

A)

	TM3	TM4	TM5	
Mga VAD161302	TRVMSVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	ANFLVILTMVLVLSGSLAAFFHVIDQFYD-RNSETILEQ----	NLSVGRRHGCFRFAAGVWLTILVICV	224
Mco CAC5373169	TRVMSVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	ANFLVILTMVLVLSGSLAAFFHVIDQFYD-RNSETILEQ----	NYSVARRRHGCFRFAAGVWLTILVICV	224
Cgi JP 011443887	VHLSLSDVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TVLIVATVMTALICGNIILVDFEGRNQLQWEGF-FDSALNLA-GVYNKVLKVKVYGF	FIHFAAGVWLTILVICV	218
Cgi_XP 014443870	TLALPWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	ACILVILTMVTFISVGHIRLLQYRM-HEIDYSG-ANSSINSE----	EDTLPLHACFRFAAGVWLTILVICV	214
Cgi_XP 014443710	ASAMVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TVLIVVITLMTFFCCGNIIFLLQYD-VYNNMG-FDSALNLA-GMRNKKQKV	YVCFRFAAGVWLTILVICV	235
Cvi_K 1223715654	TLSPMFWPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	ATILALITSTFISGHTLILQYD-LEDFG-ENSETILHVE----	KETPLHACFRFAAGVWLTILVICV	219
Nye_XP 021374964	TLSPMFWPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	ITVILVITLMTFISGHTLILQYD-LEDFG-ENSETILHVE----	DIIDFKAFLDLSORCFRFAAGVWLTILVICV	227
Bgi_XP 005079945	TEGLPWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TWFAIAVVMITLCGNTLILQYD-GRVYHSG-KNVSQSSALNLA-DELAGNKA	FGCFRFAAGVWLTILVICV	240
Ngl_XP 013068722	AGALFWPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	THAAILMTLILCGNTLILQYD-GRVYHSG-KNVSQSSALNLA-DELAGNKA	FGCFRFAAGVWLTILVICV	240
Obl_XP 014776263	AKVLPWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	CLIMVITVWILIAALNITLDFPL-LVYVHG-EQOSSYNTA-SEEDPLNIT	LYVAFRFAAGVWLTILVICV	237
Lgi_XP 009052675	SGALPWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TSIAVILTMVLSVCMNILLMLLEYE-VPEHNF-ECSTANVE-ELKNNGVM	RYGVYFARFAAGVWLTILVICV	203
Cte ELT98433	INLPMFWPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TSIVLVLITLILSVNITVLYEYEF-FLDHNG-EBSTAVPPRFTHLHYGR	IVGICVYFARFAAGVWLTILVICV	158
Fdu AGK63073	ELAMPWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	CCGICVFPICFICITVILYHSE-GRVYHYN-ECSTMS-SELENGAKGV	YGVCFRFAAGVWLTILVICV	220
Dme NP 0021263042	TDLMVYVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TENITLAIATVITMVLVLSVVFATHDVTDQAKNITVGMPTT----	NDFLGPTQYVTFRISSSLILPMITIC	225
Dme NP 524700	TDLPVYVWFPTTLKRTSSIMYVQNSRVSVLVLSLDRILAVVHPTIRKINR	TEITLAIATNCACTITVITLALSHSV-RITQYV-NAGTAVFST----	EEFSLGTVGVYVTFRISSSLILPMITIC	226

Mga_VDI61602	MLNN	---LHNTHNEV	---STKDKNCNNTENTVT	: 381
Mco_CAC5373169	MLNN	---LHNTHNDC	---STKDKNCNNTENTVT	: 381
Cgi_XP_0114438887		---IINCNEKI	---NDTKITDVI	: 360
Cgi_XP_011447302	TLNN	NATPKLPDVTSEKCLLNLT	KTIKENGDSKNSIELEMTVTITCNTQDE	: 398
Cgi_XP_011447302	TLNNG	---SKSKSKE	---NGDKNCNINCEVLEKALTE	: 397
Cvi_XP_022315654	TLNN	NATPKNSPNSSEKCLLNTT	KTAEGNCKNSSEASLEMTVITCN	: 399
Mye_XP_021374964	TLNN	---TKTVINC	---SKRNSNSENALPLQTLNKI	: 380
Aca_XP_005097945		---TVNCT	---VSNKNTTFV	: 393
Bgl_XP_013086272		---TSTKQTC	---VNSKNTTFV	: 378
Obt_XP_014776263			---SEAV	: 368
Lgi_XP_009059272			---PGKLANENNV	: 345
Cte_ELT98433				
Pdu_AKO63073		---EEGV		: 352
Dme_NP_001263042			---STTGL	: 357
Dme_NP_524700			---SNTML	: 394

Mga_VDI61602	MLNN	---LHNTHNEV	---STKDKNCNNTENTVT	: 381
Mco_CAC5373169	MLNN	---LHNTHNDC	---STKDKNCNNTENTVT	: 381
Cgi_XP_0114438887		---IINCNEKI	---NDTKITDVI	: 360
Cgi_XP_011447302	TLNN	NATPKLPDVTSEKCLLNLT	KTIKENGDSKNSIELEMTVTITCNTQDE	: 398
Cgi_XP_011447302	TLNNG	---SKSKSKE	---NGDKNCNINCEVLEKALTE	: 397
