

>CORE_REP|Org34_Gene4576#

MSENTASQIAAPQNAQASGRTILLFLALALMSALLNSSAPTPLYPLYQQQLTLSSVSLTVIYGAYAAG
VLISLFGVGNLAGKVKDLRSMIVPALLVVLGALLFAQADTFAMMLMARLLAGVGTGALTGAANIALV
RFGPRDGGKNAALIATLSFTTGLALGPIFSGIALQTGFHPTTLPFVFIMVMAAVAALGVMFSWPRGVV
TAPSHVTSAETEKSSLLDGLRATGGKFFVCAGALFICWALAASILAIKPGVAETLLGLHARGVFGYAI
AVYLLIAGISQILSRRVNARHSLFGLAQVLAADVFTMAIQWHSGLAAVGLLVAGYAYGAIFVGSA
TLVNLISPPTSHARLLSLFYVIAYIANWVPILLGVVVDRLNQATHLLFLGSTVVCLLLAWKTSRVG
FLANYFVMNIIFYN

>CORE_REP|Org34_Gene1366#

MNPLFTPYLQRWQLEQDGKAFETHSSLLMPVRYRGEAAMLKIAREQEERFGGQLMCWWRGEGAAQVLA
WHEDGILLERAQGESSLAQLVRDGDDEQATAILCRAIAALHAPRAAPLPELIPLQEWSSSLWPAAQAH
GGMLRLSATTAELLSSPRDESVLHGDIIHDNVLDGFERGWLAIDPKRLYGERGFDYANIFCNPNYGI
ATDPAIFQRRVEQVCRLAGLERRRLQWILAWAGLSAAWFMEDGQAADIDFRVAELARALDLPLPAG
DSGFILPVIERG

>CORE_REP|Org9_Gene1317#

MKGHFAAQRHESVNGEKAGMKAIGAFSSVFLGVCSLAIGNVNAAETKSNETYQDAETLLVTGEKVKR
SIFDTSSSVQVFDNSRIASMPDAVQIPDLLRMTPNVVDLGIGNELPTVRGIDGSGPNVGANAFSLGTR
PRLNLSLDGRSLTYNEQAFGPQSLWDLDRVEVFLGPQSYIQGRNAIAGAIVMASKDPTFEWESAFKGG
AGNQHSSQLAAMASGPLVEDQLAFRVSVDRQRRRSEADLPAYAPVGDPREVEATTARAKLLFNPAGLR
DLTTKLTFNHFGSTAPQNESLNPQPHPTNPRHDPRAVFKSNMNSTIWDLAWEASDALLENRVIYTD
FNINRPTAYNIQYAEIDGQEVHVEPVVRFGGADSRLHGLAGLRYFHGTQDEFVNIFFGGSTFKDKTDTH
SAFAELTYALTPQVDVTAASRLEREHRRRDGGSQAVRIDFDETYTVFLPKLDVAWKPTDTQTYGAKIA
RGYNAGGGGITIGTPVVSITYGSEYVWNYELYTRHHLKDANVLTGNIFYNDYKDMQLPYSLGENSSV
IRNADKVETYGAIEGATWQPRWDFELFGNLGLLKTDIKKFSGSGVEGHELARAPAYTANMGAKYQFLK
GWELSSNVAFSDSYYSAYDNDSRGRIGSYWTANAQLAYTFDYGRATLYAKNLFSDSRREMVRSDIYT
ATLQGRRLVGAAVELNF

