

gi	18857981	ref	NP_572475.1	-----	MYPVAF	-----	VLLLLVAPN-ADANLGRDDE	-----	FHEE	30
gi	158293278	ref	XP_314651.3	-----	MWKLIS	-----	LWTVLVMAGGLKGSQAQFSDI	-----	FDEE	31
gi	76633701	ref	XP_870165.1	-----	MAAAPVRIE	-----	LLVLLLLPGGGWGRAEPPRDS	-----	LREE	33
gi	73992513	ref	XP_534436.2	-----	MAAACLRIV	-----	WLAPLLLGLVDGGRAEPPRDA	-----	LREE	34
gi	120587021	ref	NP_598540.2	-----	MAAAMPLGLPL	-----	RLLVLLLLVGRGCCGCAEPPRDS	-----	LREE	37
gi	34860689	ref	XP_215919.2	-----	MAAAMPLG-I	-----	SLLLLLLVGGCCGRVEGPRDS	-----	LREE	35
gi	23397653	ref	NP_057021.2	-----	MAAAMPLA	-----	LLVLLLLPGGGWCLAEPFRDS	-----	LREE	33
gi	114682189	ref	XP_001155968.1	-----	MAAAMPLA	-----	LLVLLLLPGGGWCLAEPFRDS	-----	LREE	33
gi	118100578	ref	XP_417358.2	-----	MLAVG	-----	LVLLLAAGLG-----QGTTRGV	-----	LREE	26
gi	68401542	ref	XP_684608.1	-----	MAAARCCGLYLAL	-----	LIILLRIVHPGIADTLEKANDT	GEKQASADAPRDNADAREVDLNERQWOKTDVEPYTGDDPONTIPSVRPAKDQFEFE	90	
gi	18397852	ref	NP_566299.1	-----	MASLLR	-----	SLILLLVQSFLVAIAFGSKEV	-----	EFSEEA	34
gi	50302957	ref	XP_451416.1	-----	MRLQNWTPVLLLAIV	IAEVDPEVNPVDNETES	VGQDVIDESWNAEPGESRII	QSSKFLSLEHPTEY	NFRSH	73
gi	45188206	ref	NP_984429.1	-----	MKAS-IIGLWALSSLLIGVSNGLNNMEGRERINASMSGVDVNSGSDIS	IEIAVVGAAANGCGAVGGVADERRGLVSLAAPAKY	-----	PVMEH	87	
gi	6321982	ref	NP_012058.1	-----	MIL-L-LAYFMLGTLI	-----	-----	LGVFAEDTVSQIGINDSLWY	PVDEA	39
gi	39943496	ref	XP_361285.1	-----	MOSLFAFL	-----	-----	LFPLLAQAQ	VHEE	21
gi	32410037	ref	XP_325499.1	-----	MRPFPFSFLLSLLSLICFS	-----	-----	PYTAIANASSSPADISNSRS	DVHEE	46



gi	18857981	ref	NP_572475.1	LVVRPLSGDHVNTYFQPTTRMWHYG	-----	EKDN-LYHTQLTPRVIAELIQQFAVKELHIGLTCGLWRYEYWG	-----	YPIVEATGAEMWAFSGANLNRDVRQWKLAVFGVLCASLNVFDN	TNSIAPRHLIRFQ	160
gi	158293278	ref	XP_314651.3	LFIKPLPKDFVYSYFQPTTRMWHYG	-----	KNDS-LLHTNLVSRPLAELFHHFGVQELHLSFTYGLWRYEYWG	-----	YPVTDAGPGAEEVWAWFEPIDHRASIDHRWKLMLCGTSLGLFCASLSFIEP	SNTFPEVYTLRFPQ	163
gi	76633701	ref	XP_870165.1	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	162
gi	73992513	ref	XP_534436.2	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	163
gi	120587021	ref	NP_598540.2	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	166
gi	34860689	ref	XP_215919.2	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	164
gi	23397653	ref	NP_057021.2	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	162
gi	114682189	ref	XP_001155968.1	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	162
gi	118100578	ref	XP_417358.2	LVITPLPSGDVAATFQPTTRMWHYG	-----	OREG-VSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	PPFLQAPSGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	155