Cvi_XP_022315654	TLNN	NATPKNSPNSSEKCLLNTT	KTAEGNCKNSSEASLEMTVITCN	: 399
Mye_XP_021374964	TLNN	---TKTVINC	---SKRNSNSENALPLQTLNKI	: 380
Aca_XP_005097945		---TVNCT	---VSNKNTTFV	: 393
Bgl_XP_013086272		---TSTKQTC	---VNSKNTTFV	: 378
Obt_XP_014776263			---SEAV	: 368
Lgi_XP_009059272			---PGKLANENNV	: 345
Cte_ELT98433				
Pdu_AKO63073		---EEGV		: 352
Dme_NP_001263042			---STTGL	: 357
Dme_NP_524700			---SNTML	: 394

B)

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Mga_VDI58805 : -----MTENATGNPNPPTPF-----MNRMTE-----I-EWAVPINYFS : 35
Mga_CAC5393141 : -----MTENATGNPNPPTPF-----VNLRMTE-----I-EKAVPINYFS : 35
Cgi_XP_011423218 : -----MEGEDEFFPMN-----TMFFHMAFVY-----I-POAFPINYFS : 35
Cvi_XP_022371311 : -----MSST-----KLEFSNNVSAMAEYNTDF-----TRRQLRDGRNKKLE-----GQTIVPINYFS : 53
Cvi_XP_022321887 : -----MEGLDELFLPM-----TXPFHFIAYI-----I-PEAFPINYFS : 35
Mye_XP_021368937 : -----MAEIQMNNNSFENV-----TTDAFFLLDTVSF-----I-RKAVPINYFS : 42
Aca_XP_005107230 : -----MASYTSINTSSVSSELGQCTRLCQVLCIRGLSSPPMMSRQVLMCEVCVMSIAYGPNDTSLISEQALMA-----SNESAILPADTMECNTDRAIRKDDF-----K-EKSVPINYAS : 113
Lgi_XP_009055372 : -----E-----E-NKSVPINYIS : 13
Obi_XP_014770415 : -----MSVTSYDLMKEMTNTDSSTW-----ETTSFSLRNTYFPIIKRESIDELAVPILYIA : 55
Cte_EL795205 : MTTTAAAVAKMNDSVAFTPSH-----SPLASTDEARYNQSLPYD-----GFHGCNVVSNISCTPFPHLETDA-----FTRSVVYVYFS : 78
Pdu_AFV92892 : -----MEVVS-----YSGNESESIYSHNETSTM-----GDALSNSESEAFNLQMLN-----DLSLTAYIYFS : 56
Dme_NP_001284892 : MDNYTDLVQYRLAPASPEMEMELADPRQVGRGFLPTN-----ESQLEIPDYGNESLDYPNY-----QQMVGGPCRMEDNNISYWNLCDSF-----L-EKAVPINYCM : 96
Aga_ABW86945 : MIEKNFKSYHLFRGDQYLSNMIEPKKNRAPIILFNSPHMATYYFNESTPLSSQIFPKESSEYNTTGINTSTSYTHMNLNNDSTSYSYNCLASEGNTSYLVNVCETI-----L-NKSVPIYICI : 124
Tca_NP_001106940 : -----MGE-----MAS-----NSTLIFPNQTYANETVSNV-----TSVEKVQYINITME-----I-AKAVPINYVM : 53
Mga_VDI58842 : -----MRHNTAN-----QTAQLDMINTYMLSSNV-----SSGHLVLPD-----LKGHLVFN : 49
Mco_CAC5421131 : -----MKHNAEAN-----QTAQLDMINKMTLSSNF-----STEIGHVLPN-----VKGHLVFN : 51
Cgi_XP_011424701 : -----MEGS-----MKGTMPLGNISLGNPLN-----SFAAANGSFEDKMKF-----P-EVAVIRN : 51
Mye_XP_021378058 : -----MAVNLSEFRSQNNISDE-----STNVATMD-----DNSLLIIN : 40
Mga_VDI06072 : -----MNNNSTGDF-----FCRANNYV-----A-GFWIVVIC : 27
Mco_CAC5422180 : -----MNNNSTVDF-----YRRANNYV-----A-GFWIVVIC : 27
Cvi_XP_022346186 : -----MNASQNTLSN-----ETVLCISFPYF-----A-SFEYIVLIC : 32
Mye_XP_021378058 : -----MAVGDF-----YQDFRPEGSGNTSNIIVNL-----KGNFENETCLPHAYF-----F-AGFYVVIC : 49
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Mga_VDI06072 : RLICTFTVNNILVVLKHHMRTNNAIAGNMLMFMGLFPLVFLVFEFEG-NYREKVLAWY-IYVYGEYITIFERASNTALAI RNIIYHSFQRKWKMCNVLGLTAIVAI : 165
Mga_VDI58805 : RLICTFTVNNILVVLKHHMRTNNAIAGNMLMFMGLFPLVFLVFEFEG-NYREKVLAWY-IYVYGEYITIFERASNTALAI RNIIYHSFQRKWKMCNVLGLTAIVAI : 165
Mga_VDI58842 : RLIIFFFTVNNILVVLKRRHMSNTNIIAAMALMFMGLFPLVFLVFFHFFLE-NYHDDVPEYHWY-IYVYIGELITIFERASNTALAI RNIIYKTAAARFQINQVIFATFIML : 165
Mco_CAC5422180 : RLIIFFFTVNNILVVLKRRHMSNTNIIAAMALMFMGLFPLVFLVFFHFFLE-NYHDDVPEYHWY-IYVYIGELITIFERASNTALAI RNIIYKTAAARFQINQVIFATFIML : 165
Mco_CAC5393141 : RLIIFFFTVNNILVVLKRRHMSNTNIIAAMALMFMGLFPLVFLVFFHFFLE-NYHDDVPEYHWY-IYVYIGELITIFERASNTALAI RNIIYKTAAARFQINQVIFATFIML : 165