>CORE_REP|Org41_Gene4663#

MPDLSRRDILRAAAIGSAFSLLPASIRKALAIANNRTGTLRDVEHVVIILMQENRSFDHYFGTLPGVR
GFSDRFTIPLPGDRHVWQQGAERLVLPHYLD SKRGNAQRVTGTPHSWVDEQAAWDHGRMSAWPTYKT
PASMGYRQHELPPQFALANAFTLCDAYHCAIHAGTNTNRLFWHTGTNGPSAADVAVVVNEWDSPGPA
EIGYQWTTYPERLEASGVSWKVYQFLPDNFTDNPLAGFRQYRAASIQVGNPARPPKDFNAFVPYRDAL
NEAAPLYKGNNTLPAADGNDLDAMLAGFRADIQQGKLQVSWIIAPAAYSEHPDPSSPVQGGWFTQE
ILNALTDNPEVWSKTVLLVNYDENDGFFDHMPSPSAPSLREDGSFAGKSTVPFDTEIFQHVAPPGSQD
QPPPDGRIYGPGRVPMLVLSWRSRGGWNSQVFDHTSVLQFLEKRFQVHEPNISAWRRRAVCGDLTSA
FNFVDPNSEALPSLPVTSRHAADGLRQRQEQLPQVPLPSPA HQRLPHQRRQARPSRALPYQLHVEATV
VAEQRRVTLNLFNTGEQGAVFHVYDRDLAQIPRRFTVEAGKAVSDDWQTEDEYHLWLLGPNGFHREL
RGALNRPQPEVRLRPTGRSLQLQLNNPGTEAIAVTLERCPYTQQGPWHITLPAGGSHQQSFDAHASGG
WYDLTLQSPGGWLRRLAGRLEDGEHSVSDPLMGQE

>CORE_REP|Org13_Gene3724#

MSEALTCFKAYDIRGKLGSELNEDIAYRIGRAYGEYLRPKTMVLGGDVRLTSESCLKLALARGLQDSGT
DVIDIGLSGTEEIYFATSHLKVDGGIEVTASHNPMDYNGMKLVREESKPISGDTGLRDIQRLAENNSF
PAVNDAAARGGYQQLSILDAYVQKLLSFVALDNFTRPLKLVINSGNGAAGHVIDAIEARFKNAGLPVEF
IKVHHAPDGNFPNGIPNPLLPECRQDTTDAVLKHGADMGIAFDGDFDRCFLFDERGNFIEGYIIVGLL
AEAFLEKSPGSRIIHDPRLSWNTIDIVEKAYGIPVMSKTGHAFIKERMKEDAVYGGGEMSAHHYFRDF
YYCDSGMIPWLLVAELLCIKGRSLGELVNDRVAAYPASGEINSSLNNPKEAIGRVLGKYEMEADAVDH
TDGISVEYDNWRFNLRSSNTEPVVRLNVESRANVELMQEKTEEILQLLRSE

>CORE_REP|Org41_Gene2975#

MNQRLDIIGIGLGPSNLSLAALGSEIEGFTGQFLERKPHFSWHPGMILADCSMQTNFLKDLVSAVAPT
NRYSFNLVYLVKNRKFYRFLTTEQRTASREEFADYLTWAAGGMDSLAFNQDVQQIEFDDRQRQFVTTSS
NKVFHAKHVSIGIGKKIKLPDCVTAQSDRCFHASEMMLRNPDLTGKRVAIVGGGQSGADLFLNIFKGE
WGQPDQLDWISRRNNYNALDEAAFANEYFTPDIYVESFYSLDSAAKRHMLAEQKMTSDGITSESLLAIY
RAMYHRFDVLREKLWVRLLPSRSLTAVKHTLDNAYQLETRHHLDHGEEAFKADVIFATGYQTATPEF
LEPLAHRLLTTADGEYRIAPDFTFEWEGPAENCLFAMNASMHNHGIADPQLSLMAWRSARILNRALDH
KPFDLGTTPTAIQWRSESVPHAF

>CORE_REP|Org23_Gene4353#

MKSLASTLQGQSIAAAITAVENDIKAKPADADLRAALVQLLCLSGNWTRANAQLKSWQALKPIAQPTT
LLLMQSVNAELQRQAVFAGAAAPALLRQDQPWLQLLVQALHQDAQGAAEQATLRDEALEAAPAGAGQ
LTLAEGNQERQLSFDWLTGDGRLGPVCELALNGVYYWLPFADIAAIQFQAPQSAIDLWVSHALVRLT
DGREQVCQLPARYPLAEGSDDALLLGKRTEWQPLGDGTHYAGLGLKTWLSSEDEFPLHSLRQLSFDAS
A

