYDPFGRRVGKRCDQ----------KAEE-IR
YLWDGDQIAEIRHY-RHGQLIQRRHWVYNG---WELVVQ------QRQHTGGDW------------------
----------ETDFVTSSQNGTPQALFTPDGTLRWQAPKATLWGQRQAEKS--------ESPDP-GLAFAGQ
LRDSESGLCYNRFRYYDPAGGCYVSPDPIGIAGGESNYGYVSN-PMCWVDPFGL
>Tse5
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
---------------MSGLPVSHVGEKVSGGV---ISTG-SPTVHVGSSAV---------------------
-------------------------------------------------GLADRVSACV-------------
---------------------------------PL--------V----------GKPVNPMLGSKLL--PEEV
DFALAAPDTFTFARGYLSSN-PRI-GRLGRGWWLPGESMHLELSEDA---------------CVLVDAQGRR
IGFPALAPGAQHYSG-SEELWLRRGGSSGGEAQAWRGRWAAVPAELQTQEGSVLVLSGHSYLHFQRCPDGIW
RLQASFGRAGYRTE---FRWSGR-----GLLTGVRDSAGRS-Y-ALVYQQACEPSEGDDGLRLFGVILASHD
GPPPDYIDPQSPGLDWLVRYQFSDSGDLIAVRDRLGQVVRVFAW-REHMLVAHGEPGGLEVRYEWDVH----
------------------------APHGRVVKQIEAGGLTRT-FRYLRDA--TEVSDSLGRVERYEFAGEGGQ
RRWTALVRADGSRSEFDYDLFGRLVAMRDPLGRETRRRRDGQGRMLEEESPGKARYRKRVDEETGLLVELED
AMQRRWTFERDERGNATTVRGPAGST-RYAYEDPRLPDRPTRIVDPRGGERRLEWNRFGLLAALTDCSGQ-V
WRYDYDNEGRLVASSDPLGQLTRRRYD-----------------PLGQL-------------IGLELADGSA
LSYEYDALGRQTRIADAEGHATLFSWGHGDLLARVSDAGGGELSYLHDEAG-RLVALTNENGVQAQFRYDLL
DRLVEETGFDGRRQRYRYNA-ADELIARED---------ADGR---------ETTYAYDRDGRLASIRVPAT
```

```
EH----APALVERYRWLADGRLASAG------------GADCEVRYTYDEVGNLRLESQV----HADGWVYS
VEHSHDALGVRQTSRYG-DAP---------PVAWLTY--GPGHLHG-ALVGAVELAFERDALHREVRRDARR
DGQDDALFTQERQHAPLGRLQRSRLRLAGG----FDWQ------------------RGYRYDGLGQLVGI--
--------------------------------DDNQYPSVRYEYDLGGRLL-----ASRRAGAAASTYRYDA
AGNRLEGVGEHAREDARQAFAENELYRSGFSRSETRASQAGEGPARWAGNRVERIAGNRYRFDALGNLVERI
GADGERL----RLAYDGAQRLVHLTRD--YADGTRLEARYRYDALSRRIAKVVLR---------DGVEQQVR
FGWDGDRQ--CAEA----FARELRTTVHEPGG-FVPLLR------LEQACEPDPPELLQLRQAFAAEGQPLP
AQCVPALGEARIAFFHTDHLGTPLQLSDERGQLRWQGVPDD-WRAVAPERQ---------PGAQ-PIRFQGQ
YHDEESGLYYNRYRYYLPEAGRYASQDPLGLGGGPNPYAYALNAPTLAYDPTGL
>Tke4
---MAQTVHAARMGDAILHPSLAAEMISAVAEAVIYAAATAA---VAAAISLAVVGTVATGG----AAGVAI
AAVAGVAVGAV-STLSVGEDQTVGDAISSFCDSLGNSVDSPDP-YGKIESGSTNVLINSEPAARAAGITGPP
GGGAADTEQEEPSILENVGSMAMAAVPYLVPFVGLGMAIRDIFNPPVTTPANPGSEPAEGDKISCSRHPPLP
DTFIAQGSDKV---FINGQPAARSGDKTTCDATIDVNENVSPNVRIGGGTATVRDIRN--------------
----------------------------------------GKSKIAMFTGIIAGMLISR-RFGRIKG-----
-----------------------CTL----------------------------GNPVAVATGSKLQEGPEDI
DFNLPGLLAIQWARRYDSRDMRSD-GLLGMGWSVPYEVELARVPHPQG-----------GTLWIYIDNDGNR
LELGRLSAGDAFISA-VDGLAFFQLED---------GQTV-----VEDINEGLY----RVFDTDPLNPKRS-
RLIRLGDRNLNCLD---LLYDEQ-----GRLKALYDKYGQTVV-QLHYAARHP-----QRVSEVSRVFLKNG
G------TPTVERSELLVSYRYTDNGQLHEVLDATDQRVRRFTYTPEGYLNSHQLASGAVREYEWARFAIPE
TRPTPKRLDGTPYRLPPLLEPQPDHEWRVIRHWGSDGEEYR-FEYNLEAGETLVTDNLGRRDHYYW---GPL
YEVYKHIDPQGN-CWLAEVIAGQLIKRIDPQGGEWRYSYDDIGRLIETRDPLGRSEHIKYLRHWALPIQVTD
TAGRTRQYGYDSHGNLLWQQDPLGRETQYQYDP---EGRVTQVTDALEKSKYLSWNTCGQLLSYRDCSNA-Q
TLYHYDAHGRLRESINARGEHTHFRYD-----------------ARGYL-------------VESERPDGRI
DRYEIDVAGQLTRYIDPAQKTLQFRYDPSGRLVERTDAMGYSVKFRYDAYG-RLLQLTNENDESYRFGWDEL
DRLVAQKDLDGSGRLYAYNV-LDEVIRLTHVPSPDEQPPLSDNAPPTRTTAIRHDFERDAIGRLVSKRTEDG
TT----------DYRYDAADNLLSIT-------FTDNKGEKQQLDYTYDANGQLLSETNS---------AGL
LQYRYDELGNLQTLVLP-DQR---------ELNHLYY--GSGHLHQINLNGRVISDFERDAVHDEVLRTQGK
-------LVTRTRYDTSGRLAGKAIHYRDAPAEVLPLLD-----------------KAYRYDASDNLIAEVL
TQTQRRGMSNAANDENANLEQIIGRFLDLPHTGKTYSGHNRYGYDLNEQLQTVHQSRPNWQATQVEDFKYDK
AGNLFDG--------PKLN------------------------GLIKHNRVLVYQDKRYRYDRFGRLCEKR
IGSNWVQ----YFEYDAEQRLVCVEQY---RSGERERVVFAYDPLGRRISKEVYQ------RDYPEPRRRVL
FHWQGFRL--LQEV----QSGLASLYVYATVESYDPLAR------VDGKP----------------------
```

```
-------GSEAIHYFHTTLVGQPEQLTDSDGNTIWRSDHHG-WGKIINEWH-----SQQNGREQ-NLRNQGQ
YIDRETGLHFNIFRFYDPDIGRFTTTDPLGIEGGVNLYSYAPN-IVNYSDPLGL
>Rhs1
---MAE-IWAARKDDELIHTSALADIASAVAEVAVYAVATAAVSAAAAAAAPALAGVAVLGA--AATAASGC
VG-AGLIVGFATSLTGV------GEHISNGCDAVANWLFPPSV-SGVILTGSPNVFTNAKPAARAAGRLLTP
AEIKALPAPQPPQSFWDYG---------AELLAAGGNILSQLWQPGVAGPSQPSQ-PLEEDKISCDKHPLPQ
Y--LAEGSSKV---FINGQPAVRSNDRSTCEA--KVSTDVSKNVQIGGGTVVVRD-----------------
----------------------------------------IKSGKLPGIGLALTVLPLL--LGNPAK--LVK
NLPCMIGGGLAAAGVNALGEAIHAA----------------------------FNPVHAATGAKVLNDEEDL
DLLLPARFPLIWQRNYNSRN-GYQ-GLFGHGWRTPFEIWVDLNDRDG------------VIECCLHDETGRE
LRFPLPEVNQPSFSA-GEGLMFRRGEE---------GQLL-----IADTDGSVW----RLFVPLPQTPSRL-
RLVSLSDEYDNALL---LNYDER-----QRLSHIVDSAGTMTL-RLEYGDP-------RFDDRVTALRHND-
-------EPR-------VRYRYDGGGDLHQVIDAGGLVTREFHYNAQHLLTRHQQAGGPSFAYRWAMF----
------------------------DDWRVVEHRDSAGGGCT-IDYDLAAGLTTVTEYDGLRHQHRW---NAQ
RLIVEYTDERGEVWHYQWNDEDMLIATRDPLGHGWHFRYDEAGNLVEEEDPLGHIRLTGWLPQRALPISVKE
PNGATQHFYYDERHALIAEIDALGHTQRYLRDG---YGQVVQAVDANGGISHFAYDEHGQLLRARDCSGK-Q
TLYKYTAQGWLSEVTDAAGERVHYRYD-----------------AAGRL-------------TQLQRAEGWQ
ETLSWNAQGQLDRYQGADGRLTHYRYDAAGRLLATRNPLDGEVVRHYDARG-RLTALRNENAESYLFHWTAC
NLLQEEIGLDGVSTRYRYDE-CRRVVERRFAANTSAAF--------------SHYFSHDGAGQLVSKQTPDG
ET----------RYRYSPLGQLLHAASYRGNAWHDEPTTAQSEVSFDYDLLGRVTREQGA---------NGT
LRYDYDPMGNRTQTTLP-DGR---------TLRALYY--GSGHLLQLALDEITLSEFERDNLHRELSRTQGR
-------LTSRVHYDRLGRKDRREIFNDNR-QRPAPASS----------------SRQWSYDYQNNLTRE--
------------------------------EHNANPFSYQRYQYDATGRLL-----SRDGTRPDTERYRYDP
ASNLLDE-----------------------------------GQFRQRHNRVLHYQGIDYRYDVFGRTVEKR
KGHYRW-----QYLYDADHRLCEVVRYSQHRSEAQQHVHFHYDPLGRRTQKRVWQQSQDLRQPAGKCQT-TT
FLWEGFRL--LQET----RDGMPLTYVYADQGSYEPLAR------IDGH-----------------------
-------APAQVFYFHTAPNGEPESLTDSDGTLRWQSHSSA-WGRIKYEEN-----QQDLDYSQ-NLRLQGQ
YLDRETGLHYNLFRYYDPDIGRFTQHDPIGLAGGINLYQYAPN-PLGWVDPWGW
>Tke2
------MFEAARFGDEISHTSALGGFLIG----------------------------AALGI-----ALVAT
VAIATFTCGFGVALLAGLAAGIGGSLLTAAGEAIGSMFSSPS---GTITTASPNVFINSRKAARV-------
-------------------------------------------------------------EKSIGACDKHPGPV
Q--IAEGSTNV---FINSVAAARKGDKLTCGA--TISGG-SDNVIIGGGTYRYLPVDDEVPEWLRT------
```

```
----------------------------------------TVDVLMAIAGAAGGIAQLI-KAGTQAG--MKA
VMPCALKFTAGFVAGEVASRYVVEPVAR---KAI---------------GGLVGNPVDLTTGRKLI--PDEI
DFSLPGLMPIEWSRFYASDL-TVD-SVLGRGWVLPWEQSLRRQ----------------GAFIYLTDNQGRE
VPFVTLQPGQRIYNP-HEQVYLVCTEG---------GHYI-----LQTLDNLFF-----YFGEVPDTNTEV-
PLQRIENVLGHFLH---FTRTPD-----GTLTDISATGGTRVH--LHYDNPL------GRLTDIKRVVNNEA
V------ETL-------TQYRYDEHGQLSAVINRNGDTVRSFSY-ADGLMVTHSNALGLGCHYRWQTL----
-----------------------GDKPRVVEHWTSDGEHYH-FRYDLDSRTSWATDVLGRELEVQY---NAD
HRVVASRDYGGERYAIELDEHGNMVGLTLPDGNRLQFKYDEFSRLLEETDPLGRKTQYEYHHLTTLVTQVSY
PDGSTWRARFDDKGNLLAEFDALGQMTEYLNSD---DGLPHTIIDATYKSKYLWWNTLAQVERYQDCSGK-S
TYYRYDERQHLVAVTDALNQTTTLARK-----------------PDGEV-------------LRISHPDGTT
ESFTYNVYGQVLSHTDGKGQTTRLMRTARGLPSSRQDAKGQRVRYEYDKAM-RLTALVNENNATYSFAYDAS
DRLSEEVRVDNLTRRFSYDV-GGHLTRLDEIGY-GENAERPER---------HTLFERDAIGRLIAKLNSDA
QQ----------RFTYDDGDRLLSIE-RQPTGIGKQLGITEEKLEYAYDLLGRLTKEISP---------DGT
LGYEYDPLSNLTTLTLP-DGR---------KVNHLYY--GSGHLHQLNLDGQVISDMERDDLHREVYRTQGK
-------LTSCFGYDAMGRKAWQFASTLPA-DKLSQVHNTGINTSLLVEHAYNPIHRRYQYDPAGELVRT--
--------------------------------LDKLRGEIKYEYEANGQLR----SRDTGSLIGSEEFRYDP
AANRLDF------NARQFD--------------------------KVKDNRIKQWRDQEYRYDPWGNLIEKR
SGHSKLQ----HFSYDCENRLVRAETL--VNGKLESQGEYRYDSLGRRIAKQAEI--------NGEVEQ-KR
FLWQGLRM--LREE----TPGQSILYLYEPGS-YAPLAR------VDQVEG---------------------
-------EGQKVYYFHTDQIGTPLELTDSEGEIVWQATYRS-WGTIETLSI--------KEVDQ-NLRFQGQ
YFDAETGLHYNTFRYYYSEVGRYVTQDPIGLDGGLNLYRYGQN-PAGWIDPWGW
>Rhs2
------MTEAARVGDTIGHSHALAGMIAG----------------TLVGGLIAAAGALAAGALFVAGLAASC
IGVGVLLIGAS-LAVGYLT----GEAATAARDGIADAGAGSLTPKGNIVTGSPNVFINGKPAALA-------
------------------------------------------------------------TNSQVACSDDGPSM
Q--MAQGSDKV---SINGQPASRVGDKTNCDA--QVMEG-SPNVFIGGGTVTTLPIKPEVPDWLYK------
----------------------------------------VSDLTLLFAGLVGGVGGAAGKLGALGK--LLG
KLPGI----------NKLARIACRAGTLMTATAA---------------VGIIARPVDIVSGQKFLDGEDDL
DFVLPSRLPVAWQRYWRSGN-PGD-SVLGRGWNLFWESSLQPY----------------QDGLVWRAPSGDF
VAFPMVPRGHKTYCE-AEKCWLMHNDD---------GSWQ-----LFDVGEQIF-------HYPPLAGEQPS
RLSMITDAIGNATS---LFYDDE-----GLLSELVDSAGQRLM--CRYAQ--------GRLREV-ALQTAEG
E------RTL-------ARYGYDEQGQLTTVSNRAGEVTRRFGW-RDGLMISHQDAAGLLNEYQWQEI----
-----------------------DGVPRVTAYRNSAGESLE-FGYDFAGGRRSAVRGDGKRAEWRL---DDD
```

```
DNVAQYTDFDQRRYGFIY-QRGELCSVLLPGGAQRQSEWDPYGRLLSETDPLGRVTRYQYSRNSGRLFAVAY
PDGSSEAQHWDTLGRPTRYVDALGNTTLYRYPDDE-ESLPASVIDALGGEVKLEWDARGQLTRYTDCSGS-V
TAYTYDALGQLTAQTDAEGHQTRYRWD-----------------NGGRL-------------HTLIHPDGGE
ERFNWNAHGQLAEHQDALGSLTRWQYNALGLPVSITDRINRTRRYHYSPQG-WLTRLENGNGGDYRFSYDAV
GRVVAEERPDDTRHYYRYGA-AGLLEEHREVGLPGGAGELTQR---------EQRFRFDEAGQLVWRSNASA
EW----------HYRFDAMGRLRELN-RLPTASGVALGIEPDSVQMRYDAAGRLLGEQGV---------NGE
LQYQWDALANLQALTLP-QGD---------RLQWLYY--GSGHASAIKFNQQVVSEFTRDRLHRETGRSQGA
-------LQQQRRYDAMGRRSWQSSAFGHD-KLTRPEDG--------------VLWRAYRYTGRGELAGV--
--------------------------------SDALRGEVHYGYDAEGRLL---QHREPNQGKPGARLVYDL
ADNLLGE------RSPQSD------------------IDAHLPLAPIADNRLTHWQKLFYRYDAWGNLISRR
NGLYEQ-----HYRYDADNRLVQAHGR---GPQGEFEAQYHYDALGRRSRKTVHY--------KGKTEQTTH
FLWQGYRL--LQEQ---RDDGSRRSWSYDPASPWSPLAA------LEQAGDS--------------------
-------RSADIYWYHTDLNSAPLEVTDAAGNLCWSGQYDT-FGKLQGQTVAGAAKRQGAQYQQ-PLRYAGQ
YQDDESGLHYNLFRYYEPEVGRFTTQDPIGLEGGLNLYAYGPN-PLTWIDPFGL
```

Supplementary file S4d

```
>ab736_7
--------------------MLPVVIGIIELAGYAITAYEL--------YRTAANAYDEVKNYQDNIK---K
AKEEIKKIMKNLDKE-----ITDKIDRQREKVLLTTLTTGDKQTN--STKSASGRPQVKSNVITA-----AI
KQKIPFRPIISQIC-EKADHLPMIQLRKQKGKKLKDVIPKSKVDIVAKLL----KMTAQELAGASVDEYIII
RLKQLAVNFMFEFMDELLKWRSPLKSEVCFGYDIKTRKYLAPQ----LDGQTRIKRVGSELNPFWPMPYKGK
GVIGADIIIPEYRGEPLTLTNIFALVEIKFQNDRIDEKQFNNYNDLKKQCADVKHAGKITGSEGFKLSLFRY
PEDASTTEAKDSKPATMNKKRKTN
>ATCC19606_7
--------------------MLPVVIGIIELAGYAITAYEL--------YRTAANAYDEVKNYQDNIK---K
AKEEIKKIMKNLDKE-----ITDKIDRQREKVLLTTLTTGDKQTN--STKSASGRPQVKSNVITA-----AI
KQKIPFRPIISQIC-EKADHLPMIQLRKQKGKKLKDVIPKSKVDIVAKLL----KMTAQELAGASVDEYIII
RLKQLAVNFMFEFMDELLKWRSPLKSEVCFGYDIKTRKYLAPQ----LDGQTRIKRVGSELNPFWPMPYKGK
GVIGADIIIPEYRGEPLTLTNIFALVEIKFQNDRIDEKQFNNYNDLKKQCADVKHAGKITGSEGFKLSLFRY
PEDASTTEAKDSKPATMNKKRKTN
>AB030_24
------------------------MKRSLTLLLSTFISIQA------------------------------
--------------------FAE---------------ENACEKI--WDSFKNKNESIKIDKVNV-------
```