gi	68401542	ref	XP_684608.1	LVIRPLSGDIIYAFQPTTRMWHYG	-----	QEGQKLSHYRFPKALGOLISKYSLRELEHLSFTQGFWRTRYWG	-----	QPIASPPGAELWAWFQDT	VTDVDESWKELSNVLGGIFCASLNFIDE	221
gi	18397852	ref	NP_566299.1	LLIKPLPDRKVLAFHFFENRAPS	-----	SHGR-----HHHLPKAIISQLVQKFRVEMELSLQRWNEHWGGFDP	LSMNAKPPVGLWAWFQDT	QSQVDTSWKNLTHALSGLFCASLNFIDE	SYAAPTWGFQNS	166
gi	50302957	ref	XP_451416.1	LDLTPLNPNLLASLQFYMSEPFQDRD	CHESSEYS	HHTVFPKVPVGPIMSQNTROLHLRFTHGLWDSEWG	OLPHNGLKSGGTGVELWAVI	EAPE	-----	218
gi	45188206	ref	NP_984429.1	LGLRPLPRNALLASLQFYMSEPFQDRD	CHESSEYS	HHTVFPKVPVGPIMSQNTROLHLRFTHGLWDSEWG	OLPHNGLKSGGTGVELWAVI	EAPE	-----	231
gi	6321982	ref	NP_012058.1	LVLKPLPNDLLSFAFLQSEPFDAV	SMSYDAVEHYT	FPRRAIPPLLES	ATROFHLRFTHGLWDSEWG	OLPHNGLKSGGTGVELWAVI	EAPE	182
gi	39943496	ref	XP_361285.1	LVLKPLPNDLLSFAFLQSEPFDAV	SMSYDAVEHYT	FPRRAIPPLLES	ATROFHLRFTHGLWDSEWG	OLPHNGLKSGGTGVELWAVI	EAPE	155
gi	32410037	ref	XP_325499.1	LILRPLPNDLLSFAFLQSEPFDAV	SMSYDAVEHYT	FPRRAIPPLLES	ATROFHLRFTHGLWDSEWG	OLPHNGLKSGGTGVELWAVI	EAPE	180



gi	18857981	ref	NP_572475.1	MPANGQRFVRYATLPREIVCTENLTPWKLLPCSGASGFASLNSGHVHNTKYHSLGLKVRVLCEDHEDNCIVELTQANLYVDLRLRF	-----	ELSNDFSLRRLFCMGLNGYCELAES	-----	KIVORNE	-----	LGERYQLVPEFV	296
gi	158293278	ref	XP_314651.3	FPGRPEPILRYAALPREIVCTENLTPWKLLPCSRREGLLSLLVDSIYSNYSGLVHIRKLCDEACEFQLEVKQTVSVVQDLRLF	-----	GGPN-WSIRKLFQCGMEGSCALATTN	-----	VVVD	-----	SEGALBISQPD	297
gi	76633701	ref	XP_870165.1	ANGTDHYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVYFPPL	301	
gi	73992513	ref	XP_534436.2	ANGTDHYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVYFPPL	302	
gi	120587021	ref	NP_598540.2	ANDTDDYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEACPLASQSLVVDITGYS	-----	QDNETLEVSPPT	305	
gi	34860689	ref	XP_215919.2	ANDTDDYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEACPLASQSLVVDITGYS	-----	QDNETLEVSPPT	303	
gi	23397653	ref	NP_057021.2	ANDTDDYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVHPPPT	301	
gi	114682189	ref	XP_001155968.1	ANDTDDYFLRYAVLPREVCTENLTPWKLLPCSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVHPPPT	301	
gi	118100578	ref	XP_417358.2	ANGTDHRLRLRYAVLPREVCTENLTPWKLLPCSKAGLAVLLKAERLHSSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVHPPPT	301	
gi	68401542	ref	XP_684608.1	GNADHDSFLRYATLPREIVCTENLTPWKLLPCSGKAGLAVLLKSEKLFHSSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVHPPPT	294	
gi	18397852	ref	NP_566299.1	-----	DKLRYGSLPREAVCTENLTPWKLLPCSKAGLAVLLKSEKLFHSSQAVHIRPVCNRNARCTSVSWELRQTLVSVVDFAFV	-----	GQKKDWSLFRMFSRRTL	TEPCPLASESRVVDITGYS	-----	QDNETLEVHPPPT	359