Mco_CAC5421131 : RVILILITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cgi_XP_011424701 : RVILILITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cgi_XP_011423218 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cvi_XP_022346186 : EVAVITITISNLVILVLMRNKMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cvi_XP_022321887 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cvi_XP_022371311 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Mye_XP_021378058 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Mye_XP_021378058 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Mye_XP_021368937 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Aca_XP_005107230 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Lgi_XP_009055372 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Obi_XP_014770415 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Cte_EL795205 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Pdu_AFV92892 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Dme_NP_001284892 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Tca_NP_001106940 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
Aga_ABW86945 : RLIVFLITVNNILVVLKRRHMSNTNIIAAGNMLMFMGLFPLVFLVFEFEG-NYKEYIYKWKY-TKYVASELITIFERASNTALAI RNIIYHSFQRKWKITNVLGTAIVAI : 172
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Mga_VDI58805 : VSRRLDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mco_CAC5393141 : VSRRLDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cgi_XP_011423218 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cvi_XP_022371311 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cvi_XP_022321887 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mye_XP_021368937 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Aca_XP_005107230 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Lgi_XP_009055372 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Obi_XP_014770415 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cte_EL795205 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Pdu_AFV92892 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Dme_NP_001284892 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Aga_ABW86945 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Tca_NP_001106940 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mga_VDI58842 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mco_CAC5421131 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cgi_XP_011424701 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mye_XP_021378058 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mga_VDI06072 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mco_CAC5422180 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Cvi_XP_022346186 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
Mye_XP_021378058 : LTRERDEEYIDFEAPSNVNNFVTVNAVRVLKPVVRNH--MDLIVYVFWFVICTHILPCTFLWLADLTLMRQAQIRRMOLL-KQKKSSRKLLKDSNCTIMLAVAVGLDLEPFLMIMILINVO : 294
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Mga_VDI58805 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 381