```
--PCKQIWED----------SNKAKLVKTIGLNPKDAQWM--------------STGECQVIEVNKNKYQVY
YAYLKN--------DHSDINIINDTNGNYFSYYRNLGRYDM------FEDKFYPTKKAN-------------
-KNGVELSCP----GLGNFEKMKPILSSYINNKKIDIKRF--------SFEDLNK-----------------
------------------------
>AbH12O-A2_24
------------------------MKRSLTLLLSTFISIQA------------------------------
--------------------FAE---------------ENACEKI--WDSFKNKNESIKIDKVNV-------
--PCKQIWED----------SNKAKLVKTIGLNPKDAQWM--------------STGECQVIEVNKNKYQVY
YAYLKN--------DHSDINIINDTNGNYFSYYRNLGRYDM------FEDKFYPTKKAN-------------
-KNGVELSCP----GLGNFEKMKPILSSYINNKKIDIKRF--------SFEDLNK-----------------
------------------------
>AF-401_24
------------------------MKRSLTLLLSTFISIQA------------------------------
--------------------FAE---------------ENACEKI--WDSFKNKNESIKIDKVNV-------
--PCKQIWED----------SNKAKLVKTIGLNPKDAQWM--------------STGECQVIEVNKNKYQVY
YAYLKN--------DHSDINIINDTNGNYFSYYRNLGRYDM------FEDKFYPTKKAN-------------
-KNGVELSCP----GLGNFEKMKPILSSYINNKKIDIKRF--------SFEDLNK-----------------
------------------------
>AR_0063_24
------------------------MKRSLTLLLSTFISIQA------------------------------
--------------------FAE---------------ENACEKI--WDSFKNKNESIKIDKVNV-------
--PCKQIWED----------SNKAKLVKTIGLNPKDAQWM--------------STGECQVIEVNKNKYQVY
YAYLKN--------DHSDINIINDTNGNYFSYYRNLGRYDM------FEDKFYPTKKAN-------------
-KNGVELSCP----GLGNFEKMKPILSSYINNKKIDIKRF--------SFEDLNK-----------------
------------------------
>AR_0101_24
------------------------MKRSLTLLLSTFISIQA------------------------------
--------------------FAE---------------ENACEKI--WDSFKNKNESIKIDKVNV-------
--PCKQIWED----------SNKAKLVKTIGLNPKDAQWM--------------STGECQVIEVNKNKYQVY
YAYLKN--------DHSDINIINDTNGNYFSYYRNLGRYDM------FEDKFYPTKKAN-------------
-KNGVELSCP----GLGNFEKMKPILSSYINNKKIDIKRF--------SFEDLNK-----------------
------------------------
>AB031_25
```

```
-------------------------MKVLKIVIGTYIL---------------------------------L
NSISLYAES-----------------------------TNECMKY--WSEKSAASLKV---LGEV-------
--ECENIWEYG----KSNVTQGRLKLLNQLKLKPNNNQW---------MS-----TGECSKVSYNKNNYYIY
RAYYKE--------DRDEIWIAYNDKGSFSY----------------FRKVSSPKKEGE-------------
-NSKVSLSCA----KNGEYDEARSVLNTYLKNNTSVSMSYYKVGDWYKGD----------------------
------------------------
>Ab04-mff_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLDGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>BJAB0715_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLDGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>LAC-4_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLDGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>WKA02_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLDGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
```

```
------------------------
>XH858_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLDGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>AR_0088_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>CIP70.10_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>HWBA8_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>R2091_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KGI
AKSNLFFICIDGKKV-----FEQVKEDLLQNLSRNKNITNDCYFVHGFGVAMTRSLEELRDQIKAKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESRSIL-
```

```
--NLKKVNLE-QSIELDLIEIANNVFQQLSEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMDYVTKDLYEQ---IAKELNG-----------------
------------------------
>D1279779_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KEI
AKSNLFFICIDDKKV-----FEQIKEDLLQNLSRNKNITNDCYFVHGFGVAKTRSLEELRDQIKTKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESQSIL-
--NLTKVNLE-QSIELDLIEIANNVFQQLNEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMNYVTKDLYEQ---IAKELNG-----------------
------------------------
>R2090_12
MSLSVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KEI
AKSNLFFICIDDKKV-----FEQIKEDLLQNLSRNKNITNDCYFVHGFGVAKTRSLEELRDQIKTKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESQSIL-
--NLTKVNLE-QSIELDLIEIANNVFQQLNEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVTNVLYDHCVMNKMSFTDAMNYVTKDLYEQ---IAKELNG-----------------
------------------------
>ZW85-1_20
MSLLVFNTTQYEDLKDITSKIEEQCIQILNEYGQIIFLLDTTLNDSIFNGVIDNLSNKNIAYIPLAHK-KEI
AKSNLFFICIDDKKV-----FEQIKEDLLQNLSRNKNITNDCYFVHGFGVAKTRSLEELRDQIKTKLVISDQ
GKKILFRWYDPRVM-IYLDEIFKTEYVGGLLNGFKEWHF---------LH----PKGLFSFKSYDESQSIL-
--NLTKVNLE-QSIELDLIEIANNVFQQLNEFEQVDLIKIHPVEIHQNLKEAYYDFGIQNHLDLVTYGLYSQ
IIHKNFIQHP----MVINVLYDHCVMNKMSFTDAMNYVTKDLYEQ---IAKELNG-----------------
------------------------
>Ab04-mff_11
----------------------MNMIEILQSKRSQFYLLDINS------LIILALAFCGVIISSTVYA---K
DIFNVELKCKGNDQE-----YCDIVK------------NSDNKTT--FILRNMRYPEVDKVNENIFHAYGSC
GSPCQYHFFI-----SKIQEDQTKEFIAL--DKKNN-----------------------CLIESDSKKNIIY
ARKLFN---------KNKKIIANLKNKEFNNVPIDSAIYNS------FQEKSYFDDKGQLH-----------
-LVAMLADVD----KNGNSLYFNKIIKKT--------------------CE---------------------
------------------------
>BJAB0715_11
----------------------MNMIEILQSKRSQFYLLDINS------LIILALAFCGVIISSTVYA---K
```

```
DIFNVELKCKGNDQE-----YCDIVK------------NSDNKTT--FILRNMRYPEVDKVNENIFHAYGSC
GSPCQYHFFI-----SKIQEDQTKEFIAL--DKKNN-----------------------CLIESDSKKNIIY
ARKLFN---------KNKKIIANLKNKEFNNVPIDSAIYNS------FQEKSYFDDKGQLH-----------
-LVAMLADVD----KNGNSLYFNKIIKKT--------------------CE---------------------
------------------------
>WKA02_11
----------------------MNMIEILQSKRSQFYLLDINS------LIILALAFCGVIISSTVYA---K
DIFNVELKCKGNDQE-----YCDIVK------------NSDNKTT--FILRNMRYPEVDKVNENIFHAYGSC
GSPCQYHFFI-----SKIQEDQTKEFIAL--DKKNN-----------------------CLIESDSKKNIIY
ARKLFN---------KNKKIIANLKNKEFNNVPIDSAIYNS------FQEKSYFDDKGQLH-----------
-LVAMLADVD----KNGNSLYFNKIIKKT--------------------CE---------------------
------------------------
>XH858_11
----------------------MNMIEILQSKRSQFYLLDINS------LIILALAFCGVIISSTVYA---K
DIFNVELKCKGNDQE-----YCDIVK------------NSDNKTT--FILRNMRYPEVDKVNENIFHAYGSC
GSPCQYHFFI-----SKIQEDQTKEFIAL--DKKNN-----------------------CLIESDSKKNIIY
ARKLFN---------KNKKIIANLKNKEFNNVPIDSAIYNS------FQEKSYFDDKGQLH-----------
-LVAMLADVD----KNGNSLYFNKIIKKT--------------------CE---------------------
------------------------
>ab736_9
-------------------------MSGANIVVPKISLPTIKTP---------------------------
--------------------F-----------------SNKINYN--WNINSEGKKELFIINKKN-------
--NILIRSHK-----NELDKNNNLSSLRFYTPEEVD----------------------FTAMIFNSD-YIQL
KQNIPD-----------SENIDEL-----------------------FEETLLYDEEND-------------
--------------DVYTEEEF-----------------------------------------------
------------------------
>ATCC19606_9
-------------------------MSGANIVVPKISLPTIKTP---------------------------
--------------------F-----------------SNKINYN--WNINSEGKKELFIINKKN-------
--NILIRSHK-----NELDKNNNLSSLRFYTPEEVD----------------------FTAMIFNSD-YIQL
KQNIPD-----------SENIDEL-----------------------FEETLLYDEEND-------------
--------------DVYTEEEF-----------------------------------------------
------------------------
```

```
>ab736_10
----------------------MEIFTQSADFLENIFAPTEEIDESFYYFLIDSSSFSGVDSFCKDFPFDGG
QKINLYLDFSENLQENGALLYSFTHEECIKNIELIKNIRDQGGLN--FFNSYFEIEQIKEHLEELMEIKQPN
GKSALFRFQDSFAFHATVSVLNELKWRKILSFKINYWIWQNIDNTFHRLDNFPTNRSILTTLSFSEDEFKDI
NINLKPMRLM-PLLKEYDENLKDLPFYQLYEIAINLLKEAKKQQLISFEDEILFSTLYH-------------
-KFGEFLLAE----GPFKKALNKTQMTAMSFQKTTDEIDLEELDDWYKRYQEVQV-----------------
------------------------
>ATCC19606_10
----------------------MEIFTQSADFLENIFAPTEEIDESFYYFLIDSSSFSGVDSFCKDFPFDGG
QKINLYLDFSENLQENGALLYSFTHEECIKNIELIKNIRDQGGLN--FFNSYFEIEQIKEHLEELMEIKQPN
GKSALFRFQDSFAFHATVSVLNELKWRKILSFKINYWIWQNIDNTFHRLDNFPTNRSILTTLSFSEDEFKDI
NINLKPMRLM-PLLKEYDENLKDLPFYQLYEIAINLLKEAKKQQLISFEDEILFSTLYH-------------
-KFGEFLLAE----GPFKKALNKTQMTAMSFQKTTDEIDLEELDDWYKRYQEVQV-----------------
```

Supplementary file S4e

```
>6200_21
---------MSIDNLEYFLD---KELLLPLKVP-----------SNWYISKNYL---------------YQV
SC-----NWLNQ------------------------------------------------------------
---------------------------LNDEDKFK------------MSEIFLYKNIFYAKLE---------
RIINNLTYSFVIDISIY-----PEIEEGLYTKFEYE--IGVGLYEISKKNKLIFMRNF--NFYN-IVEVCE-
-------FLNIILIDVCHSL-------------------------------------GESI-----SEID---
IFKNVD---NFFEKNK--------------------------------------------------------
---------------------------
>KAB01_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>ACICU_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
```

```
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>A1296_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>AbPK1_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>AR_0056_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>KAB03_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
```

```
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>1656-2_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>DU202_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKVSVLS-----EINGFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECNYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>R2090_8
------------MRSKIFIS----VILFGLSAC------AAKADQNQLKDRELD----KLVACNGGNTEYTN
ID-----GYFTI----------------PDFGC---PYDGKNNKIGNA---MVYLIAPDHNNDYIQLNNMKN
IKGKYIYIVPFKFLNQD-----------KKSGSFY----------IAKDNYSYEVYFNEGGKW---------
VRKPDIIVSNNKISVLS-----EINSFLNDRAKSFS--KKTEKKLKKYKMDINHDGVE--DFIE-VVGKDNK
P------SSIHILNGLDNSL-------IYKNDKIF--------NNSFNECDYSSFDNISI-----SKNN---
FTLEYS---TCADSSQIGYRYATFKTDKNKEPILIQDNYLVS------------------------PREETS
DNFKPKKVNCLTSSKITFNQFNGRCG-
>6200_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------IEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
```

```
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>WKA02_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>AR_0083_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>USA15_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>IOMTU433_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
```

```
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>A1_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>A388_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>A85_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>AB0057_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
```

```
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AB307-0294_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AB5075-UW_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AR_0078_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>D36_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
```

```
---------------------------
>SDF_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>WCHAB005078_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFIDKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>AB030_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFINKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
>AbH12O-A2_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ---------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFINKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS-------------------------------------------------------------
---------------------------
```

```
>AF-401_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFINKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AR_0063_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFINKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AR_0101_15
----------MQTWNKAFFK---FMTIILMGTC--------CIACDLRKKNEVT----V----------VEN
KN-----IIIKK----------------FESDA----EYIFGNQ----------------------------
---------------------------ILGKKIFS--------------------SYNAERLI---------
FQVKDLEQNSDNFINKI----------------------DGRLNKRGWNYKEKYKEAY--IYCD---RDMN-
-------QLELVPPIKIGTV--------------------MQSGEGQSLNQLVDYWNIGF-----IHSR---
HKRYVC---NMNS------------------------------------------------------------
---------------------------
>AB030_24
-------------MNKILIA----LSFLFLTAC-----------NDFNKLEKES------------------
NA-----SIEHQ--------------------------------------------------------------
---------------------------NESNSVIK-------------------------------------
---SQLSNSNDSLIKET-----TVSQVKDKKIENSK--PQMDAQDKITCMGKTLNDWY--TFDE--------
-------KLEQPKCKKLNGY-----------------------KLKNYQCSVEKNVFDLN-----SDAI---
RITMKD---TRVFAFHSLEQCQEAVEMWEANGI-----------------------------------------
---------------------------
>AbH12O-A2_24
```

```
-------------MNKILIA----LSFLFLTAC-----------NDFNKLEKES------------------
NA-----SIEHQ-------------------------------------------------------------
---------------------------NESNSVIK-------------------------------------
---SQLSNSNDSLIKET-----TVSQVKDKKIENSK--PQMDAQDKITCMGKTLNDWY--TFDE--------
-------KLEQPKCKKLNGY----------------------KLKNYQCSVEKNVFDLN-----SDAI---
RITMKD---TRVFAFHSLEQCQEAVEMWEANGI-------------------------------------
----------------------------
>AF-401_24
-------------MNKILIA----LSFLFLTAC-----------NDFNKLEKES------------------
NA-----SIEHQ-------------------------------------------------------------
---------------------------NESNSVIK-------------------------------------
---SQLSNSNDSLIKET-----TVSQVKDKKIENSK--PQMDAQDKITCMGKTLNDWY--TFDE--------
-------KLEQPKCKKLNGY----------------------KLKNYQCSVEKNVFDLN-----SDAI---
RITMKD---TRVFAFHSLEQCQEAVEMWEANGI-------------------------------------
---------------------------
>AR_0101_24
-------------MNKILIA----LSFLFLTAC-----------NDFNKLEKES------------------
NA-----SIEHQ-------------------------------------------------------------
---------------------------NESNSVIK-------------------------------------
---SQLSNSNDSLIKET-----TVSQVKDKKIENSK--PQMDAQDKITCMGKTLNDWY--TFDE--------
-------KLEQPKCKKLNGY----------------------KLKNYQCSVEKNVFDLN-----SDAI---
RITMKD---TRVFAFHSLEQCQEAVEMWEANGI-------------------------------------
---------------------------
>AR_0063_24
-------------MNKILIA----LSFLFLTAC-----------NDFNKLEKES------------------
NA-----SIEHQ-------------------------------------------------------------
---------------------------NESNSVIK-------------------------------------
---SQLSNSNDSLIKET-----TVSQVKDKKIENSK--PQMDAQDKITCMGKTLNDWY--TFDE--------
-------KLEQPKCKKLNGY----------------------KLKNYQCSVEKNVFDLN-----SDAI---
RITMKD---TRVFAFHSLEQCQEAVEMWEANGI-------------------------------------
---------------------------
>AB031_25
-----------MRFIFAFFI-------IFLSAC---------SHSNTIADKKSY---------------LDF
```

```
NS-----VNLKD--------------KSYIIGN---KYSDVN------------------------------
---------------------------FSSKGIAK---------------------DQIGSCT---------
-TFSDFNNSISYTLNNQ-----KLVEVLIGNENKSI--YTSKNIRNGMGVENIYKNYK--GYNI--------
-------KKMKS--------------------------------DGAGDSQDDYTYIVTDN-----LQKN---
NSLIFD---VVHGKIQGIHLGKKGFDLSDCE----------------------------------------
---------------------------
>Ab04-mff_11
-------------MSRLF-----LLFVISLMYA--------CTTEADQPKSSNT----K----------LYF
SY-----RICEK----------------AGKCK---NFTPTKKMDNYLFKRLDPAYDEFYI-----------
---------------------------KDNNGNFT--------------LYYKNVYSEDVQVG---------
WAEAKADKNNSSELSLN-----IDKVNLALGGIDFI--KNGYATKQAESKNFKSGIYY--LADN--------
-------YTGAPYYQKQKIF--------FKK------------NAGDLVLDCNSYLNNPS-----VKNESYG
VFYGVC---SEGEKVYFKQVN--------------------------------------------------
---------------------------
>BJAB0715_11
-------------MSRLF-----LLFVISLMYA--------CTTEADQPKSSNT----K----------LYF
SY-----RICEK----------------AGKCK---NFTPTKKMDNYLFKRLDPAYDEFYI-----------
---------------------------KDNNGNFT--------------LYYKNVYSEDVQVG---------
WAEAKADKNNSSELSLN-----IDKVNLALGGIDFI--KNGYATKQAESKNFKSGIYY--LADN--------
-------YTGAPYYQKQKIF--------FKK------------NAGDLVLDCNSYLNNPS-----VKNESYG
VFYGVC---SEGEKVYFKQVN--------------------------------------------------
---------------------------
>WKA02_11
-------------MSRLF-----LLFVISLMYA--------CTTEADQPKSSNT----K----------LYF
SY-----RICEK----------------AGKCK---NFTPTKKMDNYLFKRLDPAYDEFYI-----------
---------------------------KDNNGNFT--------------LYYKNVYSEDVQVG---------
WAEAKADKNNSSELSLN-----IDKVNLALGGIDFI--KNGYATKQAESKNFKSGIYY--LADN--------
-------YTGAPYYQKQKIF--------FKK------------NAGDLVLDCNSYLNNPS-----VKNESYG
VFYGVC---SEGEKVYFKQVN--------------------------------------------------
---------------------------
>XH858_11
-------------MSRLF-----LLFVISLMYA--------CTTEADQPKSSNT----K----------LYF
SY-----RICEK----------------AGKCK---NFTPTKKMDNYLFKRLDPAYDEFYI-----------
```