>CORE_REP|Org42_Gene4092#

MHNIDLEDRLAALSAAIADRTRARMLCLLMDGRAYTATELSAAVEVAPSTASAHKALLEQRLIACVK
QGRYRYFRLAGQPVAEALEGLMALAGVPRPSVKSSPTTLQYARTCYDHIMAGEVAVKLHDLRHLNWL
NGEEDYRLSDAGQAALARLGVDCSPAPTRRRFACGLDWSERRSHLGGALGAALLAAFIHRGWIVRRL
DSRELQLTPAGKKALAAHFDLTV

>CORE_REP|Org4_Gene1541#

MNEKIDYHIEKYHFAPLDEAPRLAHQWSEVLNECRETQAGAEERLRIALLNV DYVTSFELPFRLLLVR
APQLIAGIREELPLSQKNVVFNGKRFQCVYSLKSDLSGVPEAFQYSLSTRIHRAASGVDALPYREIA
KALKAPRERLRLALEQGLPVTALDGLFWFGIQRIAAEVRRRLRKTGMAIVTAETEIFDTLTGTTTRKVPV
YRLAES

>CORE_REP|Org26_Gene3903#

MFRGLKAFLLLTLSLLFCQRAFADCATTNGTVTLPGSSSFVVYNGQINAQGTAGLNCTGLGLSLLSQN
TVTVKVA STTNGMAVANTDGS GDKIAYLIYPDANYQYPYSIGQTIDYSSLNLLSLILISSNVNFPLYI
KTTAGANVRSGTYTDTINLIWNYHICGLGVLGLCIWWDGVNKVSTVSVSVAITKDC LIGTAPNVNFGS
MALVGQFNPVNQSITLTCTKTEGYNTYFTNGNNPVSGWRRMKSGTSNFMQYQIYLPNTTTVWDSTNKQ
SGAGTGLAQSI PYKAAVNAAQTEVAVGSYQDNLSFVVEY

>CORE_REP|Org6_Gene2783#

MHHLMLDIETLDIKPSAVILVVAAVFFDPRTGALGAEFETAVSSQKDQPGRTISLDTVAWWAKQSDEA
RKQAFGGTESLKRVLSSLSRFIHMNSTDTVKVWNGNGKEFDCAILEHAFQQLEMPCPWKFWDTQDVRTV
ITLAELHGFNPKKARPFEGMPHRALDDARHQARYVADTVSALYYRQGAQR

>CORE_REP|Org8_Gene789#

MAKTVVVFHSGYGHTERLAKVVAEGAGAELIAIDQNGDISDEAWQTLDEADAIIFGSPTYMGGPSWQF
KKFADASSKAWFGRKWQDKVFGGFTNSASLNGDKQVT LIALQTLASQHGGLWVSLGLLPANTKSAQRT
DVNNLGGSVGLLVQTPADAGVDEMLSGDLATAKLYGQRVAGFAAKLA

>CORE_REP|Org7_Gene4762#

MKTVKRTGIALAIALTFPLALPAATAAQTSLTNSKAATMTEKHGQFI AVGKV VQVTFGDFAFKLDFTD
DKTMTFTGIGEASQGITDTVQYTAVEIRPKVYVMVYWHEPQSGDNVTHIEDFERGEVYT NIAAKDGSFT
HLKGQLKIVGHSGN

>CORE_REP|Org42_Gene757#

MLNDIEEIRFTARSEENLRGVHPDLVRVIRLALRYS LVPFSVSEGLRSMARQREMVRAGSSQTLRSRH
LTGHAVDVVAMPAGVVSWEWDYYAQIAVAVRRAARECGINVEWGGEWKTLKDGPHFQLAFRDYPA