gi	50302957	ref	XP_451416.1	LNQSNHLYLMRATLANPVCENLTPFKLLPTRGKSGISLSDGKHFDSNWHLSIDVNTVCDES	TANCHVMEEF	ETVVNVPNALARADRP	PKPLPGDELRCDD	CKH-HDAFCQCFPLPQ	SKVEFSIS	363	
gi	45188206	ref	NP_984429.1	LNQSNHLYLMRATLANPVCENLTPFKLLPTRGKSGISLSDGKHFDSNWHLSIDVNTVCDES	TANCHVMEEF	ETVVNVPNALARADRP	PKPLPGDELRCDD	CKH-HDAFCQCFPLPQ	SKVEFSIS	375	
gi	6321982	ref	NP_012058.1	FNSTEKLVMRASLPNPEICTENLTPFKLLPTRGKSGISLSDGKHFDSNWHLSIDVNTVCDES	EDDADLCHVEMDAR	ETVVNVPNALARADRP	PKPLPGDELRCDD	CKH-HDAFCQCFPLPQ	SKVEFSIS	328	
gi	39943496	ref	XP_361285.1	NVTAANMHLVGTLPREVCTENLTPFKLLPTRGKSGISLSDGKHFDSNWHLSIDVNTVCDES	EDDADLCHVEMDAR	ETVVNVPNALARADRP	PKPLPGDELRCDD	CKH-HDAFCQCFPLPQ	SKVEFSIS	300	
gi	32410037	ref	XP_325499.1	DANATNMHLVGTLPREVCTENLTPFKLLPTRGKSGISLSDGKHFDSNWHLSIDVNTVCDES	EDDADLCHVEMDAR	ETVVNVPNALARADRP	PKPLPGDELRCDD	CKH-HDAFCQCFPLPQ	SKVEFSIS	450	



gi	18857981	ref	NP_572475.1	HEVKTIRGGHVVVSVYDME--EQFKEAGER-LFNVAWLAPKSNR--RRNLAKPSLPPVIVHRYLLGHQERGRIVTEVTSNH-YDALP-----IMLQVPIPVVHAYLHLSIRR	402
gi	158293278	ref	XP_314651.3	ETILSVRGGARTQLHRFDVKQFEALITAKGRRAMFNVAVMKRDPN--VIVVAGPPPIYAKRFLIGVGOERGRIVQITNAH-WGALD-----LIVFETIPWFVYVYLHTLIRR	403
gi	76633701	ref	XP_870165.1	ITYQDVILGTRKTYAVYDLDLDAAVSN--SRSLNIIQLKWKRPPENE--APPVPFLHAORYVSGYGLQSGQLSILLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	404
gi	73992513	ref	XP_534436.2	ITYQDVILGTRKTYAVYDLDLDAVINN--SRNLNLQFKWKSPPENE--APPVPFLHAORYVSGYGLQNGELNLLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	405
gi	120587021	ref	NP_598540.2	ITYQDVILGTRKTYAVYDLDLDAVINN--SRNLNIIQLKWKRPPENE--ALPVPFLHAORYVSGYGLQKGLSILLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	408
gi	34860689	ref	XP_215919.2	ITYQDVILGTRKTYAVYDLDLDAVINN--SRNLNIIQLKWKRPPENE--ALPVPFLHAORYVSGYGLQKGLSILLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	406
gi	23397653	ref	NP_057021.2	ITYQDVILGTRKTYAVYDLDLDAVINN--SRNLNIIQLKWKRPPENE--APPVPFLHAORYVSGYGLQKGLSILLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	404
gi	114682189	ref	XP_001155968.1	ITYQDVILGTRKTYAVYDLDLDAVINN--SRNLNIIQLKWKRPPENE--APPVPFLHAORYVSGYGLQKGLSILLYNTHPYRAFP-----VLLLDVVPWYLRLYVHTLITIS	404
gi	118100578	ref	XP_417358.2	SVHEAIVQGDKTYAVYDLDLDAVLENT--SRSLNIIQLKWKRPPESS--ELSPIMHAORYVSGYGLQGEISILLYNTHPYRAFP-----VILLETVPWYLRLYVHTLITIS	397
gi	68401542	ref	XP_684608.1	LLSQAVVLGDRRTYVSYDLDLDAETFGQ--LRSNLNLLRWKGG--ESG--DMLRPLHAEORYVSGYGLQGEIHTVIYNTHPYRAFP-----VLLMDVVPWYLRLYVHTLITIS	460
gi	18397852	ref	NP_566299.1	FELSLKPERVIRE--CSFLTFIDDKSSD--EPPDLGLTWKRPSKWS--CQQAPLHSRFRMLGSGNERGAIATLLKATESQEKLSGRDLTNGCQITKANIFQIPWYIKVYVHTLQIPV	425