```
---------------------------KDNNGNFT--------------LYYKNVYSEDVQVG---------
WAEAKADKNNSSELSLN-----IDKVNLALGGIDFI--KNGYATKQAESKNFKSGIYY--LADN--------
-------YTGAPYYQKQKIF--------FKK------------NAGDLVLDCNSYLNNPS-----VKNESYG
VFYGVC---SEGEKVYFKQVN-----------------------------------------------------
---------------------------
>LAC-4_11
-------------MSRLF-----LLFVISLMYA--------CTTEADQPKSSNT----K----------LYF
SY-----RICEK----------------AGKCK---NFTPTKKMDNYLFKRLDPAYDEFYI-----------
---------------------------KDNNGNFT--------------LYYKNVYSEDVQVG---------
WAEAKADKNNSSELSLN-----IDKVNLALGGIDFI--KNGYATKQAESKNFKSGIYY--LADN--------
-------YTGAPYYQKQKIF--------FKK------------NAGDLVLDCNSYLNNPS-----VKNESYG
VFYGVC---SEGEKVYFKQVN-----------------------------------------------------
---------------------------
>15A34_23
--------MMMKKLISLLVL---IIVAFPTVAR-----------------------------------IPK
GD-----YIMID------------------------------------------------------------
----------------------------KKKGGFV-------------------------------------
RLCKSESTEELENIILT-----DKSLHLALPESTEY--LILKEKMNKNEHILEVRNPY--NIVY-TYKIKK-
-------INNSDVYKWDAYL------------------------GNKRIEDLSFFSIAK-----NKAK---
NIISVG---ICK------------------------------------------------------------
---------------------------
>A1_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK--------------------------------------------------
---------------------------
>A388_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
```

```
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>A85_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P-----------------------------------
---------------------------INGDEVIE-----------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>AB307-0294_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P-----------------------------------
---------------------------INGDEVIE-----------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>AB5075-UW_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P-----------------------------------
---------------------------INGDEVIE-----------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>AR_0083_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P-----------------------------------
---------------------------INGDEVIE-----------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
```

```
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>AYE_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>D36_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>WCHAB005078_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDNLV----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK-------------------------------------------------
---------------------------
>6200_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDSLV----------------------TVKVEYHQYSEFINFVI-----NKES---
```

```
SCKKIGNIKYDDGSDLIKMLRK--------------------------------------------------
---------------------------
>ZW85-1_17
--------------MKLLIL---EILCLSLLSG-----------CASAKEAEC----------------YNT
SK-----ALITD----------------LYNKF---P-----------------------------------
---------------------------INGDEVIE------------------------NKNI---------
KTLSNFFDKNLTNLLIK-----DQECSAR----------NNGVCNIDFNILIHSQDTP--NKYK--------
-----------ILQDTDSLV-----------------------TVKVEYHQYSEFINFVI-----NKES---
SCKKIGNIKYDDGSDLIKMLRK--------------------------------------------------
---------------------------
>ab736_9
-------------MKKYFTT--VLLIISSLIYS-----------QNIFANDQCN----I---------EETV
NL-----TIFKK------------------------------------------------------------
----------------------------NDYKFYN-------------------------------------
YMCDSVEGSYLKGYLGS-----QEKKIFVSDYSDFA--AKESPKLLAVSIYKSKKRKP--PILI--------
-------TLNSSYYCCTPQM-----------------------EGEMYQVNLYQISENKT-----LNLK---
NITNIL---GVNAEGFEGRAEGKVYYKYKNISEIKKWLDKNY------------------------------
---------------------------
>ATCC19606_9
-------------MKKYFTT--VLLIISSLIYS-----------QNIFANDQCN----I---------EETV
NL-----TIFKK------------------------------------------------------------
----------------------------NDYKFYN-------------------------------------
YMCDSVEGSYLKGYLGS-----QEKKIFVSDYSDFA--AKESPKLLAVSIYKSKKRKP--PILI--------
-------TLNSSYYCCTPQM-----------------------EGEMYQVNLYQISENKT-----LNLK---
NITNIL---GVNAEGFEGRAEGKVYYKYKNISEIKKWLDKNY------------------------------
---------------------------
>DU202_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
```

```
---------------------------
>TCDC-0715_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AF-673_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>CMC-CR-MDR-Ab4_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>CMC-CR-MDR-Ab66_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
```

```
>CMC-MDR-Ab59_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>15A34_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>15A5_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>1656-2_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>3027STDY5784958_6
```

```
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>AB07_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>AB34299_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>Ab4568_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>Ab4653_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
```

```
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>Ab4977_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AbPK1_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AC29_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AC30_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
```

```
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>ACICU_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AR_0056_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AYP-A2_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>BJAB07104_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
```

```
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>BJAB0868_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>CBA7_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>HRAB-85_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>JBA13_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
```

```
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>KAB01_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>KAB02_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>KAB03_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>KAB04_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
```

```
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>KAB05_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>KAB06_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>KAB07_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>KAB08_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
```

```
---------------------------
>KBN10P02143_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>MDR-TJ_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>MDR-ZJ06_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>NCGM237_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
```

```
>SAA14_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>SMC_Paed_Ab_BL01_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>SSA12_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>SSA6_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>TYTH-1_6
```

```
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>USA2_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>WCHAB005133_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>XDR-BJ83_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG------------------------------------------------------
---------------------------
>XH386_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
```

```
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>XH856_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>XH857_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>XH859_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>XH860_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
```

```
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT-----QHDVNVVYINHNSG---EIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>YU-R612_6
-----------MNFNDLLKK---IDECNEIIYG-----------ERFLINQDNS-----------------V
ND-----DLFKS----------------YLSCI---PENDFN-----------------------------
---------------------------IDLGGNIN----------------DFLGKDSLENIQ---------
YMFEDIFDGESTTVFLT------QHDVNVVYINHNS--GEIGACISGDELHIIAKNLF--DFFS-QINVIQ-
-------NLIIDLYDSNPRG-----------------------ENGGYKTGFLEELKKTL-----IKEN---
VVLDVD---YFLEFFYG-------------------------------------------------------
---------------------------
>AB030_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE-----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP-------------------------------------------------------
---------------------------
>AbH12O-A2_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE-----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP-------------------------------------------------------
---------------------------
>AF-401_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
```

```
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP------------------------------------------------------
---------------------------
>AR_0063_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP------------------------------------------------------
---------------------------
>AR_0101_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP------------------------------------------------------
---------------------------
>IOMTU433_22
----------MRNNQE-------LDDLIDQLYD-----------------------------------LEL
EQ-----AYFVY----------------IKFCY---KI---------------------------------
---------------------------IPLLSNIN--------------------------SE---------
YIIESIQKAKSFWFDSK-----SNIDEKEIINRRVK--IIKYMEEKDIDFNINSEPEL--KFSI--------
----------IPLWTKPPSE----------------------DIGDSLDWAFTLLKVIN-----IPDD---
IVKTKL---YEALNDIP------------------------------------------------------
---------------------------
>ATCC17978-mff_2
---------MNQEDIDYFYE----------KYG-----------------QPID----K----------VEV
TE-----DIIKK----------------YRGKL---PESILE-----------QWHLFGFAGYLNGLYWITN
PDDYAEVIYDWLEETP-----------LPDDDVYH-----------VLARSAFGELLIWGERN---------
YGRYYIKTMEGILHDNG-----EQLESAEFYGSDF---FFLPKKNYLDYTDKNGNKLF--DRAVKKLGVLK-
```

```
---------ADEMYAFEPAL----------------------ALGGEESLQHLTKVNLP------VHMK---
LLKQVT---PLRLRTFEDLTAALYGTSYSVDDLTSGQDAESQYQESVQAGEVCPRTGYWTTPAQPNTRHYCK
KGEVLPEIKEQDWGEVYWYWDGEN---
>CIP70.10_2
---------MNQEDIDYFYE----------KYG-----------------QPID----K----------VEV
TE-----DIIKK----------------YRGKL---PESILE-----------QWHLFGFAGYLNGLYWITN
PDDYAEVIYDWLEETP-----------LPDDDVYH-----------VLARSAFGELLIWGERN---------
YGRYYIKTMEGILHDNG-----EQLESAEFYGSDFF--FLPKKNYLDYT-DKNGNKLF--DRAVKKLGVLK-
---------ADEMYAFEPAL----------------------ALGGEESLQHLTKVNLP------VHMK---
LLKQVT---PLRLRTFEDLTAALYGTSYSVDDLTSGQDAESQYQESVQAGEVCPRTGYWTTPAQPNTRHYCK
KGEVLPEIKEQDWGEVYWYWDGEN---
>R2091_2
---------MNQEDIDYFYE----------KYG-----------------QPID----K----------VEV
TE-----DIIKK----------------YRGKL---PESILE-----------QWHLFGFAGYLNGLYWITN
PDDYAEVIYDWLEETP-----------LPDDDVYH-----------VLARSAFGELLIWGERN---------
YGRYYIKTMEGILHDNG-----EQLESAEFYGSDFF--FLPKKNYLDYT-DKNGNKLF--DRAVKKLGVLK-
---------ADEMYAFEPAL----------------------ALGGEESLQHLTKVNLP------VHMK---
LLKQVT---PLRLRTFEDLTAALYGTSYSVDDLTSGQDAESQYQESVQAGEVCPRTGYWTTPAQPNTRHYCK
KGEVLPEIKEQDWGEVYWYWDGEN---
>CIP70.10_31
--------------VSNFTE---QRRQQFLTED------------YYLKTKEYNEEGIP----------LYL
ES-----DAFED---------------DQYNCG---EASRWTAITDIYTSLLYLTYTAGHSIQELIPVFEKV
IDGYEKQSEALALFHKSEKPSVITSQNETLNILSLAFLLHRNDLFLRIHSLVNGEGDSHTGED---------
EIINKFFKLNDSTHPTI-----NEGNLFSLSYAKLC--DVIDNVLVKSDKKHSVELLD--EYLS-NWYQM--
-------NRNEIWYNSHLDL-----------------------ENKSSYVGYWAFEAAAL-----VYLL---
DLDDSS---LYKHLFYPKDIVQWARNQTKIKALNDDVIQIKL-----KGGEKCTRTGYWQTPAQPNLRRYFV
QDEVLPTLIEMDWGEVYWYWDGEN---
>R2091_31
--------------VSNFTE---QRRQQFLTED------------YYLKTKEYNEEGIP----------LYL
ES-----DAFED---------------DQYNCG---EASRWTAITDIYTSLLYLTYTAGHSIQELIPVFEKV
IDGYEKQSEALALFHKSEKPSVITSQNETLNILSLAFLLHRNDLFLRIHSLVNGEGDSHTGED---------
EIINKFFKLNDSTHPTI-----NEGNLFSLSYAKLC--DVIDNVLVKSDKKHSVELLD--EYLS-NWYQM--
-------NRNEIWYNSHLDL-----------------------ENKSSYVGYWAFEAAAL-----VYLL---
```

```
DLDDSS---LYKHLFYPKDIVQWARNQTKIKALNDDVIQIKL-----KGGEKCTRTGYWQTPAQPNLRRYFV
QDEVLPTLIEMDWGEVYWYWDGEN---
>AR_0088_32
MKLEYQVNDQEIDWQKWFDQ----ENKDSDSYR-----------DSFLETEMYQ----R--RFNTFLNGIYS
VT-----DGFRK----------------YKTSA---KAGKMMSAGHQRLQDVLNLMSLQYSAGGDISFIKEL
YPYLLHWMEEYAETHAAYHQTEE----AGGRYVWHISLGTEDYWYIALRLICFGLLTGYADQM---------
ARIMPIIDYVEATPEGQ-----EKDGLIERLVAPFV--ADRGTPPDEARRHLPYRKLI--KVFNAAPEQRP-
-------ALMLQYLESWYEA-----------SRREPYYNQHPQADIDEGFLYYGYWSWEA-----AAVT---
WLLDIDDALYREHEFYPKDLVDFARTQSNVVPNEEQPERIKV-----KGGEACIKTGHWITPAKPDTRLYFT
QGTILPILSETDWGEVYWYWDGEN---
>AR_0088_14
--------MKNTSVSSTMLIVLSILGCSSNTSIAKGINKIDVKDCSIDYDEVDFCSKER----------LKD
YN-----NILKN----------------KVSNF---DKNKFLMNFKEKNYLYFAVIDLEKLKVFTFPASLSV
MSNIKPIEFSSDSNS------------FCLNGNFN--QYQNSYRAVKTCYTYNNGSFDFKSRV---------
ELDKDINNSNNVIKKLN-----LPISSDFFSKCREK--NSAKKCTQLENSNNRAYSFS--ELEKISPDFINV
LNDTKVDSLNVNTFRFLPQF------------------------KDSFYAIAEKYIDTDE-----SSSS---
EFYLIKIKPDLKVEKIGDYYSIDSSGVISYRDKNSKILKKNLR-----------------------------
---------------------------
>CIP70.10_14
--------MKNTSVSSTMLIVLSILGCSSNTSIAKGINKIDVKDCSIDYDEVDFCSKER----------LKD
YN-----NILKN----------------KVSNF---DKNKFLMNFKEKNYLYFAVIDLEKLKVFTFPASLSV
MSNIKPIEFSSDSNS------------FCLNGNFN--QYQNSYRAVKTCYTYNNGSFDFKSRV---------
ELDKDINNSNNVIKKLN-----LPISSDFFSKCREK--NSAKKCTQLENSNNRAYSFS--ELEKISPDFINV
LNDTKVDSLNVNTFRFLPQF------------------------KDSFYAIAEKYIDTDE-----SSSS---
EFYLIKIKPDLKVEKIGDYYSIDSSGVISYRDKNSKILKKNLR-----------------------------
---------------------------
>HWBA8_14
--------MKNTSVSSTMLIVLSILGCSSNTSIAKGINKIDVKDCSIDYDEVDFCSKER----------LKD
YN-----NILKN----------------KVSNF---DKNKFLMNFKEKNYLYFAVIDLEKLKVFTFPASLSV
MSNIKPIEFSSDSNS------------FCLNGNFN--QYQNSYRAVKTCYTYNNGSFDFKSRV---------
ELDKDINNSNNVIKKLN-----LPISSDFFSKCREK--NSAKKCTQLENSNNRAYSFS--ELEKISPDFINV
LNDTKVDSLNVNTFRFLPQF------------------------KDSFYAIAEKYIDTDE-----SSSS---
EFYLIKIKPDLKVEKIGDYYSIDSSGVISYRDKNSKILKKNLR-----------------------------
```

```
---------------------------
>R2091_14
--------MKNTSVSSTMLIVLSILGCSSNTSIAKGINKIDVKDCSIDYDEVDFCSKER----------LKD
YN-----NILKN----------------KVSNF---DKNKFLMNFKEKNYLYFAVIDLEKLKVFTFPASLSV
MSNIKPIEFSSDSNS------------FCLNGNFN--QYQNSYRAVKTCYTYNNGSFDFKSRV---------
ELDKDINNSNNVIKKLN-----LPISSDFFSKCREK--NSAKKCTQLENSNNRAYSFS--ELEKISPDFINV
LNDTKVDSLNVNTFRFLPQF------------------------KDSFYAIAEKYIDTDE-----SSSS---
EFYLIKIKPDLKVEKIGDYYSIDSSGVISYRDKNSKILKKNLR----------------------------
---------------------------
>TYTH-1_14
--------MKNTSVSSTMLIVLSILGCSSNTSIAKGINKIDVKDCSIDYDEVDFCSKER----------LKD
YN-----NILKN----------------KVSNF---DKNKFLMNFKEKNYLYFAVIDLEKLKVFTFPASLSV
MSNIKPIEFSSDSNS------------FCLNGNFN--QYQNSYRAVKTCYTYNNGSFDFKSRV---------
ELDKDINNSNNVIKKLN-----LPISSDFFSKCREK--NSAKKCTQLENSNNRAYSFS--ELEKISPDFINV
LNDTKVDSLNVNTFRFLPQF------------------------KDSFYAIAEKYIDTDE-----SSSS---
EFYLIKIKPDLKVEKIGDYYSIDSSGVISYRDKNSKILKKNLR----------------------------
---------------------------
>15A5_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE----------------------------------------------------
---------YEK------------------------------------------------------------
---------------------------
>Ab4568_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE----------------------------------------------------
---------YEK------------------------------------------------------------
---------------------------
```

```
>Ab4977_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>JBA13_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>KAB04_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>KAB07_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>KAB08_28
```

```
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>KBN10P02143_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>SAA14_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>SMC_Paed_Ab_BL01_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>SSA12_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
```

```
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>SSMA17_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>YU-R612_28
-----------MPKIHILER---PLKISSNGDN----------YSEYTILPAGT----V----------LYD
DS-----DSLNR------------------------------------------------------------
-------------------------------RVMV--------------------YFNLQGVD---------
FNFEEQDPEISKQPSEV-----RSIRSTELSDILK----TIPLTKKDIYLIIKYDDSI-NDSVR--------
-------SILFKKYKIDPSE---------------------------------------------------
---------YEK-----------------------------------------------------------
---------------------------
>BJAB0715_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP----------------------------------YPE
D---------------YFSKNTTSE--
>XH858_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
```

```
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP----------------------------------YPE
D---------------YFSKNTTSE--
>Ab04-mff_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP----------------------------------YPE
D---------------YFSKNTTSE--
>AR_0088_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP----------------------------------YPE
D---------------YFSKNTTSE--
>CIP70.10_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP----------------------------------YPE
D---------------YFSKNTTSE--
>HWBA8_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
```