Mco_CAC5393141 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cgi_XP_011423218 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cvi_XP_022371311 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cvi_XP_022321887 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mye_XP_021368937 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Aca_XP_005107230 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Lgi_XP_009055372 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Obi_XP_014770415 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cte_EL795205 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Pdu_AFV92892 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Dme_NP_001284892 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Aga_ABW86945 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Tca_NP_001106940 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mga_VDI58842 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mco_CAC5421131 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cgi_XP_011424701 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mye_XP_021378058 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mga_VDI06072 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mco_CAC5422180 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Cvi_XP_022346186 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
Mye_XP_021378058 : NTFEHVNICDDRTFAIMLSMNSFFILLSYELNFIYVQVROFFEDFKRMFIGGS---MPIDRECSQVMTL---PIENGKNTQMTVG-----GGETVVL : 379
```

TM

	TM2	TM3	TM4	
Mga_VD1085660	: ISASDLSISLFLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mga_VD1153419	: VSDAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHAVASQRRFPMSPMAFFLITAFISVLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mga_VD115122	: ISQVLSISLFLITLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mga_VD160978	: ISASDLSISLFLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mco_CAC5416355	: ISQDPTISLM-LMTLWLRFFSPACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHAVASQRRFPMSPMAFFLITAFISVLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mco_CAC541393	: VSDAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mco_CAC5413924	: ISQVLSISLFLITLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mco_CAC5413929	: ISQVLSISLFLITLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mco_CAC5413925	: ISQVLSISLFLITLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cgi_XP_011429560	: VSDAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cgi_XP_011429601	: VSDAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mye_XP_021363764	: VSDPVLILHL-LISTVLYKYKMAACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Mye_XP_021375026	: ISQAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Aca_XP_005095139	: LQDILITVL-MMATLTMHGFSPACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Lgi_XP_009065270	: VSDAPVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Obi_XP_014781588	: IADVLVLSISLFLITLITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cte_EL788806	: IADVLILGLL-LITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cte_EL794371	: ISQDPTISLM-LMTLWLRFFSPACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Pdu_AK630777	: IADPCLVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Pdu_AK62999	: IADPCLVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Pdu_AK621080	: VADQDPTIGL-LITLIDHDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Dme_AAL021225	: IADPCLVLSISLFLITLVLGHEDEETACAFKINFLVYSINFTVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cgi_XP_009241886	: LQDILITLHMTAMTIDIKHDEFEVIFWTNFTSSITVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239
Cvi_XP_012331357	: LQDILITLHMTAMTIDIKHDEFEVIFWTNFTSSITVSVLLLVLS	GORLAVCHPERSCKLRNINFFVICILSLSLSVLWFLV	ISTVSHYKQDRLKTRKQKNSGLVLPQGGFTWFDL	: 239