>CORE_REP|Org25_Gene3681#

MKRLLLDTHALLWMLIDDA CLGVNAKRQIADPGNAVYVSAASIWEISIKQALGKLALPEDIFAIIEAE
DFLALPMDAFHCQQAGQLPPYHQDPFDRMLIAQAQAEGLTLISADTVFPQYGV RVADARR

>CORE_REP|Org3_Gene2772#

MLKTAGWLLPAILALAGCSSSGQRHEQTL SQALTALGQDKALIGASNGVMVRDAESGTVLYQAH AQQR
LAPASNMKMFTSLAAFV LGADYRFETRLLTTGEQRGDTLRGDLYLQSGSDPTLHPDDLDTFAATLAQ
RGIRHIHGRILIDASAFDQTPFGAGWSWDEPF AFAAPISALNYAFTPGGDINVVRVDVQPGARAGAP
GRVSFY PANDAVTLVNRTTTTGGDTALT FDRQPGSNRIVVSGTVAAQAEASSRLITVDQPARVVGALL
QNALRAHGITLRGNAEEGVT PAGARLLAEKTS PPLSRLAVTFLKVSNNGYGEVLT KAMGRKTQKGDW
AAGLQAIGRFVQSQGIEAGAYRQVDGSGLSRMNQITPQQLTLLLAARKQPFADWYNALPIAGQPGL
LVGGTLRSRMVKSAAAGRAHAKSGSMTGVSSLSGYVDSATGRPLAFAIISNNYLVPGA EVKALEDRLV
ETLAACDATV VCR

>CORE_REP|Org1_Gene2196#

MSTRRTFIKQLSAVAGVSLTASLGIPLRGHAKAALNPAWRMPDEGEPQQRAFLAFGAQR AIWGGFTAD
VQAAQGRIARAIADFQPLTVFCRGNERQLAEATCGSHNVSYVVT ELDDIWMRDIGANFVVNDAGELGA
VDFNFNGWGD KQQHARDARLAGFVARRYGVAQPRRSALVGE GGGIEVDGHGTGIMTESSWVNANRNPG
WSRDRVEQELKAMLGLRKIIWLP GIKGRDITDAHVD FYARFVRPGVVVANLDTDPASYDHA VTQAHLA

ILRAATDADGRTLQVHTLSPPRAPRESRFSRRNPDAAGYINYFVINGAVIAPEFGDLQADKAAFELL
SALYPQRKVVQLEIDAIAAGGGGGGIHCVTSQLPVHGKPDQ

>CORE_REP|Org13_Gene3194#

MNYQFENLVFEGGGVKGIAYGGALELLEAKGIMPQIKQTSGASAGAIALLVGLGCSSADVTKILSAM
DFKKFLDYNGGFFGTLQDAYRLFNQYGIAPGDYFYQWSRDIIKQYTGKPDITFEQFEAMKAAKGFKSI
YFIGANLNSGQREVYSHRTTPRMKVADGLRISMSFPFAFVAKNNTLGDLCIDGGMIDNYPVRLFDYDF
SATPPYIDSSSQRINTRTLGLRLDSAGEIAQAAGQAGPRTPVNNLFDFTLAVANVMLDIQTKVHLDSD
DWKRTVYVDTLDVGTLEFGISEEKKRALIESGRRGVERYFAWYDTAMKQAA

>CORE_REP|Org17_Gene537#

MKKIMLMLAAAAALSACAQPAAPPEDAKLKQAYSACINTAEGSPERLQPCKAVLNVLKQEKQHQQFAA
QETVRVMDYQNCIMAVHSGNGQAYDAKCGKLWQEIRDNNN

>CORE_REP|Org2_Gene3975#

MGINPVFARRLYLCWLISHSERPNVPRLMALTGWPRRTLQDVLKALPGMGIELQFVQQGVRNNDGFYQ
LESWGPFNKSWVHHQALLSAIE