```
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP---------------------------------YPE
D---------------YFSKNTTSE--
>LAC-4_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP---------------------------------YPE
D---------------YFSKNTTSE--
>R2091_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP---------------------------------YPE
D---------------YFSKNTTSE--
>WKA02_12
--------------MKVIQG---EIQKLTIEDS------------KILPLKNIE----K----------QAV
GS-----AMLGA----------LASSSTLMTNA---PIMLMAARGIDAKTFTCEINGYKVIGQFTTVQFQEN
DPLVIV---ISDEQEQG--RHLAYSILDPRTGLLY----------------------MLYEMG---------
RSLKNSYKNIWQLVFIW-----SISASIIFTGLFFI--FDIFSGKEIFNFSYLIENLK--LFFL-----IL-
-------CVLLIFFSLFMNL-------VFRRSFK---------QAAELSEKIFSILGFKN-----VDEQ---
DFYNDF---IIKDGVHV----SVMEYRKNLKGPDP---------------------------------YPE
D---------------YFSKNTTSE--
>ZW85-1_20
----------LKLNLKLVKG---PIHSLEKAKT-----------------------------------KIP
IN-----QNIGGIAAGTAFAGVLAESSSLLTSA---PILVMAGKAKDGITFTGEIEEHSLLGQFTTVRFKEN
DELIAVINDSPVDGRYQ-----VYAILDPKSGLLY----------------------MIYEMG---------
RSVKKGYKAIFMQTYYF-----T------LLSWAVI--SISLLLFYIFRFSYSWDSFL--RLIV-----WSF
```

```
GGVFGIAALMAFVNYFG-----------YRKSYE---------NFGILSEQIFEKLGFEY-----PKEQ---
DFYNDF---LTDDGVQI----SVMKYRKNLKGPDP---------------------------------YPE
D---------------YFSKNTTSE--
>TCDC-AB0715_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>Ab4653_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NS---PIEYIDS----------------YNKYTVLNPNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>BJAB07104_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>BJAB0868_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
```

```
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>CMC-MDR-Ab59_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>KBN10P02143_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>SMC_Paed_Ab_BL01_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>SSA6_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
```

```
---------------------------
>USA2_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>WCHAB005133_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>XDR-BJ83_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>XH859_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
```

```
>YU-R612_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>MDR-TJ_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>MDR-ZJ06_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>KAB05_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>SSMA17_18
```

```
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>15A5_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>3027STDY5784958_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>AB07_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-----------------------------
---------------------------
>Ab4568_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
```

```
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>Ab4977_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AC29_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AC30_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AF-673_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
```

```
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AR_0102_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AYP-A2_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>CBA7_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>CMC-CR-MDR-Ab4_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
```

```
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>CMC-CR-MDR-Ab66_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>HRAB-85_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>JBA13_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>KAB02_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
```

```
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>KAB04_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>KAB06_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>KAB07_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN------------------------------
---------------------------
>KAB08_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK-----------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
```

```
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>SSA12_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>XH386_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>XH856_18
--------MKVLNSFAIMIA---CSVSFNICYA--------KENSEWNDYLQDS---------------TQI
NSPIEYIDSYNK----------------YTVLN---PNLKIK------------------------------
---------------------------LVDFGNIN-----------KIKKDIKYSLKKYGVQI---------
LNRKEVYNIFEGKVPLK-----SNVDFTLLYNDKNIVAFRIRENSNIDYVKEPYKNFTANAYFY--------
-------NLINNKFIEVPVL-------NSDSEDKSKSTDILQGDQLTYDSKKGQYIYLAN-----IKSY---
KTGKTQ---SIKTIFNSNLKCISSTLGCETIGVLPATKAN-------------------------------
---------------------------
>AR_0078_29
----------MFGKYVFYTGWLLATLSLSVSAC----------ADNSKVNCNTN----N----------VYG
DL-----KCLEK----------------ENKKL---INQLDNKKNKERKDYNQWIKEIKNKCEGKISYAS--
---------------------------GEGAGLIK----------NQCYREEYLSRLSFINTG-------KV
KKSDTNIHGLELTYLPY-----NSNDHLKCIMKKEV--NSCSKVNLVKSSNLIKYYPF--ISPA-YGDSIVL
PETDDSKQIIVSPFEDNED-----------------------EGPQLEISIINAFGVVEQKTISANKN---
VIIDKNYNLIYKEGNKEKILKLK-----------------------------------------------
```

```
---------------------------
>AF-401_30
----------------IF-----LLSSLFLIGC----------------------------------------
-S-----ESFSN-------------------------------------------------------------
--------------------------------------------------------------------------
FTIDNVVKSNEKLNFSI-----NFKNNEVLDKVK-----ESSSKKIVCKNTANNNQML--DAYIDKIEN---
-------NKIDVSVEFCANN----------------------DNRSCEPIDISSVKKIN-----LECQ---
AIFSAMIGNVSKSEKFPIIWEKK--------------------------------------------------
---------------------------
>AYE_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>A1_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>A388_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
```

```
>A85_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>AB307-0294_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>AB5075-UW_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>AR_0083_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>D36_16
```

```
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>USA15_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>WCHAB005078_16
--------------MKYFVL---SATQSSLCPI---------------SLVDDA----V----------LYM
NK-----EQASQ----------------NIECG------------------SLPWYSYKTSKNCD-------
---------------------------LPIEGVLI-----------LKSKKIEISIRNINENI---------
YVVDEIFKNIFGKYINS-----DFIRVEVLSE-------SLEKINNKNYYIFRFNQIF--DFKN-----VL-
-------DLNKSTYRLDNDF---------------------------LVLEKAEFLSDLD-----IDIL---
KIDNMD---SAQDTFFISEFVKKEIEKNKYQGINIFELTLAQ----------------WRDSDDFSFMFLSE
D---------------EVNKFVWPI--
>3207_1
--------------MKYFLL---TLLSITLSAC-----------NPFINNEKAS-----------------N
NN-----AEIKS---------------LTYSRL-------------------------------------
---------------------------DGMSGDIF--------------------KFNLETND---------
-DLNKIYQENNYKYSHF-----KCDNIKNYF-------VTGAISVEGEKLKKGKYTSS--GYFKVCEDESM-
-------NVCIDKNQLEKLL----------------------TSNMSCRVVFGGLLQSSKV----VADN---
ILISKE---AIRKSNFQ-----------------------------------------------------
---------------------------
>AB042_1
--------------MKYFLL---TLLSITLSAC-----------NPFINNEKAS-----------------N
```

```
NN-----AEIKS---------------LTYSRL----------------------------------------
---------------------------DGMSGDIF--------------------KFNLETND---------
-DLNKIYQENNYKYSHF-----KCDNIKNYFV-------TGAISVEGEKLKKGKYTSS--GYFKVCEDESM-
-------NVCIDKNQLEKLL----------------------TSNMSCRVVFGGLLQSSKV----VADN---
ILISKE---AIRKSNFQ-------------------------------------------------------
---------------------------
>AR_0088_1
--------------MKYFLL---TLLSITLSAC-----------NPFINNEKAS-----------------N
NN-----AEIKS---------------LTYSRL----------------------------------------
---------------------------DGMSGDIF--------------------KFNLETND---------
-DLNKIYQENNYKYSHF-----KCDNIKNYFV-------TGAISVEGEKLKKGKYTSS--GYFKVCEDESM-
-------NVCIDKNQLEKLL----------------------TSNMSCRVVFGGLLQSSKV----VADN---
ILISKE---AIRKSNFQ-------------------------------------------------------
---------------------------
>ATCC17978-mff_1
--------------MKYFLL---TLLSITLSAC-----------NPFINNEKAS-----------------N
NN-----AEIKS---------------LTYSRL----------------------------------------
---------------------------DGMSGDIF--------------------KFNLETND---------
-DLNKIYQENNYKYSHF-----KCDNIKNYFV-------TGAISVEGEKLKKGKYTSS--GYFKVCEDESM-
-------NVCIDKNQLEKLL----------------------TSNMSCRVVFGGLLQSSKV----VADN---
ILISKE---AIRKSNFQ-------------------------------------------------------
---------------------------
>HWAB8_1
--------------MKYFLL---TLLSITLSAC-----------NPFINNEKAS-----------------N
NN-----AEIKS---------------LTYSRL----------------------------------------
---------------------------DGMSGDIF--------------------KFNLETND---------
-DLNKIYQENNYKYSHF-----KCDNIKNYFV-------TGAISVEGEKLKKGKYTSS--GYFKVCEDESM-
-------NVCIDKNQLEKLL----------------------TSNMSCRVVFGGLLQSSKV----VADN---
ILISKE---AIRKSNFQ-------------------------------------------------------
---------------------------
>ATCC17978-mff_4
----------MIKYKLCLAL---LLGASTVANA------------EFNIENNPN----QPVYIKLGYQNVLN
SS-----FIYTD----------VSKNVDLKKNI---VTVPYGEVTVLLNPVLNNNNEIKGKDYYFINYQPKI
```

```
LLGKIQYKLPFVISDVGAIGTSI-IYNDNNISIFS--------IESYANPVSNNNSKKFKSDI---------
YIFNKKNLGIYNPSFLS-----INVKLKSLNDASMK--FTKLSSIKYNKNDKSYQVVY--DFQK-VTEDFT-
-------STGKVNYEKFPIQ---------------------------YSFSLIPDKNKPF-----LIKD---
IIEKRK---GDKNIISKIENNDMYSYSLK-----------------------------------------
---------------------------
>3207_4
----------MIKYKLCLAL---LLGASTVANA------------EFNIENNPN----QPVYIKLGYQNVLN
SS-----FIYTD----------VSKNVDLKKNI---VTVPYGEVTVLLNPVLNNNNEIKGKDYYFINYQPKI
LLGKIQYKLPFVISDVGAIGTSI-IYNDNNISIFS--------IESYANPVSNNNSKKFKSDI---------
YIFNKKNLGIYNPSFLS-----INVKLKSLNDASMK--FTKLSSIKYNKNDKSYQVVY--DFQK-VTEDFT-
-------STGKVNYEKFPIQ---------------------------YSFSLIPDKNKPF-----LIKD---
IIEKRK---GDKNIISKIENNDMYSYSLK-----------------------------------------
---------------------------
>AB031_26
-------------MLTMLVE---VIMSVFI-----------------------------------------
-------ANFKA-------------------------------------------------------------
----------------------------SEHPIIN-------------------------------------
IIVRGLLVAVIGFFIAL----------------------FSSIVEGWDFSIGFALIF--SLAI--------
-------GMLVSVFLLVVEI--------------------------------FFNY----------IDKK---
---------------------------------------------------------------------
---------------------------
>AB031_27
--------------MKLEQI---ETADMDVKSI-----------------------------------KIY
GD-----KFY----------------------------------------------------------
---------------------------ILFSAVYD-----------------------------------
TCLKQYIKNVELVFSNW----------------------SSFKIEKYDGNIEEYKQLD--LLEI--------
-------NQSKDLFTLIQII-----------------------HVSEDVVELEGFNDDGE-----WNKV---
VFFNPS---YSLNIIDI---------------------------------------------------
---------------------------
>ab736_10
----------MKNIFKLVLS---AALLPLMVAC-----QAQTVDLTFLVYNYST------------------
-------EGLGE--------------------------------------------------------
---------------------------IQVNGKGS------------------TIADAAERLG---------
```

```
-SIGEAGTACCVHLVEN-----SDTADVSFYT-------DRGDGYKQYHIKVPVENLK--DTPR--------
-------SYAVLHYFPNNTG------------------------VIEVSMRRPSFRKDLF-------DK---
ALGNKA---KNIQLDSPTMWRTISENQAARMQFPD-------------------------------------
---------------------------
>ATCC19606_10
----------MKNIFKLVLS---AALLPLMVAC-----QAQTVDLTFLVYNYST------------------
-------EGLGE-------------------------------------------------------------
---------------------------IQVNGKGS------------------TIADAAERLG---------
-SIGEAGTACCVHLVEN-----SDTADVSFYT-------DRGDGYKQYHIKVPVENLK--DTPR--------
-------SYAVLHYFPNNTG------------------------VIEVSMRRPSFRKDLF-------DK---
ALGNKA---KNIQLDSPTMWRTISENQAARMQFPD-------------------------------------
---------------------------
>ZW85-1_19
-----------MSQFEIRPQ---EIYLLERYSSPAYFEELVIAFKNMLDAAENALELFM----------QDL
PY-----DYRDR----------------HISEQ---PDVVWGEHVLPNFRSTMQSLHYGYKQLLDGDLSA--
---------------------------LQFAGNVV--------------------TDFRNQRV---------
DYFPDWMDEANLAVFDE-----EQMKASRLAS-------NIKATVMGNWVTGNLSHRY--NSQS-RGELNL-
-------PLSLPIYRLNLNV--------------TVKTGETVPEDGIYIPSIQDASAQLL-----LKGH---
DAIEALVGLSRSGLQYAREESTTWLLVKRIADEGGSVETIQAENLKGYAGQSCQQSGHWWSPANQSQTRYFE
KGEIFPEIPNNAWGETIWYLEVTNKAE
>ATCC19606_7
-------------------M---ITTCLFLVAC-----SKPASNNRMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG-------------------------YHIDE
S---------------YIDPDIWPYVQ
>ab736_7
-------------------M---ITTCLFLVAC-----SKPASNNRMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
```

```
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>ACICU_7
-------------------M---ITTCLFLVAC-----SKPASNNRMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>KAB06_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTA-T---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>LAC-4_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>Ab04-mff_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
```

```
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>BJAB0715_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>D1279779_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>KAB02_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>KAB05_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
```

```
S---------------YIDPDIWPYVQ
>MDR-TJ_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>R2090_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>WKA02_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
>XH856_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG------------------------YHIDE
S---------------YIDPDIWPYVQ
```

```
>XH858_13
----------MKNYLSLFIC---IITCIFLTSC-KPANNTTQGNKSMNQNQDVI----A----------LHF
GE-----QGMQD----------------FSKNS----TTPVDRQPAGMNFLSLDWTPPKLGRVRVFSEKSNL
EIENVISVLGTQVARRSNDGIQI----MDINASLH-------------PNEYTTSQEAYTAYT---------
KLVHQINDKQWKQYFLP-----FSARIDKQDNLKHM--TETMGEVIDPTYILNFKEWQ--DVLS-KTN----
-------RLVFNLYNGDVEL-------GISLRRTYKD------DKKEQYMVRYSFENFKY-----AGRN---
AISDSD---KMNSEQLKQAFETEVANNKKARKTEENNMKKEG-------------------------YHIDE
S---------------YIDPDIWPYVQ
```

Supplementary file S4f

```
>SDF_16
-MLNSIHQVLDSLGISPQKRAIHVQFMSPILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEQY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSADHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGFRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDANEVKQQIEGGLNNAKALSEVAKNQKTDEIESL--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEILITGASSQITLNGSGISPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQHINPLR
RLAQASSDKTAITKIQSPFETFV
>A1_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
```

```
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>A388_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
```

RLAQASSDKTAITKIQSPFETFV
>A85_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
--EQLKDFASQIQQ--------------------
---QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>AB0057_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
--EQLKDFASQIQQ--------------------
---QIAKF

```
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>AB307-0294_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>AB5075-UW_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
```

```
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>AR_0083_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>D36_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
```

KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ----------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>USA15_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI

```
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>WCHAB005078_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>AYE_16
-MLNSIHQVLDSLGISPQKRAIHVQFTSSILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTETPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDRINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYSPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGVRFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKDVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNMGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
```

```
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRAQGVLELLHDYSHGAFVKGAGYTVT--DNLGKVVNGKLDDKGFARVSGLAT-GS
VKVLFDPDPRNPWDEASDFKRKVEWPNQNDVEGSI---GIESGSKGLTETLKNDFKKLSQLASNVKSVQQKI
ESVKKIKDQGAKALLPMAMEQVLGGSDGSKLSQ--------------------SFVSQNSFMPSSQQSNPLR
RLAQASSDKTAITKIQSPFETFV
>6200_21
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEQY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNSIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>1656-2_6
-MLNSIHQVLDTLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
```

PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>15A34_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>15A5_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ

```
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>3027STDY5784958_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
```

```
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AB07_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AB34299_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
```

```
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>Ab4568_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>Ab4653_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
```

```
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>Ab4977_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AbPK1_6
```

```
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AC29_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
```

```
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AC30_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>ACICU_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
```

```
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AR_0056_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AR_0102_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
```

```
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AYP-A2_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
```

```
>BJAB07104_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>BJAB0868_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
```

IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>CBA7_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>HRAB-85_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF

```
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>JBA13_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB01_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
```

```
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB02_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
```

IDGNSLVNNTLHQYLQSPFKKNS
>KAB03_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB04_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF

EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB05_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB06_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT

```
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB07_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KAB08_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
```

KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>KBN10P02143_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI

```
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>MDR-TJ_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>MDR-ZJ06_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
```

```
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>NCGM237_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>SAA14_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
```

PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>SMC_Paed_Ab_BL01_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>SSA12_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ

AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>SSA6_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA

```
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>TYTH-1_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>USA2_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
```

----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>WCHAB005133_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XDR-BJ83_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE

```
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XH386_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XH856_6
```

```
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XH857_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
```

SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XH859_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>XH860_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA

```
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>YU-R612_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRVQGVLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>AF-673_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
```

```
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKR---VLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>CMC-CR-MDR-Ab4_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKR---VLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
```

```
>CMC-CR-MDR-Ab66_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKR---VLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>CMC-MDR-Ab59_6
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
```

IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKR---VLELFHEYAHGEFVKGGSYRVV--DNFGKEVTGKLDDKGFAKVSGLAT-GA
VKVFFESDHRDPWDTASDFKRPVEWPNKNDADSEQSDSLIAQMSK----TAQSKLGELSKQLTNPTNIMKNI
QTAQSIKSEGAKALMPMLKTQAQGLVTDQVKSF---------LPISEAGQKIGNNIELTSIQKMNDFNKSGS
IDGNSLVNNTLHQYLQSPFKKNS
>IOMTU433_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVFEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEQY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLNNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDQINGLLAQSNWSIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGEHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESL----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVKSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAI-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSIGQGWMHRKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>3207_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF

GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>AB030_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>AbH12O-A2_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL

```
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>AF-401_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
```

KNTETALNPMSFKFK--------
>AR_0063_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
--EQLKDFASQIQQ--------------------
---QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>AR_0101_22
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNDQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQT
KNPLFAASLSLDLSGLT-QTYEVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHIVPSTDTPIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYAPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESSDKSFLIVSKNFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PTTPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
--EQLKDFASQIQQ--------------------
---QIAKF

```
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTSQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>AB031_27
-MLNSIHQVLDSLGISPQKRAIHVQFTSPILNAQVFLQRIDGVHALNDGLKAELLCLSTNATIQLKSFIGVQ
AAVDIVTERGELTRVTGIITHAQQGQSDGSLTLYKLTLEDPTALWKYRRNSRVFMNKSVVEIWEILFKEWQS
KNPLFAASLSLDLSGLT-QTYDVRPFVMQHNESDWNFLTRLLRSENISWLIDEAQHTVPSTDTSIQAQKLRL
IDANSQYQPLDRKTIRYHRSSAVEQYDSMTRLTAERSLQPNVMHIQRWQAEILDQEEGIGSVQSKHQHSEHY
DNATLGLEQAWNYSPAWIGDLKGEDGVTKSGNQQVERLNQNLHNYYEAQAKRFIAQTTVRDAYVGYYFELNE
HPEIDQ-HESTDRSFLIISKSFFNQNNLPKDLNDQINGLLAQSNWAIQNPE----NSDERQANQLILQRRHI
PITPAYNPQIHSPVTHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDYA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKIE
IQAQSDALDVLANKGITISSTEDCIEISSPKEIVITGASSQITLNGSGIFPKTGGKFQVNAGQHVFQGGASA
SVQSSLPP------PPKRGQGVLELFHEYAHGEFVKQGGYTVT--DSLGKQFKGQLDDKGFVRVSGLAT-GS
AKIVFEEDKRNPWDEASDFKRPPMWPSDNDTSAQTLMGKADSVLKGAVTEAKKALG---QTFTNPSSIMRTI
DTAKQLKENGASALLPMVQQGVESHLTGQLTNFTSKVLSQSSTGQGWMHGKTNPVAPVTSGLNVNPLRAQDS
KNTETALNPMSFKFK--------
>VgrG2Abay
-MSFHLFGALERLGLSAQQRALHLTLSDVSLNSQVYLQRIQGQQHLNQGSSAELICFSSYAHLPLKQFIGCQ
AAVDQVTDTGQLFRSSGIITAATQGQSDGALTLYTLTLQDPTALWHKRRNSRVFMNKSVRDISEILFKEWQN
KSPLFAASLTLDTSGLS-RDYDIRPFSMQANETDYDYLTRLWRSEGINWLIDEAQLIVPSITSPIQPQILRL
IDDNTAYQPLPRTSLRYQRSSATEPFDSITQFTATRSLQPTSVYLQRWQADALQQQEGSGSVQSTQHHSQHY
DNASLNLEDAWQISPAWTQDLNGEDQVTASSNTQIEQLNQQINAYHHLQSKQFTATGSVRDAQVGYWFQLDG
HPELDQ-HSNEERQLLIISKYYHNQNNLPKELAQQIQHLLPQ------QPN----SKEQRHSTELTLVRRNI
KTVPEYHPQQHQPQTHPQRAKVVGPEGEQVHVDEWGRIKVRFLFTRSEDHSHDGGAGSNDNDTDSAWVDVLT
```

```
PWAGEGYGARFLPRIGEIVVIDYFDGDIDRPFVLGRIHEAERSPTKFDIKGQLPHTRHLSGIRSEEIQGSGY
NQLRFDDTTGQISSQLHSSHGATQLNLGNLSHPKEQLESEGRGEGFELRTDQWGAVRAGEGLHLTTHKQEQA
QGQHLDAKEASQQLESSLNNAKALSEVAKNQQTDPLEVL--------------------------------
----------------------------------------DNLKQFLKQIEQ--------------------
-----------------------------------------------------------------QDQNKAAAF
KQALMILSAPSSIAMSSNQDIHLSADGQLSQHAGESLSFSTQKSLIAHASDKISLFAAQQGARLYAGKGKIE
LQAQGDGADLIARKDIQIISTEDVINISAQKRILITAKTSQVEINEQGIILRTGGKAEFKAGQHVFMGGQNI
NETILDLP-------------------------ELKDCEY-----KMKDAASTGKSSVRIK-----------
---------------------------------------------------------------------
---------------------------------------------------------------------
-----------------------
>VgrG3Abay
-MSFHLFGALERLGLSAQQRALHLTLSDVSLNSQVYLQRIQGQQQLNQGSSAELICFSSHAHLPLKQFIGCQ
AAVDQVTDTGQLFRSSGIITAATQGQSDGALTLYTLTLQDPTALWHKRRNSRVFMNKSVRDISEILFKEWQN
KSPLFAASLTLDTSGLS-RDYDIRPFSMQANETDYNYLTRLWRSEGINWLIDEAQLIVPSTTSSIQPQILRL
IDDNTAYQPLPRASLRYQRSSATEPFDSITQFTATRSLQPTSVYLQRWQADALQQQEGSGSVQSTQHHSQHY
DNASLNLEDAWQISPAWTQDLNGEDQVTASSNTQIEQINQQINAYHHLQSKQFTATGSVRDAQVGYWFQLDG
HPELDQ-HSNEERQLLIISKYYHNQNNLPKELAQQIQHLLPQ------QPN----SKEQRHSTQLTLVRRNI
KTVPEYHPQQ--PQTHPQHAKVVGPEGETVHVDEWGRIKVRFLFTRSEDHSHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDYFDGNIDRPFVLGRIHEAERSPTKFDIKGQLPHTRHLSGIRSEEIQGSGY
NQLRFDDTTGQISSQLHSSHGATQLNLGNLSHPKEQLESEGRGEGFELRTDQWGAIRAGEGLHLTTHKQEQA
QGQHLDAQEASQQLESSLNNAKALSEVAKNQQTDPLEVL--------------------------------
----------------------------------------DNLKQFLEQIEQ--------------------
-----------------------------------------------------------------QDQNKAAAF
KQALMILSAPSSIAMSSNQDIHLSADGQLSQHAGDSLNISTQKSLIAHASDKISLFAAQQGARLYAGKGKIE
LQAQGDGADLIARKDIQIISTEEAVYITSPKEINLTVNGSQLKLNDSGVFSTTGGKFEVKAGQHIFEGGEKV
TVSKAAEN----------KPCYLTFEIVDLDGNPAKNIEYIAF--RADGTHQEGRTDVSGKTQTFQTEG---
-----------------SEQISIHISDKNASKYKLITKG-------------------------------
---------------------------------------------------------------------
-----------------------
>AB042_3
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
```

KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGKDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNVDRPFVVGRIHEAERQPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML----------
----------ENIQTFLEVLKQ----------
----------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGIQITSTEDTVFITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGEQV
T-----PP-----KKQENKPCYLTFEITDLDGKPAKNVEYIAF--RMDGSRQKGQTNAQGLTQRFETDG---
----------SEQISIHICDENASKYKLAAKG----------

>ATCC17978-mff_3
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGKDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNVDRPFVVGRIHEAERQPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML----------
----------ENIQTFLEVLKQ----------
----------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGIQITSTEDTVFITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGEQV
T-----PP-----KKQENKPCYLTFEITDLDGKPAKNVEYIAF--RMDGSRQKGQTNAQGLTQRFETDG---
----------SEQISIHICDENASKYKLAAKG----------

```
------------------------------------------------------------------------
-----------------------
>ZW85-1_20
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRD-TRILFKEWQG
KSPLSAASLTLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILNKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
-----------------------------------------ENIQTFLEVLKQ--------------------
-------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNDSGIFPVTGGKLEVKAGQHLFRGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>XH858_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITFDTSGLS-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESRLFVADPNASIQSQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERHLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRVDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
-----------------------------------------ENIQTFLEVLKQ--------------------
```

```
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>D1279779_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHISLKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDRSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
-----------------------------------------ENIQTFLEVLKQ--------------------
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGIQITSTEDTVFITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>R2090_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHISLKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDRSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
```

KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML----------
----------ENIQTFLEVLKQ----------
----------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGIQITSTEDTVFITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP----------DCSAKQTQAAQNGSAKVDLS-------

>AR_0088_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLECLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML----------
----------ENIQTFLEVLKQ----------
----------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP----------DCSAKQTQAAQNGSAKVDLS-------

>CIP70.10_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ

```
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLECLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP--------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>HWBA8_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLECLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP--------------------------------------DCSAKQTQAAQNGSAKVDLS-------
```

```
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>R2091_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLECLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>BJAB0715_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSGAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERHLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRVDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
```

```
----------------------------------------ENIQTFLEVLKQ--------------------
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP--------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>Ab04-mff_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-----------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP--------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>LAC-4_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
```

```
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>WKA02_12
MMSHKIFQILDSLGLVAQNRVLHVQFSNASLNNQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDML--------------------------------
----------------------------------------ENIQTFLEVLKQ--------------------
-------------------------------------------------------------EDPKKAAEF
QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINMSTQKNIVNHASQKISLFAAQEGARLFAGKGKVE
IQAQGDGLDVIARKGVQITSTEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGSSI
NPPALDLP-------------------------------------DCSAKQTQAAQNGSAKVDLS-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------
>CIP70.10_31
```

-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVAEPNASIQPQVLRL
IDDNQNYQALEHRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPIELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFQSGEKV
PYNLPPLG---------ELKSFLELNYHWPTLEPMKGAPYLVV--FESGQEFKGNLDDKGFAKIPNVPTNES
YTVWYGEDQRKVEIEVLEESILENFTDQDEIELDELLKNWDVEN----------

>R2091_31
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVAEPNASIQPQVLRL
IDDNQNYQALEHRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPIELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWIDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFQSGEKV

PYNLPPLG---------ELKSFLELNYHWPTLEPMKGAPYLVV--FESGQEFKGNLDDKGFAKIPNVPTNES
YTVWYGEDQRKVEIEVLEESILENFTDQDEIELDELLKNWDVEN----------

>ab736_7
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSYPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDANEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGGSA
NANVPALP----KLEFAQSPYSAQYQLFKADGRNFQGYKYFIHD-SKNNLIKQGITDNQGFTEQVVTES-KE
RIIGYKSVMRESERITENWEAKLEQVANKMSSVGK----------

>ACICU_7
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSYPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA

```
QGVHLDANEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGGSA
NANVPALP----KLEFAQSPYSAQYQLFKADGRNFQGYKYFIHD-SKNNLIKQGITDNQGFTEQVVTES-KE
RIIGYKSVMRESERITENWEAKLEQVANKMSSVGK-------------------------------------
-----------------------------------------------------------------------
-----------------------
>ATCC19606_7
---MSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSYPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDANEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGGSA
NANVPALP----KLEFAQSPYSAQYQLFKADGRNFQGYKYFIHD-SKNNLIKQGITDNQGFTEQVVTES-KE
RIIGYKSVMRESERITENWEAKLEQVANKMSSVGK-------------------------------------
-----------------------------------------------------------------------
-----------------------
>ZW85-1_19
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFAASLTLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSESINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
```

```
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILNKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSA
NANVPALP-------EFNKTNWIALEHLDVDNQPFANLGYKIF--FENNQVIEGKLDEQGKAHHENVPD-KA
IRVEYQELPAKPDTPWDTYDAVLKELNSFEEGDIRD-------------------------------------
-----------------------------------------------------------------------
-----------------------
>15A5_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
-----------------------------------------------------------------------
-----------------------
```

```
>Ab4568_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
-----------------------------------------------------------------------
-----------------------
>Ab4977_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
```

IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

>JBA13_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

>KAB04_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF

```
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
---------------------------------------------------------------------
-----------------------
>KAB07_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
---------------------------------------------------------------------
-----------------------
>KAB08_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
```

IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

>KBN10P02143_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

```
-----------------------
>SAA14_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
-----------------------------------------------------------------------
-----------------------
>SMC_Paed_Ab_BL01_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
```

```
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
-----------------------------------------------------------------------
-----------------------
>SSA12_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML---------------------------------
-----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
-----------------NDELVVNWFEQEDLVNGE-------------------------------------
-----------------------------------------------------------------------
-----------------------
>SSMA17_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
```

PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

>YU-R612_28
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNIVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRTDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLLFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NANVPALP----DLRIKTEHRNFQAIDSSKN-EPLEGIPYSILN-KRTGIKFYGFTNEKGMTKTIKSAE---
----------NDELVVNWFEQEDLVNGE----------

>BJAB0715_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSGAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE

```
KSPLFASSITFDTSGLS-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESRLFVADPNASIQSQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERHLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRVDDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
---------------------------------------------------------------------
-----------------------
>D1279779_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
```

```
------------------------------------------------------------------------
-----------------------
>MDR-TJ_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
-----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
------------------------------------------------------------------------
-----------------------
>R2090_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLISTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
-----------------------------------------ENLKTFIEQIEE--------------------
```

```
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
---------------------------------------------------------------------------
-----------------------
>XH858_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSGAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
-----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
---------------------------------------------------------------------------
-----------------------
>Ab04-mff_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
```

```
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
-----------------------------------------------------------------------
-----------------------
>KAB02_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
-----------------------------------------------------------------------
-----------------------
>KAB05_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
```

VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV----------

>KAB06_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---

```
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
-----------------------------------------------------------------------
-----------------------
>WKA02_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV-------------------------------------
-----------------------------------------------------------------------
-----------------------
>XH856_13
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFVADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
```

----------ENLKTFIEQIEE----------
----------NDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGAEV
GMNLQGLP--------AYEAYNERFKMLLPSGEPLSFIDYKI---SSEGKEIFANSDKKGQTKEIHSPK---
---EQELKLDLLWLDLETVDETEVWVDPAQGSKNV----------

>AF-401_30
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQE
KSPLFASSITLDTSGLT-EDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVVESQLFVAEPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNE
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNV
KAVPEYNPLEHRPAAYPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEE----------
----------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHVFMGGGSV
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTDYIIFDENDKEIERGKLDRTGLVKLETEEP---
----------NKQYKIHVEI----------

>3207_1
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIVDPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND

```
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTEYIIFDEHDKEIERGKLDRTGLVKLETEEP---
-----------------NKQYKIHVVN----------------------------------------------
---------------------------------------------------------------------
-----------------------
>AR_0088_1
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIVDPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTEYIIFDEHDKEIERGKLDRTGLVKLETEEP---
-----------------NKQYKIHVVN----------------------------------------------
---------------------------------------------------------------------
-----------------------
>HWAB8_1
```

```
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIVDPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTEYIIFDEHDKEIERGKLDRTGLVKLETEEP---
-----------------NKQYKIHVVN----------------------------------------------
-----------------------------------------------------------------------
-----------------------
>AB042_1
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
```

```
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTEYIIFDEHDKEIERGKLDRTGLVKLETEEP---
-----------------NKQYKIHVVN---------------------------------------------
-----------------------------------------------------------------------
-----------------------
>ATCC17978-mff_1
-MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQ
VAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSITLDTSGLT-KDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIADPNASIQPQVLRL
IDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHY
DNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELND
HPELDQ-HDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLD--SQNPEQRHFAELNVVRRNI
KAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGSGLLVSTHKQDQA
QGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-----------------------------------------------------------------KDQDKAAAF
KQALMILTAPNSIALASNEDIHLSADGQLNQTAGDSINLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKAVQVISTEDKIEATAAKEIVLTAGGSQVKITGSGIFMTTSGKFEVKAGQHLFMGGGSV
NSSLPYLP------EQGKQKYGVWFDVMDKQGNKLKPGTEYIIFDEHDKEIERGKLDRTGLVKLETEEP---
-----------------NKQYKIHVVN---------------------------------------------
-----------------------------------------------------------------------
-----------------------
>AB5075-UW_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFINKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
```

```
KGDHLYAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>A1_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>A388_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
```

DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>AB307-0294_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK

```
>AR_0078_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>D36_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
```

IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>A85_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLYAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>AB0057_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF

GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLYAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>WCHAB005078_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLTVSDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRVIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQIEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLYAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>SDF_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFCTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYEFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL

```
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTD-------ERQANQLILQRRHI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESL--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQITGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRTKK
>WKA02_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGVSQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLLQQSDWQASNTN-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQSDALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
```

FKTTNQESPIQQGDLDTFVRSKK
>AB031_26
-MFNNISQVLESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYEFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGALDTFVRSKK
>AB030_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTSGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF

```
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMAGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQG-D----------
--------------LDTFVRSKQ
>AbH12O-A2_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTSGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMAGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQG-D----------
--------------LDTFVRSKQ
>AF-401_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
```

```
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTSGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMAGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQG-D----------
--------------LDTFVRSKQ
>AR_0063_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTSGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMAGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQG-D----------
--------------LDTFVRSKQ
>AR_0101_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
```

KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTSGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMAGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLA
NLAGQTVGQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQG-D----------
----------LDTFVRSKQ
>6200_15
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRYPTKFDNKGKLPDTKKLSGIRSKEVSGSGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESL----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD

```
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGNLDTFVRSKK
>TCDC-AB0715_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVIDFFNGDIDRPFVMGRIHEAQRQPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>JBA13_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
```

```
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB02_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB04_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
```

PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB05_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB06_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ

VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB07_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP

```
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>KAB08_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>SAA14_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
```

```
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>SSA12_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>SSMA17_0
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
```

```
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>15A34_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>15A5_5
```

-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>3027STDY5784958_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA

```
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>Ab4568_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>Ab4653_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
```

```
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>Ab4977_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI---------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>AF-673_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
```

```
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>AR_0056_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
```

```
>AR_0102_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>BJAB07104_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
```

IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>BJAB0868_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>CMC-CR-MDR-Ab4_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF

GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>CMC-CR-MDR-Ab66_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>CMC-MDR-Ab59_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL

```
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>HRAB-85_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
```

FKTTNQESPIQQGDLDTFVRSKK
>KBN10P02143_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>MDR-TJ_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF

EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>MDR-ZJ06_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>NCGM237_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT

```
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>SSA6_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>TYTH-1_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
```

KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>USA2_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD

```
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>WCHAB005133_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-------------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>XDR-BJ83_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
```

```
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>XH386_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI--------------------------------
----------------------------------------EQLKDFASQIQQ--------------------
-----------------------------------------------------------------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>XH856_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
```

PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>XH859_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>YU-R612_5
-MFNNIFQILESFGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGVQ

VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNMDNIQPQKLRL
IDDNNQYQALTRRAIRYHRSSATEQFDSMTSLMADRSLQPTSIFVQRWQPDVLQQTDGAGSVQSKHQHSTNY
DNQSLSLEEAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYYDAQSKQFIAKTTVRDTQVGYWFELNE
HPEIDQ-HESTDKEFLIIGKNYYNQNNLPKDLNQQIQTLVQQSDWQASNTD-------ERQANQLILQRRYI
PTTPAYNPQTHSPVAHPQRAKVVGPEGEEIYVDEWGRIKVRFLFTRSDDHSHDGGAGTNNNDTDSAWIDVLT
PWAGEGYGARFLPRIGEIVVINFFNGDIDRPFVMGRVHEAQRHPTKFDNKGKLPDTKKLSGIRSKEVSGGGF
GQLRFDDTPGQISTQLQSSHGASQLNLGKLSHPKDKAESEDRGEGFELRTDQWGALRAGQGLLVSTHKQDNA
KGDHLDAEVAKKQLEGSQTNSKALSDIAKNQKTDEIESI----------
----------EQLKDFASQIQQ----------
----------QIAKF
EKALLLLSSPDGIALSSSEDIHISADAQINQIAGDSINISTQKNVIAHAQNRLSLFAAQSGLKAVAAQGKVE
IQAQADALDVLSKLGITISSTDDKVIISSPKEVKITGGSSQITLNGSGIFPKTGGKFQVNAGQHLFMGGASA
NASAPELP------KAKPMQGALELLRSYGGDNFFKQNSYKVI--DSLGKQITGKLDGNGFAQVTGIAP-GP
AKVVFEKDNTSAWLQSSDFKRNYTWAEPVKSVQGLMKNALEAVGQNTMSQLQNNLLSTDKNSFKNLGKNTLD
NLAGQTVAQIKNQVTNTALNTVSKQLNLNLSAD----QMKSLGQMATNPSQSLEMLKEQGGDFLSDQMTAKL
FKTTNQESPIQQGDLDTFVRSKK
>AB031_0
-MFNNISQVLESLGFLSQHRSVHLQFSDASLNSQVFLQRIEGQHYLNEGMTAELICLSTNAHIALKTFIGVQ
VAIDQVTDQGQLFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVREITEILFQEWQG
KSPLFASSLTLDLSGLK-QAYDIRPFVMQLNQSDYDFLTRLWRSEGINWLIDEAELTVPSNTDHIQPQKLRL
IDDNSQYQALSRRTIRYHRSHATEQFDSMTSLMANRSLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTNY
DNQSLSLEDAWHFSPAWMQDLKGEDGATSASNQQLEKFNQNLSAFHDAQSKQFIAQTTVRDTQVGYWFELNE
HPEIDQ-HNGSDKEFLIIGKHYYNQNNLPKDLNQQIQALVRQSHWSINNEE--------RQGNELILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIHVDQWGRIKVRFLFTRADDHRHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKEKAESDGRGEGFELRTDQWGAVRAGSGLYVSTHKQDQA
QGTHLDAKETKQQLDGNLNNAKALSDVAKNQQTDPLEHL----------
----------ENLKTFLEQIEE----------
----------QDQGKAAAF
KQALMVLTAPNSIALASNEDIHLSADGQLSQTAGDSISLSTQKNLIAHAQNKISLFAAQEGARLYAAKGKLE
VQAQGE----------KSLIVSF----------QRLYKG----

```
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>AB031_00
-MFNNISQVLESLGFLSQHRSVHLQFSDASLNSQVFLQRIEGQHYLNEGMTAELICLSTNAHIALKTFIGVQ
VAIDQVTDQGQLFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVREITEILFQEWQG
KSPLFASSLTLDLSGLK-QAYDIRPFVMQLNQSDYDFLTRLWRSEGINWLIDEAELTVPSNTDHIQPQKLRL
IDDNSQYQALSRRTIRYHRSHATEQFDSMTSLMANRSLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTNY
DNQSLSLEDAWHFSPAWMQDLKGEDGATSASNQQLEKFNQNLSAFHDAQSKQFIAQTTVRDTQVGYWFELNE
HPEIDQ-HNGSDKEFLIIGKHYYNQNNLPKDLNQQIQALVRQSHWSINNEE--------RQGNELILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIHVDQWGRIKVRFLFTRADDHRHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKEKAESDGRGEGFELRTDQWGAVRAGSGLYVSTHKQDQA
QGTHLDAKETKQQLDGNLNNAKALSDVAKNQQTDPLEHL---------------------------------
----------------------------------------ENLKTFLEQIEE--------------------
-----------------------------------------------------------------QDQGKAAAF
KQALMVLTAPNSIALASNEDIHLSADGQLSQTAGDSISLSTQKNLIAHAQNKISLFAAQEGARLYAAKGKLE
VQAQGE------------------------KSLIVSF-------------------------QRLYKG----
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>ab736_0
-MFNNISQVLESLGFLSQHRSVHLQFSDASLNSQVFLQRIEGQHYLNEGMTAELICLSTNAHIALKTFIGVQ
VAIDQVTDQGQLFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVREITEILFQEWQG
KSPLFASSLTLDLSGLK-QAYDIRPFVMQLNQSDYDFLTRLWRSEGINWLIDEAELTVPSNTDHIQPQKLRL
IDDNSQYQALSRRTIRYHRSHATEQFDSMTSLMANRSLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTNY
DNQSLSLEDAWHFSPAWMQDLKGEDGATSASNQQLEKFNQNLSAFHDAQSKQFIAQTTVRDTQVGYWFELNE
HPEIDQ-HNGSDKEFLIIGKHYYNQNNLPKDLNQQIQALVRQSHWSINNEE--------RQGNELILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIHVDQWGRIKVRFLFTRADDHRHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKEKAESDGRGEGFELRTDQWGAVRAGSGLYVSTHKQDQA
QGTHLDAKETKQQLDGNLNNAKALSDVAKNQQTDPLEHL---------------------------------
```

```
----------------------------------------ENLKTFLEQIEE--------------------
-----------------------------------------------------------------QDQGKAAAF
KQALMVLTAPNSIALASNEDIHLSADGQLSQTAGDSISLSTQKNLIAHAQNKISLFAAQEGARLYAAKGKLE
VQAQGE------------------------KSLIVSF-------------------------QRLYKG----
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------
>ATCC19606_0
-MFNNISQVLESLGFLSQHRSVHLQFSDASLNSQVFLQRIEGQHYLNEGMTAELICLSTNAHIALKTFIGVQ
VAIDQVTDQGQLFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVREITEILFQEWQG
KSPLFASSLTLDLSGLK-QAYDIRPFVMQLNQSDYDFLTRLWRSEGINWLIDEAELTVPSNTDHIQPQKLRL
IDDNSQYQALSRRTIRYHRSHATEQFDSMTSLMANRSLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTNY
DNQSLSLEDAWHFSPAWMQDLKGEDGATSASNQQLEKFNQNLSAFHDAQSKQFIAQTTVRDTQVGYWFELNE
HPEIDQ-HNGSDKEFLIIGKHYYNQNNLPKDLNQQIQALVRQSHWSINNEE--------RQGNELILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIHVDQWGRIKVRFLFTRADDHRHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEIVVIDFFDGNVDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKEKAESDGRGEGFELRTDQWGAVRAGSGLYVSTHKQDQA
QGTHLDAKETKQQLDGNLNNAKALSDVAKNQQTDPLEHL--------------------------------
----------------------------------------ENLKTFLEQIEE--------------------
-----------------------------------------------------------------QDQGKAAAF
KQALMVLTAPNSIALASNEDIHLSADGQLSQTAGDSISLSTQKNLIAHAQNKISLFAAQEGARLYAAKGKLE
VQAQGE------------------------KSLIVSF-------------------------QRLYKG----
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------
>AR_0088_32
-MFNNISQVLESIGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDQGQQFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNTDNIQPQKLRL
IDDNSQYQALTRRTIRYHRSSATEQFDSMTSLIAGRHLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSASY
DNQSLSLEDAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYHDAQSKQFVAQTTVRDTQVGYWFELNE
```

```
HPEIDL-HSGADKEFLIIGKHYYNQNNLPKDLNQQIQTLITQSHWQSSHTK-------ERQGNQLILQRRHI
KTVPEYQPLQDRPQAAVQRARVVGPEGESIYVDQWGRIKVRFLFTRANDHSHDGGAGSNDNDTDSAWVDVVT
PWAGKGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPAQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAVSQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGKGLLVSTHKQDQA
QGTHLDAADAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEQ--------------------
-------------------------------------------------------------QDKEKAAAF
KQALMILTAPNSIAVASNEDIHLSADGQLSQTAGDSINISTQKNLIAHAQNKLSLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKGIQIISTEDKIEINASKEIVITSGSSQIKINSSGIFPVTGGKFEVKAGQHVFMGGGSA
SSTLPALP------QLNIPPKELELKYVYDDLKPVAQAPYKLI--FQDGSMQEGILDSNGYAKVQVPAD--K
VQPKVYYGFSNMEAKPDQPKQQNSFKDKKVMSIVEAEQLIEQYNKQELDHLLDEYFPDEIQAMIDGQGVEYD
DHINDYVEKDLEQQNNPDDAIADQAEEIPLNKQSTPHSGFGEGI----------------------------
-----------------------
>HWAB8_32
-MFNNISQVLESIGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDQGQQFRTTGIITGASQGQSDGALTLYKLTISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNTDNIQPQKLRL
IDDNSQYQALTRRTIRYHRSSATEQFDSMTSLIAGRHLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSASY
DNQSLSLEDAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYHDAQSKQFVAQTTVRDTQVGYWFELNE
HPEIDL-HSGADKEFLIIGKHYYNQNNLPKDLNQQIQTLITQSHWQSSHTK-------ERQGNQLILQRRHI
KTVPEYQPLQDRPQAAVQRARVVGPEGESIYVDQWGRIKVRFLFTRANDHSHDGGAGSNDNDTDSAWVDVVT
PWAGKGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPAQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAVSQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGKGLLVSTHKQDQA
QGTHLDAADAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEQ--------------------
-------------------------------------------------------------QDKEKAAAF
KQALMILTAPNSIAVASNEDIHLSADGQLSQTAGDSINISTQKNLIAHAQNKLSLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKGIQIISTEDKIEINASKEIVITSGSSQIKINSSGIFPVTGGKFEVKAGQHVFMGGGSA
SSTLPALP------QLNIPPKELELKYVYDDLKPVAQAPYKLI--FQDGSMQEGILDSNGYAKVQVPAD--K
VQPKVYYGFSNMEAKPDQPKQQNSFKDKKVMSIVEAEQLIEQYNKQELDHLLDEYFPDEIQAMIDGQGVEYD
DHINDYVEKDLEQQNNPDDAIADQAEEIPLNKQSTPHSGFGEGI----------------------------
-----------------------
>CIP70.10_2
```

-MFNNISQVLESIGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDQGQQFRTTGIITGASQGQSDGALTLYKITISDPTYLWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNTDNIQPQKLRL
IDDNSQYQALTRRTIRYHRSSATEQFDSMTSLIAGRHLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTSY
DNQSLSLEDAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYHDAQSKQFVAQTTVRDTQVGYWFELNE
HPEIDL-HSGADKEFLIIGKHYYNQNNLPKDLNQQIQTLITQSHWQSSHTK-------ERQGNQLILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIYVDQWGRIKVRFLFTRANDHSHDGGAGSNDKDTDSAWVDVVT
PWAGKGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPAQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAVSQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGKGLLVSTHKQDQA
QGTHLNAADAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEQ----------
----------QDKEKAATF
KQALMVLTAPNSIAVASNEDIHLSADGQLSQNAGDSISLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKGIQIISTEDKIEINASKEIVITSGGSQIKINSSGIFPVTGGKFEVKAGQHVFMGGAKA
DYVLPSLP------TQEIKTDDLLLEYLHSDGTPVKGADYEVL--LSDGSIRKGKLDASGKAIVSGVPA-GR
AKIQYGEDQSKDEFPALEVDDWFTQLGSSTKTGKEE----------

>R2091_2
-MFNNISQVLESIGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDQGQQFRTTGIITGASQGQSDGALTLYKITISDPTYLWHKRRNSRVFMNKSVRDISEILFKEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNTDNIQPQKLRL
IDDNSQYQALTRRTIRYHRSSATEQFDSMTSLIAGRHLQPTSVFVQRWQSDVLQQTDGAGSVQSTHQHSTSY
DNQSLSLEDAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYHDAQSKQFVAQTTVRDTQVGYWFELNE
HPEIDL-HSGADKEFLIIGKHYYNQNNLPKDLNQQIQTLITQSHWQSSHTK-------ERQGNQLILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIYVDQWGRIKVRFLFTRANDHSHDGGAGSNDKDTDSAWVDVVT
PWAGKGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPAQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAVSQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGKGLLVSTHKQDQA
QGTHLNAADAKQQIEGGLNNAKALSEVAKNQQTDPLEML----------
----------ENLKTFIEQIEQ----------
----------QDKEKAATF
KQALMVLTAPNSIAVASNEDIHLSADGQLSQNAGDSISLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKGIQIISTEDKIEINASKEIVITSGGSQIKINSSGIFPVTGGKFEVKAGQHVFMGGAKA

```
DYVLPSLP------TQEIKTDDLLLEYLHSDGTPVKGADYEVL--LSDGSIRKGKLDASGKAIVSGVPA-GR
AKIQYGEDQSKDEFPALEVDDWFTQLGSSTKTGKEE-----------------------------------
------------------------------------------------------------------------
-----------------------
>ATCC17978-mff_2
-MFNNISQVLESIGFLSQHRSVYLQFSDASLNSQVFLQRIDGQHYLNQGMTAELICLSTNAHIPLKTFIGLQ
VAVDQVTDRGSFFRTTGIITGASQGQSDGALTLYKLAISDPTYLWHKRRNSRVFMNKSVKEISEILFQEWQG
KSPLFASSLTLDLSGLK-QTYDVRPFVMQLNESDYDFLTRLWRSEGISWLIDEAELTVASNTDNIQPQKLRL
IDDNSQYQTLTRRTIRYHRSSATEQFDSMTSLIAGRHLQPSSVFVQRWQSDVLQQTDGAGSVQSKHEHSSNY
DNQSLNLEDAWHFSPAWMQDLNGEDGATSASNQQLEKFNQNLSAYHDAQSKQFVAQTTVRDTQVGYWFELNE
HPEIDL-HSGADKEFLIIGKHYYNQNNLPKDLDQQIQTLTTQSHWQSSHTK-------ERQGNQLILQRRHI
KTVPEYQPLQDRPQASVQRARVVGPEGESIYVDQWGRIKVRFLFTRANDHSHDGGAGSNDNDTDSAWVDVLT
PWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPAQFDQKGQLPDTKKLSGIRSEEVDGKGF
NQLRFDDTTGQISAQLQSSHAVSQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAVRAGKGLLVSTHKQDQA
QGTHLDAADAKQQIEGGLNNAKALSEVAKNQQTDPLEML--------------------------------
----------------------------------------ENLKTFIEQIEE--------------------
-------------------------------------------------------------KDQDKAATF
KQALMVLTAPNSIAVASNEDIHLSADGQLSQNAGDSISLSTQKNLIAHAQNKISLFAAQQGARLYAGKGKVE
IQAQGDGADLIARKGIQIISTEDKIEINASKEIVITSGGSQIKINSSGIFPVTGGKFEVKAGQHVFMGGAKA
DYVLPSLP------TQEIKTDDLLLEYLHSDGTPVKGADYEVL--LSDGSIRKGKLDASGKAIVSGVPA-GR
AKIQYGEDQSKDEFPALEVDDWFTQLGSSTKTGKEE-----------------------------------
------------------------------------------------------------------------
-----------------------
>VgrG1Abay
-MLNNIHSVFEQLGFGALKRAIHVQFSNPLLNTQIFLQRIDGKHTLNEGLEVELTCLSINAHIALKQFIGCQ
VAIDQVTDTGQLARTSGIITRATQGQSDGALTLYTLNIQDSTALWHKRRNSRVFMNKSVAEISEILFKEWQN
RSSLFAASLTLDLSGLA-QNYDIRPFTMQINETDYEFLTRLWRSEGINWLVDEKNTVVTHPLQPIAPQKLRL
IDDNQQFLALSRGLIRFHRSHATEHFDSMTHLVAHRQLQSTAAYVQRWQADGLLQDEGSGSVLSAHQHSDQQ
SNESLSLEQAWSIGSAWTTDLTGADQATASSSQQIEKLNQNLTAYQERQAKYFIAQTTVRDAQVGYWFELQG
HPEIDQ-HDLADRQFLIYEKRFFNQNNLPKDIQQQFEYLLMHSALKTSNQQ-------ERQGNELTLIRRQV
KVVPEYQPLMHRPVVYPQRARVVGPENEEIYVDEWGRIKVRFLFTRTEDHAHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRVGELVVIDFFDGHVDRPFATGRIHEAQRSPTKFDIRGQLPATRNLSGIRSQEIAGSGF
NQLRFDDTTGQISTQLQSSHGASQLNLGNLSHPKNEETSQGRGEGFELRTDHYGAVRAGKGMLISTYAQEQA
```

IADHLEAAQAQSLLAQSHENMKTLSDIALKQQTDALNVIDRLPKFIQSLELKSTEQALDRTVNLFKDNLNKD
PINALKDCGSFIEDIGRLGGNTKGVVEEFDTFFTQNKDALENLKAFIENVEEHGTDVVKGRLASVKDDIQQN
PFASLQDIGKVLANVDIKDFDLMSNCGTFSKGSKLEVTPSKALSSLQGFMEGYTQGLESSSDAKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKVSLFAAQKGLSAYAAKGAVK
IQAQDDLVDIIAKKVIKLISTEDKIELTSTKEIDIKAGGSQLIVNGNGVFIKTGGKFEVRSGQHVFTSGEKV
SYEVPELP------NTSIFSNRLDIYDLFWASDF-SQLSYKAFV-PETSSFTSGSIDEHGRTGKISTSD--P
TKVQVLVGSNDEWGLVIDGFDEDDFMTDQNVNDSESDNNIEVRDLK--------------------------
---

>ab736_9
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESKLFVPHFTAPIQGQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHSYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGLYISTHKQDQA
QGFHLNANETKQQLEGGLNNSKALSEVAKNQQTDPLEVL--------------------------------
--DHLKTFLDQIEQ--------------------
---RDKDKAAAF
KQAIMVLSAPNSMALTSNENIHVIADGQISQTADDSINLSTQKNFIAHAQNKISFLQLKMEQECMRARAKLS
YK----------HKVMVQISLHEK--------------------------------------GYRLFQQKIES
K---

>ATCC19606_9
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESKLFVPHFTAPIQGQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF

```
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHSYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGLYISTHKQDQA
QGFHLNANETKQQLEGGLNNSKALSEVAKNQQTDPLEVL--------------------------------
----------------------------------------DHLKTFLDQIEQ--------------------
-----------------------------------------------------------------RDKDKAAAF
KQAIMVLSAPNSMALTSNENIHVIADGQISQTADDSINLSTQKNFIAHAQNKISFLQLKMEQECMRARAKLS
YK----------HKVMVQISLHEK-------------------------------------GYRLFQQKIES
K-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
-----------------------
>IOMTU433_0
--------------------------------------------------MAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLSAFAAKGPIK
VQAQTEGIEILSRKNIKILSVEDKIEIVGQKEIVLNAGGSQLTISDKGVFINTPRLFHAKAGQHKFDAGAII
NYSFPNLP--------SMYYGNFNITDK--NNNPIGGQKYKMT--LPSGKEILGFTDENGNTVTGYSGE---
-------DNQNLKLEIIEDLYQDIWYQPNSTYEYETIDDLELPVNFDKEVDEDE------------------
-----------------------------------------------------------------------
-----------------------
```

```
>AB031_25
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNNQIFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGISWLIDESELFVPHFTAPIQAQKLRL
IDDNSQYQALERRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDSF
DSATLSLEQAWHVSPAWMQDLKGEDQATASGSSQLEKLNQHFTDMHASRAKYFKAYSSVRDSQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSHWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPQGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDIKGQLPATKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQETSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNAFFTDAKDAVENLKAFIENVEEHGADIVKGKLASIKDRIHKN
PFESIKEVGKVLANVETKDFDMMSVCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGATV
NAELPKMP------ESGIFSRRFDFSELINTNLLKDGFKYKAIN-HTKKTEYIGFLDEFARTRRIFSDN-PD
NIEILLLGKNDEHSDKLQLVEEIINDGQGKSSDETCCGGGDEHNHDHDSNEQIEDDDLKSDFENFRIKD---
------------------------------------------------------------------------
-----------------------
>3207_4
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPATKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQETSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTINLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNAFFTDAKDAVENLKAFIENVEEHGADIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
```

LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSGPFTKAFHFVSL--EGEKIENAIIQVY--EKINDSYKFKIGSKIDKSIFKLEE---
------SEENIEYKALVGFDDWVSWFEEEEGEEVEEIDLGEHYNPFDK-----------------------
---

>15A5_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
---

>3027STDY5784958_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF

```
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
-----------------------------------------------------------------------
-----------------------
>AB07_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
-----------------------------------------------------------------------
-----------------------
>AB34299_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
```

IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>Ab4568_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

```
------------------------
>Ab4653_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
-----------------------------------------------------------------------
------------------------
>Ab4977_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
```

RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>AC29_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>AC30_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT

PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>AF-673_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>AR_0102_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE

KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>AYP-A2_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------

```
------------------------------------------------------------------------
-----------------------
>BJAB07104_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
------------------------------------------------------------------------
-----------------------
>BJAB0868_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
```

PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>CBA7_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>CMC-CR-MDR-Ab4_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI

KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>CMC-CR-MDR-Ab66_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>CMC-MDR-Ab59_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ

VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>HRAB-85_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---

---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>JBA13_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KAB02_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND

PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KAB04_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KAB06_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE

HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KAB07_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KAB08_18

-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>KBN10P02143_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV

SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>MDR-TJ_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>MDR-ZJ06_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA

IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>SAA14_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>SMC_Paed_Ab_BL01_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF

DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>SSA12_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>SSA6_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>TCDC-AB0715_18
---------LEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE

LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>USA2_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>WCHAB005133_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF

NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>XDR-BJ83_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>XH386_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL

IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

>XH856_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------
---

```
------------------------
>XH859_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
------------------------------------------------------------------------
------------------------
>YU-R612_18
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNEADYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLTNVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
```

```
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP--------KNGPYAVDFLFASLAGNGIENAKIQLYEPDKKEIIWEGKTDLRGKSNLSLQNE---
---------SKRYEALIGFDDWSSIFDDEDDYEEEHEEEFEIGEHGMQAEENNLEE----------------
------------------------------------------------------------------------
-----------------------
>AB030_24
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSNATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVSVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNTKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ESGIFSRRFDFSDIFNLEKLKEEIRFKVIN-KTKNTEYIGMLDEMGRTPRIFSDS--S
DTIEIQFISNNENKSIIPTKELNEDIYNHDTGDFVDDGIQSQLAEALDDEYKDDLEDDFNKFGV--------
------------------------------------------------------------------------
-----------------------
>AbH12O-A2_24
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSNATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVSVLT
```

PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNTKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ESGIFSRRFDFSDIFNLEKLKEEIRFKVIN-KTKNTEYIGMLDEMGRTPRIFSDS--S
DTIEIQFISNNENKSIIPTKELNEDIYNHDTGDFVDDGIQSQLAEALDDEYKDDLEDDFNKFGV--------
---

>AF-401_24
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSNATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVSVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNTKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ESGIFSRRFDFSDIFNLEKLKEEIRFKVIN-KTKNTEYIGMLDEMGRTPRIFSDS--S
DTIEIQFISNNENKSIIPTKELNEDIYNHDTGDFVDDGIQSQLAEALDDEYKDDLEDDFNKFGV--------
---

>AR_0063_24
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE

KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSNATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVSVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNTKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ESGIFSRRFDFSDIFNLEKLKEEIRFKVIN-KTKNTEYIGMLDEMGRTPRIFSDS--S
DTIEIQFISNNENKSIIPTKELNEDIYNHDTGDFVDDGIQSQLAEALDDEYKDDLEDDFNKFGV--------
---

>AR_0101_24
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSNATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVSVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNTKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTQQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ESGIFSRRFDFSDIFNLEKLKEEIRFKVIN-KTKNTEYIGMLDEMGRTPRIFSDS--S
DTIEIQFISNNENKSIIPTKELNEDIYNHDTGDFVDDGIQSQLAEALDDEYKDDLEDDFNKFGV--------

```
------------------------------------------------------------------------
-----------------------
>Ab04-mff_11
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ETGMYSMRFDLSQIF-DTKILKNMEYKLIN-HSKKIEAVYEFEQESSARVYSDSV-DN
VELALVPGVYLTEIKELISEQEAESLDDEDIDSCGCGEEHEHD----------------------------
------------------------------------------------------------------------
-----------------------
>BJAB0715_11
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
```

PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ETGMYSMRFDLSQIF-DTKILKNMEYKLIN-HSKKIEAVYEFEQESSARVYSDSV-DN
VELALVPGVYLTEIKELISEQEAESLDDEDIDSCGCGEEHEHD----------

>WKA02_11
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ETGMYSMRFDLSQIF-DTKILKNMEYKLIN-HSKKIEAVYEFEQESSARVYSDSV-DN
VELALVPGVYLTEIKELISEQEAESLDDEDIDSCGCGEEHEHD----------

>XH858_11
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI

KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFMSGATV
NAELPKMP------ETGMYSMRFDLSQIF-DTKILKNMEYKLIN-HSKKIEAVYEFEQESSARVYSDSV-DN
VELALVPGVYLTEIKELISEQEAESLDDEDIDSCGCGEEHEHD----------

>A1296_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGGSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLQQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPATKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQEMSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>D1279779_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNPQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ

VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGTPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>R2090_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNPQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGTPYKILLKKTGDILMVGTINDDLQTERVFTKE---

```
----------EEEIELILFETNYTDFNIENLDYLFGEE-----------------------------------
-----------------------------------------------------------------------
-----------------------
>1656-2_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE-----------------------------------
-----------------------------------------------------------------------
-----------------------
>AbPK1_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
```

PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>ACICU_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>AR_0056_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE

HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>DU202_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>KAB03_8

-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTDFNIENLDYLFGEE----------

>NCGM237_8
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----EIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV

```
SMKLPHLP----VIQEGGFSQLFDLKDLSKDNPNLIGAPYKILLKKTGDILMVGTINDDLQTERVFTKE---
----------EEEIELILFETNYTYFNIENLDYLFGEE-----------------------------------
-----------------------------------------------------------------------
-----------------------
>15A34_23
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNPQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASGSSQLEKLNQHFTDMHASRAKYFKAYSSVRDSQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQGNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPQGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPATKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSKVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEDKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPQLP------STMMYSNKLDVYDLFWDFDL-SRLSYVAK--FKNGRVSTGSLDENGRTARISSDS--S
EPAEVFVDTNTDWVVEIEEEVSQVESQNQDIK---------------------------------------
-----------------------------------------------------------------------
-----------------------
>6200_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELLVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
```

IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIILTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSTPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>ZW85-1_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLDGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGENAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSTPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>A1_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF

DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>A388_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>A85_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>AB0057_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE

LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>AB307-0294_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN----------

>AB5075-UW_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF

```
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN---------------------------------
--------------------------------------------------------------------------
-----------------------
>AR_0083_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN---------------------------------
--------------------------------------------------------------------------
-----------------------
>AYE_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
```

```
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN---------------------------------
--------------------------------------------------------------------------
-----------------------
>WCHAB005078_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN---------------------------------
--------------------------------------------------------------------------
```

```
------------------------
>D36_17
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGGSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTSGAKV
SYEVPELP------SSFDYSNRIDLYKIFQWSDF-ENIKYSAI--FENQRVTQGNLDELGRTERFKSSMPDK
MKVLVGYSADKWHKETEEFEDFDDYETNNDSNLNNNSN--------------------------------
-----------------------------------------------------------------------
------------------------
>AR_0088_14
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
```

RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP------NTPTFSNRLDIYDLFWESDF-SKLSYKAFM-PETNSFTSGAVDEHGRTGKISSAD--P
TNVQVLIGSDDEWGLLIDSFDADDFLEDQSINGSNSEIDNNTEDRG--------------------------
---

>CIP70.10_14
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP------NTPTFSNRLDIYDLFWESDF-SKLSYKAFM-PETNSFTSGAVDEHGRTGKISSAD--P
TNVQVLIGSDDEWGLLIDSFDADDFLEDQSINGSNSEIDNNTEDRG--------------------------
---

>HWBA8_14
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT

PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP------NTPTFSNRLDIYDLFWESDF-SKLSYKAFM-PETNSFTSGAVDEHGRTGKISSAD--P
TNVQVLIGSDDEWGLLIDSFDADDFLEDQSINGSNSEIDNNTEDRG--------------------------
---

>R2091_14
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE
KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLKL
IDDNNQYQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEVNGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGRVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFTGGAKV
SYEVPELP------NTPTFSNRLDIYDLFWESDF-SKLSYKAFM-PETNSFTSGAVDEHGRTGKISSAD--P
TNVQVLIGSDDEWGLLIDSFDADDFLEDQSINGSNSEIDNNTEDRG--------------------------
---

>AR_0078_29
-MLFNIFSVLEKIGLNAQKRAIHVQFSNELLNHQVFLQRIEGQHQLNGGLMAELICLSTNAQIALKQFIGVQ
VAVDQVTDSGQLFRTTGIVTEASYGQSDGALTLYKLTIEDATNLWHKRRNSRVFMNKSIVEITEVLFKEWQE

KSPLFAASLSLDLGGLS-QNYDIRPFTMQHNESDYDFLTRLWRSEGVSWLIDESELFVPHFTAPIQAQKLRL
IDDNNQNQALARRSIRYHRSSATEYQDSITGFVAVRSLQPTAVHVQRWQPDALAQEEGNGSVVTTHTHSDNF
DSATLSLEQAWHVSPAWMQDLKGEDQATASSSSQLEKLNQHFTDMHASRAKYFKAYSSVRDTQVGYWFNLRE
HPEIDQ-HEGADQEFLIIAKNFYNQNNLPKDLHQQVSQLLTQSRWDQHGYD-----DIERQSNELTLIRRQI
KTAPEYNPEQHRPIAYPQRAKVVGPEGETIHVDEWGRIKVRFLFTRSDDHGHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRIGEVVVIDFFDGNIDRPFVTGRIHEAQRSPTKFDVKGQLPDTKKLSGIRSQEINGSGF
NQLRFDDTTGQISTQLQSSHAATQLNLGNLSHPKEQATSQGRGEGFELRTDAWGAVRAGKGMLISTYAQEQA
IADHLEAAQAQSLLSQGYESMKMLSEVAAKQQTDALNVINRLPKFIQSLELKTTGQALNSTVNLFKEGINND
PIHALKDCGGFIQDIGALGGNAKGVVDEFNSFFSDAKDAVENLKAFIENVEEHGPDIVKGKLASIKDRIHKN
PFESIQEVGKVLANVETKDFDLMSTCGTFSKGSKLEVSPSKALSSLQGFMEGYTQGLESSSDTKQQEQGKIF
RQALMLLASPNGIALTTPENIILQASQDIAESASGSINLSAQKNIIGHAQDKISLFAAQKGLRAYAAKGKLE
LQAQDDAIEAIAKKVIKLISTEEKIELTSPKEIVLTAGGSQLKINANGVFSTTGGKFESKAGQHLFAGGAKV
SYEVPELP------NTPTFSNRLDIYDLFWESDF-SKLSYKAFM-PETNSFTSGAIDEHGRTGKIGTPD--P
TNVQVLIGSDDEWGLLIDSFDEDEILEDQSINSNNSAIDNNIEDRG----------

>ab736_10
-MLNNIFDFLDKIGFASQKRALHIYFTNPEINNQVFLQRIDGFHSINEGLSAELICLSINPYISLKQFIGSQ
VAVEQVTDSGKLFRTTGIITGASQGQSDGALCLYKLTMQDATSLWYKRRNSRVFMNKSAVEIIEIIFKEWQN
KSSLFAASLQLDSSGLT-KNYDIRPFSMQSNESDYAYLTRLMREEGINWLIDESESMVLSNSQTIEPQKLRL
IDHNNEYKVLERRAIRYHRSDATEQNDSITSFIAQRQLQPTAIHLQRWQADNLSQEDASGSVLSAHQHSSQR
DNESLSLEQAWTIAPAWITDLNGEDQATTSSNSQIEKLNKQLNQYQALQAKYFIARSSVRDAQVGYWFKLNE
HPELERNHESSDKEFLILSKRFYNQNNLPKDIRDQVEQLLSLSHWQ-VSHD----RAQERQANELMVVRRYI
DIVPEFDPLIHRPSAHVQRAKVVGLDGEEIHVDEWGRIKVRFLFTRTDDHQHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRVGEIVVIDFFDGNIDRPFVTGRVHEGQRSPTKFDIKGQLPDTKKLSGIRTKEVSGSGF
NQLRFDDTTGQISTQLHSSHGASQLNLGNLSYPKDSATSEGWGEGFELRTDQWGAVRAGDGLLISTYKQKNA
AHDALNLEQTIADLKTHKEWNTVLEDNVKEHKVMAL----------
----------DALATLTKSIEA----------
----------LEAAGKETEVQTL
KEAIIILTSPADITLNSSKNIFLQSQSNTHISAKENINLMSDQNTVLASQKKLSLFSYEDFMQIISAKGKLE
IQTHEKSIEMIANEVVKILSVKSNIELTSPEEITLTAKESQIKINGSGVFITTNGKFEVKAGQHVFLSGAKA
D-----LP----------KLTWSFKEKTASCMKNA-------SESHEAFVGFEG----------
---

```
------------------------------------------------------------------------
-----------------------
>ATCC19606_10
-MLNNIFDFLDKIGFASQKRALHIYFTNPEINNQVFLQRIDGFHSINEGLSAELICLSINPYISLKQFIGSQ
VAVEQVTDSGKLFRTTGIITGASQGQSDGALCLYKLTMQDATSLWYKRRNSRVFMNKSAVEIIEIIFKEWQN
KSSLFAASLQLDSSGLT-KNYDIRPFSMQSNESDYAYLTRLMREEGINWLIDESESMVLSNSQTIEPQKLRL
IDHNNEYKVLERRAIRYHRSDATEQNDSITSFIAQRQLQPTAIHLQRWQADNLSQEDASGSVLSAHQHSSQR
DNESLSLEQAWTIAPAWITDLNGEDQATTSSNSQIEKLNKQLNQYQALQAKYFIARSSVRDAQVGYWFKLNE
HPELERNHESSDKEFLILSKRFYNQNNLPKDIRDQVEQLLSLSHWQ-VSHD----RAQERQANELMVVRRYI
DIVPEFDPLIHRPSAHVQRAKVVGLDGEEIHVDEWGRIKVRFLFTRTDDHQHDGGAGSNDNDTDSAWVDVLT
PWAGEGYGARFLPRVGEIVVIDFFDGNIDRPFVTGRVHEGQRSPTKFDIKGQLPDTKKLSGIRTKEVSGSGF
NQLRFDDTTGQISTQLHSSHGASQLNLGNLSYPKDSATSEGWGEGFELRTDQWGAVRAGDGLLISTYKQKNA
AHDALNLEQTIADLKTHKEWNTVLEDNVKEHKVMAL-----------------------------------
----------------------------------------DALATLTKSIEA--------------------
-------------------------------------------------------------LEAAGKETEVQTL
KEAIIILTSPADITLNSSKNIFLQSQSNTHISAKENINLMSDQNTVLASQKKLSLFSYEDFMQIISAKGKLE
IQTHEKSIEMIANEVVKILSVKSNIELTSPEEITLTAKESQIKINGSGVFITTNGKFEVKAGQHVFLSGAKA
D-----LP-------------KLTWSFKEKTASCMKNA-------SESHEAFVGFEG---------------
------------------------------------------------------------------------
------------------------------------------------------------------------
-----------------------
>VgrG4Abay
-MLNSIFGILDKLGFNQQKRAISIQFSNQELNHHIMLQRIDGYHAINDGLSVELICISTNPYLSLKQFIGCQ
AAIDQVTDTGKLFRTTGIITEASQGQSDGALTLYRLRLQDATSLWHKRRNSRVFMNKSVVEIIEIVFREWQS
KSPLFAATLKLDTSHLTNKQYDIRPFSMQSNESDYAYLTRLMREEAINWLIDESNYLVMSQTQAIEPQYLRL
VDQNTEYSCLERSSIRYHRSHATEQQDSITSLIAQRQLQSTAIYVQRWQADALSQEDASGSVLSNHQHSQQH
GNESLSLEQAWNISPAWMTDLNGEDQATASDSRQLEKLNKQLHLYQALQAKSFTAYSSVRDTQVGYWFRLVD
HPELDKNHDESDKEFLIVSKHFYNQNNLPKDIQDQIQQLLSLNHWS-IYQD----SFQERQANKLTLIRRNI
DIVPEYDPLQHRAIAHVQRARVVGSETEEIHVDEWGRIKVRFLFTRIEDHEHDGGAGSNDSDTDSAWVDVLT
PWAGEGYGARFLPRVGEIVVIDFFDGNIDRPFVTGRIHEAHRSPTKFDIKGQLPETKKLSGIRSKEVAGEGY
NQLRFDDTTGQISAQLHSSHGTTQLNLGHLSHPKDKAESEGRGEGFELRTDDWGAIRASKGILLTSEASEQA
QGEQLTRSSIKENLHFHTQSNQYFKELAQAHEVDEPDL---------------------------------
----------------------------------------EAQKSLKEKFES--------------------
```