Mga_VDI08560	: AGDTCN	YVE	-	KSS-QQ	-HGEKRN	HKPKFELDMKMTXVGTFLGSP	-	D	-	ENVNTSLV	-	ET	-SSVY	: 426
Mga_VDI13242	: EB	-NSFND	-	IRAKAKIKEITNLEMMPTGSLSHRVLT	TSNCSVSGNVGTAE	SPVNHLMNNEHV	DGTEYEVKGNNS	DNSVLI	QNSVET	DFKKTLLAEDSD	DKNSVTV	-	-	: 444
Mga_VDI53419	: IE	-NSVLE	-	KSSKKKKIKKAVPSV	-	TKAKYELATITATGASLILP	-	N	-	DGLLHPSHQ	-	ET	-TSLY	: 398
Mga_VDI15122	: NE	-NSVFT	-	KLSGKR	-KNGGNNR	KSERYELTTQTVAAKSGMLKS	-	-	-	ESVFLYNEEKRLLMD	-	KT	-TNMY	: 403
Mga_VDI60978	: AGDTCN	YVE	-	KSQK	-HGEKRN	-	-	-	-	-	-	-	-	: 375
Mco_CAC5416355	: EB	-NSFND	-	RIKAKYTIKQNTLIEDPKTGSLSHRVLT	TSNCSVSGNVGTAE	SPVNHLMNNEHV	DGTEYEVKGNNS	DNSVLI	QNSVET	DFKKTLLAEDSD	DKNSVTV	-	-	: 455
Mco_CAC5413936	: IE	-NSVLE	-	KSNKKKT	-KKAVPSV	TKAKYELATITATGASLILP	-	N	-	DGLLHPSHQ	-	ET	-TSLY	: 430
Mco_CAC5413924	: NE	-NSVFT	-	KASGKR	-KNGGNNR	KSERYELTTMTVAEKGSGIMKS	-	-	-	ESVFLHEEGTRLMD	-	KK	-TNMY	: 404
Mco_CAC5413929	: AGD	-NSVTE	-	KSS-QQ	-HGEKRN	HKPKFELDMKMTXVGTFLGSP	-	D	-	ENVNTSLV	-	ET	-SSVY	: 423
Mco_CAC5413925	: NE	-NSVFS	-	KASGKR	-KNGGNNR	KSERYELTTMTVAENAGLMKS	-	-	-	ESVFLHEEGTRLMD	-	KE	-TNMY	: 404
Cgi_XP_012419560	: HE	-NSVFE	-	KSSQKK	-STTMEDKK	KAEEKFEMATIMTTTDDNGNHRP	-	K	-	NDSASSIN	-	DGDDGDLGY	: 407	
Cvi_XP_022319641	: HE	-NSVFE	-	KSSHEK	-KTITDEKK	KAEEKFEMATIMTTTDDNGNHRP	-	K	-	HDSASSIN	-	DA	-DGLY	: 407
Mye_XP_021363764	: GE	-STLE	-	TKHRRSHDYAFGKGDMKE	-	IELKEKEKEKKTITENYQQTNGNVTEKCRLLQ	HKHFVKHTEKKNNDNSLDVEE	PPDVG	-	HSDTAALY	-	-	: 428	
Mye_XP_021375026	: TR	-ESSVE	-	ASKDOW	-RNDSCKPT	KGDKYEMALMTSLTDNDHQV	-	-	-	SGSGKSVN	-	DE	-SNLY	: 403
Aca_XP_005095139	: NE	-NSVFS	-	RTSQTYTRSGVMGEER	-	MELSAVDINPTSPNVAEGQ	-	-	-	SIK	-	SPDGEHG	: 417	
Lgi_XP_009056070	: HE	-NSMFS	-	KNNQNF	-GRSVVIT	IEDRLMSTFEPGQNNIDATP	-	M	-	LPKNHLTIT	-	TL	-PDEQCL	: 398
Obi_XP_014781588	: AE	-NSVTE	-	KGREAY	-SQTT	VTEKQELQITINHCATENKVQE	-	-	-	DFANG	-	ETQ	-TEDID	: 398
Cte_ELT78806	-	-	-	-	-	-	-	-	-	-	-	-	-	: -
Cte_ELT94371	: AE	-NSVTE	-	-	-	-	-	-	-	-	-	-	-	: 331
Fdu_AKQ63077	: AE	-NSVTE	-	HRRQGNPTSTATTATTINSDRT	-RNHNEE	EDEEEVYITKTVKVNVEFL	-	N	-	DNNSSEKARFIQ	-	AEDLKQDG	-	: 409
Fdu_AKQ62999	: MSFT	-	-	GNNWMC	-GKKYVRS	VHAEYBFTLATTMDGNG	-	-	-	-	-	-	-	: 466
Dme_AAG54080	: LE	-NSVFT	-	-	-	-	-	-	-	-	-	-	-	: -
Dme_AAL02125	: LE	-NSVFE	-	KFGKGRQSERLGGNGKGQAQALTKKCLAT	-	RNNAPMAIT	TTTTEGNLLNPNEDSLKLPWLLLP	GNSTNFTD	DFIDQYNDTRMTMPTFLYKTVKPSMKKGT	-	-	-	: 505	
Cgi_XP_019924816	: KRRVRYFLQ	-	-	GNINAVELD	-IRP	-	VSNQTAESINQDYQADSQNLQ	-	-	-	-	-	-	: 375
Cgi_XP_022313157	: KRRVRYFLQ	-	-	GRNVEFLDSRREGH	-	-	VSNQTAESINQDYQADSQNLQ	-	-	-	-	-	-	: 375

Mga_VDI08560	V	--DKESQTQQDEI	438
Mga_VDI13242	I	--DKESQTKLH	454
Mga_VDI53419	V	--DKEIQTs	406
Mga_VDI15122	V	--DKESQT	410
Mga_VDI60978		--	
Mco_CAC5416355	I	--DKESQTKLH	465
Mco_CAC5413936	V	--DKEIQTs	438
Mco_CAC5413924	V	--DKESQT	411
Mco_CAC5413929	V	--DKESQTQQDEI	435
Mco_CAC5413925	V	--DKESQT	411
Cgi_XP_011429560	V	--DKESQTLQEDV	419
Cvi_XP_022319641	V	--DKESQTLQEDV	416
Mye_XP_021363764	A	--DKQIQTRRIV	439
Mye_XP_021375026	V	--DKESQTQ	411
Aca_XP_005095139	L	--KPPVQL	425
Lgi_XP_009065270	L	--K-PVAL	403
Obi_XP_014781588	V	--DEPEVVVTELE	410
Cte_FIT88R06		--	

Cte	ELT94371	:	-----	:	-
Pdu	AKQ63077	:	L-----DKPTAV-----	:	416
Pdu	AKQ62999	:	-----	:	-
Dme	AAG54080	:	ICLSEQQEAFCTTARRGSGAVQQTDL-	:	467
Dme	AAL02125	:	CAILWFSDKHTEGTKAFILYCFFLSYA	:	532
Cgi_XP_019924186		:	T-----GMLE-----	:	380
Cvi_XP_022313157		:	T-----GP-----	:	368