```
-----------------------------------------------------------------WADN
NDALVALHSESALILDSKESLQLTSKDNIELSTPKNLQFFTGKSWIAKALDKISLFAKHAGIKIKSGEGDIE
VAAQKGKMTLSSKQQMHVYSLNDFVRIESGKGILITAGGGYIKIQNGNIEIACPGLMELKAGQIQAKSGASL
SSELPAMP-------ELKSQYDEHFILHYPDGEPAKNLKYRIT--AEDGQVFEGVSGEDGKTTVFTKDA---
-----------------MTALNIEVFSPE-----------------------------------------
-----------------------------------------------------------------------
```

Supplementary file S4g

```
>PAAR1
MTSPIFLHELPIEQLQQMSQEDIEQTLKAEQLYFQHRPKAMYYLAVNGSKTKQGGLVKASATQGKIGDLSIA
RIGDDVIY-ADGTIAKIISGAGKVCIVEGLSAALVGSQLDNGDEIIDSPNRTVAIN----------------
-----------------------------------------------------------------------
----------------------IFKGETLPEGFLIPEGTDHG-----------------------------
---------------------------------------
>PAAR3
MSRP---------------------------------------YITI-GSPTTGGGKVITANRRFLINGKAIA
CVGDKATCPTHKTVATIIAGDNHMLVM-GKAAAQHNSPLSCGCKCIADQSLTVGNN----------------
-----------------------------------------------------------------------
-----------------------------------------------------------------------
---------------------------------------
>15A34_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>15A5_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>3027STDY5784958_B
```

```
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AB34299_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>Ab4568_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>Ab4653_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>Ab4977_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AbPK1_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
```

```
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AC29_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AF-673_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AR_0056_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AR_0102_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AYP-A2_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>CBA7_B
```

```
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>CMC-CR-MDR-Ab4_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>CMC-CR-MDR-Ab66_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>CMC-MDR-Ab59_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>DU202_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>HRAB-85_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
```

```
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>JBA13_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB01_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB02_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB03_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB04_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB05_B
```

```
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB06_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB07_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KAB08_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>KBN10P02143_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>SAA14_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
```

```
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>SMC_Paed_Ab_BL01_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>SSA12_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>SSA6_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>SSMA17_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>USA2_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>WCHAB005133_B
```

```
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>XDR-BJ83_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>XH386_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>XH857_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>XH859_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>XH860_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
```

```
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>YU-R612_B
MTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>1656-2_B
LTTP----------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AC30_B
LTTP----------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>ACICU_B
LTTP----------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>BJAB07104_B
LTTP----------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>BJAB0868_B
```

```
LTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>MDR-TJ_B
LTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>MDR-ZJ06_B
LTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>NCGM237_B
LTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>TCDC-0715_B
LTTP---------------------------------------YITI-GCPTSGGGQVISGNNMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSAAKSSSAPI
SQKQPATDSFVKDEYENYYIEQNTTKYVKFTNGIFPYDEDKKNLFGAISQAVSGVCTFIVTYILKGQELFVT
VSMLPPTLSGDATIFPYATLDLVHNNQSLGK---TRLEKGKG---VWSTENSKEPVGQCKVTLPKPDLSTIE
ATLTMGYTAKFDG--GTVRPNPPHTRFSFTLNSASRRKS
>AB030_I
MATP---------------------------------------YITI-GCPTSGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGSAQSLPAS-----
--KAQTQDSFVEDKSKEY-----------------------------------------GIQFQLKDEKTQKV
```

```
FSEIPYSI-------------IYKKDGKVET--------------GWTDKEGKTHVINAD------------
--------------------SPDEVEFQTIDASKPLPPL
>AR_0088_I
MATP---------------------------------------YITI-GCPTSGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGSAQSLPAS-----
--KAQTQDSFVEDKSKEY-----------------------------------------GIQFQLKDEKTQKV
FSEIPYSI-------------IYKKDGKVET--------------GWTDKEGKTHVINAD------------
--------------------SPDEVEFQTIDASKPLPPL
>HWAB8_I
MATP---------------------------------------YITI-GCPTSGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGSAQSLPAS-----
--KAQTQDSFVEDKSKEY-----------------------------------------GIQFQLKDEKTQKV
FSEIPYSI-------------IYKKDGKVET--------------GWTDKEGKTHVINAD------------
--------------------SPDEVEFQTIDASKPLPPL
>B8342_G
MATP---------------------------------------YITI-GCPTSGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGSAQSSPVS-----
--KAQTQDSFVENKSKDIHKIQFK----------LVDDETKKPLTELMYEI----------YSKDKGQLLV-
-----------------------------------------QG---YTDKSG---------------------
--LTALYESNYTAESVEVILVDLSKPIEPI---------
>A388_J
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAVQGSQASNATQD
SFMPQTDEHGIKFQLKDQETGK-------------PLAQQYFKLQGPDGSEIEG------------------
----------------------FTDENGFTE----LIKTGTE---------------AKEIDLTTFDLSQPM
AKWE-----------------------------------
>A85_J
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAVQGSQASNATQD
SFMPQTDEHGIKFQLKDQETGK-------------PLAQQYFKLQGPDGSEIEG------------------
----------------------FTDENGFTE----LIKTGTE---------------AKEIDLTTFDLSQPM
AKWE-----------------------------------
>AB0057_J
```

```
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAVQGSQASNATQD
SFMPQTDEHGIKFQLKDQETGK-------------PLAQQYFKLQGPDGSEIEG------------------
----------------------FTDENGFTE----LIKTGTE---------------AKEIDLTTFDLSQPM
AKWE-----------------------------------
>15A34_J
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPYMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAVQGSQASNATQD
SFMPQTDEHGIKFQLKDQETGK-------------PLAQQYFKLKGPDGSEIEG------------------
----------------------FTDKNGFTE----LIKTGTE---------------AKEIDLTTFDLSQPM
AKWE-----------------------------------
>LAC-4_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFQIDGIPVA
CTGDKATCPTHKVVATIVSGDPCMQIF-GKAAARVNDSLSCGCKLLPKQNLVVQDNGSGAASSAAKSSPAPM
SQKQPATDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQMVSGACNFEVTHQVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEVKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>6200_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>3027STDY5784958_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>Ab4568_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
```

ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>Ab4977_A
MATP----------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AF-673_A
MATP----------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AR_0102_A
MATP----------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>CBA7_A
MATP----------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>CMC-CR-MDR-Ab4_A
MATP----------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>CMC-CR-MDR-Ab66_A

```
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>CMC-MDR-Ab59_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>JBA13_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB02_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB04_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB05_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
```

```
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB06_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB07_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB08_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>MDR-ZJ06_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>SAA14_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>SSA12_A
```

```
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>SSMA17_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>TYTH-1_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>WKA02_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XDR-BJ83_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XH386_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
```

```
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XH856_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XH857_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XH858_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>XH859_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>BJAB07104_A
LATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>BJAB0715_A
```

```
LATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>BJAB0868_A
LATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAANSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANDKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AB34299_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AC29_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AC30_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB01_A
MATP---------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
```

```
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>KAB03_A
MATP--------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>AB07_A
LATP--------------------------------------YITI-GCPTTGGGQVISGNSLFLIDGIAVA
CVGDKATCPTHKIVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPKQHLVVQDNGGGSASSAAKSSPAPM
SQKQPTTDSFVKDEYENYYIEQNKTTMVPFKTMLMPYDQDRTNLFGVMSQIVSGACNFEVTHRVKKDQLFVT
ATLLPPTVRADATIIPRAVLRLFKKDKQISD--TITLKVGKG---YWNTANEKQPVGSCEIKLPAPDLEVIK
AKLTMKYDAKFDG--GVVVTSPPDVTYEFTITSAARRKA
>SDF_M
MASP--------------------------------------YIMI-GCPTTGGGQVISGNSAFLIEGITIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
---------------------------------------
>IOMTU433_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDTLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
---------------------------------------
>TYTH-1_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
---------------------------------------
>15A34_M
```

```
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>1656-2_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>A1_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>A388_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>A85_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AB0057_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
```

```
---------------------------------------NQG------------------------------
--------------------------------------
>AB07_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>AB307-0294_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>AB34299_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>Ab4653_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>AB5075-UW_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>AbPK1_M
```

```
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AC29_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AC30_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>ACICU_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AF-673_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AR_0056_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
```

```
----------------------------------------NQG------------------------------
--------------------------------------
>AR_0078_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AR_0083_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AR_0088_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AYE_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AYP-A2_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>BJAB07104_M
```

```
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>BJAB0715_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>BJAB0868_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>CBA7_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>CIP70.10_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>CMC-CR-MDR-Ab4_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
```

```
---------------------------------------NQG------------------------------
--------------------------------------
>CMC-CR-MDR-Ab66_M
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>CMC-MDR-Ab59_M
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>D36_M
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>DU202_M
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>HRAB-85_M
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>HWAB8_M
```

```
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>KAB01_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>KAB03_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>MDR-TJ_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>MDR-ZJ06_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>NCGM237_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
--------------------------------------------------------------------------
```

```
---------------------------------------NQG------------------------------
--------------------------------------
>R2090_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
---------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>R2091_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
---------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>SSA6_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
---------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>TCDC-0715_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
---------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>USA15_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
---------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>USA2_M
```

```
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>WCHAB005078_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>WCHAB005133_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>XDR-BJ83_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>XH386_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>XH856_M
MASP--------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
```

```
---------------------------------------NQG------------------------------
--------------------------------------
>XH857_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>XH858_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>XH859_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>XH860_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>ZW85-1_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIEGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
--------------------------------------
>3207_M
```

```
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AB030_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AB042_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>Ab04-mff_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>ab736_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
---------------------------------------NQG------------------------------
----------------------------------------
>AbH12O-A2_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
```

```
----------------------------------------NQG------------------------------
--------------------------------------
>AF-401_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AR_0063_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>AR_0101_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>ATCC17978-mff_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>ATCC19606_M
MASP-------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG------------------------------
--------------------------------------
>WKA02_M
```

```
MASP---------------------------------------YITI-GCPTTGGGQVISGNSAFLIDGIAIA
CVGDKATCPAHKTVSTIVSGDPNMQVM-GKAAARVNDSLSCGCKLLPKQSLV--------------------
------------------------------------------------------------------------
----------------------------------------NQG-------------------------------
----------------------------------------
>AB307-0294_C
MATP---------------------------------------YITI-GCPTSGGGQVISGNSMFLIDGIAVA
CVGDKATCPTHKVVATIISGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDN-GGAASSGAKSSTAPM
SQKQQTTNSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEITR---AKLKSDKG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AbH12O-A2_C
LATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSASKSSSAPI
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AB030_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSASKSSSAPI
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AF-401_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSASKSSSAPI
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AR_0063_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSASKSSSAPI
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
```

```
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AR_0101_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDNGGGAASSASKSSSAPI
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>A1268_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPIA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDN-GGAASSGAKSSSAPM
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AB042_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDN-GGAASSGAKSSSAPM
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>AR_0078_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDN-GGAASSGAKSSSAPM
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>ATCC17978-mff_C
MATP---------------------------------------YITI-GCPTTGGGQVISGNSMFLIDGIPVA
CVGDKATCPTHKVVATIVSGDPNMQIF-GKAAARVNDSLSCGCKLLPQQNLVVQDN-GGAASSGAKSSSAPM
SQKQQTTDSFREEKYENYYIEQYKTDVYISHKAVLLGDEGVTPL--------DGAVSYFLNYKVQGKELFLS
VVINAAPLSHKGTVYPFGTAIVSREGKEIAR---TKLKSDQG---YWPTDKNKAPLGSCTIKLPEPNLQLVD
VELELGYTAVISDTVGSVHPMPPIKKYKFSLNSAARKV-
>SDF_D
```

```
-----------------------------------------------------------------MGNLFV
RAGDGHMCPKCKCWSVVIKSHDHMIMD-GKPVAYAGDKLTCGATIQPQQSHVVGDS-VSPYSYASTTSQSLS
PQNQLTTNSFVKDEYENYYIDNSKEERVEFKNFLFPYDQDKGNLIGIIAQGVSGKCTFVVNRKNQNTSLFVS
VTLLPPVLKNDAKIYPKASIQLLKKGKPLGP--IEPMPIGKG---FWNTEKDMQPVGSIELTLPPPDLEPVT
VKLRLSYTGWIDG--GQVVPNPSYINHEFTITSAARRKA
>ACICU_H
MAKS---------------------------------------FAIN-MAPTNHGGVVPATQSRTSQEGNLFV
RAGDGHMCPKCKCWSVVIKSHDHVIMD-GKPVAYVGDKLSCGATIMPQQFHVVGDSGSPYSSAASSAAPVQN
SLVEDKSNEIHKVQFKLVDVDTDQ-----------------------------------------------
---------------PLSAMLYEIHSKESGKLLVQGYTDKNGMTAIYESEHTPESVQLITVDLSKPLDPL--
----------------------------------------
>SDF_H
MSKS----------------------------------------FAVH-MAPTNHGGMIPATQSRSSQQGNLFV
RAGDGHMCPKCKCWSVVIKSHDHVIFD-GKPVAYVGDSLSCGAKIVLQQFHVVGDSGSPYSSAASSTAPVQD
SLVEDKSNEIHKVQFKLVDVDTNQ-----------------------------------------------
---------------PLSAMLYEIHSKDSGKLLVQGYTDKNGMTAIYESEHTPESVQLITVDLSKPLDPL--
----------------------------------------
>PAAR2
MAKG----------------------------------------FAIH-NAPTNHGGIIPSTQVRGSQQGNLFV
RAGDGHFCPKCKCWSTVIKSHDHVIMD-GKPVAYAGDKLTCGATIQPQQSHVVGDS-GSYYNGSTNFSQNLL
DSQKGIFDEQIQVEVNNSFSDLF-----------------------------------LGLAYRLKVDGNVIE
GTLDSNG----------KTLRFETKKQSQVTEFEIFFKENIK---YFSDLEGEE------------------
----------------------------------------
>SDF_K
-MKG----------------------------------------FAIH-NAITDHGGIIPSTQMRTSQMGNLFV
RAGDGHMCPKCKCWSVVIKSHDHIIMD-GKPVAYAGDKLSCGATIQPQQSHVVGDSGSPYSYAASSAAPA--
------QDSFVEEKKE-------------------------------------------YGIQFQLKDEKTQKI
FSDIPYSI-------------IYKKDGKIET--------------GWTDKEGKTHV----------------
----------------INAATPDEVEFQTIDASKPLPPL
>ab736_L
MAKG----------------------------------------FAIH-NAITDHGGVIPSTQAISSQMGNLFV
RAGDGHMCPKCRCWSVVIKSHDHVIFD-GKPVAYVGDKLSCGATIQPQQSHVVGESGSPYSRSSDNTNNSSF
VPTL---------QYGQRFLLQDELTGEPLSNICYEIEKGGNIIHGKTDE--NGFTDLITSENKEEIQIHI-
```

```
----------------------------------IYEEHDHG------------------------------
---------------------------------------
>ATCC19606_L
MAKG---------------------------------------FAIH-NAITDHGGVIPSTQAISSQMGNLFV
RAGDGHMCPKCRCWSVVIKSHDHVIFD-GKPVAYVGDKLSCGATIQPQQSHVVGESGSPYSRSSDNTNNSSF
VPTL---------QYGQRFLLQDELTGEPLSNICYEIEKGGNIIHGKTDE--NGFTDLITSENKEEIQIHI-
----------------------------------IYEEHDHG------------------------------
---------------------------------------
>6200_E
MAKG---------------------------------------FAIH-NAITDHGGVIPSTQSRSSQMGNLFV
RAGDGHMCPKCRCWSVVIKSHDHVIFD-GKPVAYAGDKLSCGATIQPQQSHVVGESGSPYSGKDSNTQSQKY
DEQLKITFNDETDELLKYF-----------------------------------DCRVKIGENFRNANLDIT
G----------------KTNRFYTEGKEPITEIELILKDNII---YFDEL----------------------
---------------------------------------
>A1268_F
MAKG---------------------------------------FAIH-NAITDHGGVIPSTQSRSSQMGNLFV
RAGDGHMCPKCRCWSVVIKSHDHIIMD-GKPVAYAGDKLSCGATIQPQQSHVVGDSGSPYSAKETTQKNNFV
ENNIEKKVTEITWSYGNNFNPLS----------------DKSRFFNDLN------IHVKTTGYSQGENVSIS
---IEPENSDISTFEPFAITIKVDSN-------------GEG---ILKDVFSGK------------------
---TLIIDTEY----------------------------
```