gi	50302957	ref	XP_451416.1	GE--SSKICVHVP--SHWDVMIQVDESYFATDDN--CFDLNKNKPP--HDVRLLETID--SKSVLPSKKTPIYVSRALTYGQDRGGLRIVFRNPS--NEAVE--LVYFESLPWFMGVYLSLALAE	474
gi	45188206	ref	NP_984429.1	SD--TPSKACVKVS--DNWKVLIKAGDAYFITATN--CFDVKGKKW--HDIYLDLTD--ITKVYVDSVPVFRTRSLTYGQDKGGLRIVFRNPS--DQFVS--LVYFESLPWFMRRLYSLTVKIE	486
gi	6321982	ref	NP_012058.1	AN--RPTRICAEVDRS--WTAFLSVDITFTHDN--CFDLSNDQEGGSYDFILESTD--ITKVYVDSVPVFRTRSLTYGQDRGGMRIYVFRNPS--DTFVK--LVYFESLPWFMRVYLSLQIUS	446
gi	39943496	ref	XP_361285.1	ANSDVPPVCMQIP--ESRSVYTESGVHEIKNPDGRSRCRKYVDDGAL--VELVLAEPSESSAHPSPGADFE--FELVLAEPSESSAHPSPGADFE--LVYFESLPWFMRVYLSLQIUS	432
gi	32410037	ref	XP_325499.1	LDPNVSPVCIQVP--DSRIVFAS--EGAVEKKNPDQ--SRCDFFPAEND--FEIFLPAF--BAEDGSVIVIEHVVKPE--PLLYAERSF--IGHQERGGVQ--ILRNPSPDQVEE--FIVMESLPWFMRVYLSLQIUS	449



gi	18857981	ref	NP_572475.1	KPORVNE-----YGGQRLT-----FKLLHYTPGKQRELPSHLIEIGFMLPGQ--SALISIDVDYLLKWLIEYPPDANHGHIYPS--IIISLLPSARNYTSIPR--EALFRESFNA--QLAGYFQVREALLLTLPTDFSMYPNVICLAC	537
gi	158293278	ref	XP_314651.3	-----AGGERIE-----PAFLHYTPGQREPRYGLVAFRIPARA--TVELSIDFDYIFLKWQYPPDANHGHIYPS--IIISLLPSARNYTSIPR--EALFRESFNA--QLAGYFQVREALLLTLPTDFSMYPNVICLAC	532
gi	76633701	ref	XP_870165.1	K-----GKENK-----PSYIHYQPAQDRMQPHLLEMLIQLPANS--ITKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFNLSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	533
gi	73992513	ref	XP_534436.2	K-----GKENK-----PSYVHYQPAQDRLOPHLLEMLIQLPANS--ATKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFKSLXPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	534
gi	120587021	ref	NP_598540.2	K-----GKENK-----PSYIHYQPAQDRMQPHLLEMLIQLPANS--VTKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFNLSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	537
gi	34860689	ref	XP_215919.2	K-----GKDNK-----PSYIHYQPAQDRMQPHLLEMLIQLPANS--VTKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFNLSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	535
gi	23397653	ref	NP_057021.2	K-----GKENK-----PSYIHYQPAQDRMQPHLLEMLIQLPANS--VTKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFNLSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	533
gi	114682189	ref	XP_001155968.1	K-----GKENK-----PSYIHYQPAQDRLOPHLLEMLIQLPANS--VTKVSIOFERALLKWTETPDNNGFYVSPSVL--SALVPSVVAAKPDWEEPLFNLSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	533
gi	118100578	ref	XP_417358.2	K-----GKENK-----PSYMHYQPAQDRKRRPHLLEMLIQLPANS--ATKVTIOFERALLKWTETPDNNGFYVSSVVL--SALVPSVVIAMKDNVVEESLFTSLFPVSDSSSYFVRLYTEPLLVNLTPTDFSMYPNVICLAC	526
gi	68401542	ref	XP_684608.1	K-----SRENK-----PSYIHYQPAKDRRPHLLEMLIQLPANS--MTEITVQFDRALLKWTETPDNNGFYVSGSVV--SALVPSVVMAMNTNFTLDDQPLFSFVVKES--SYFMRYTEPLLVNLTPTDFSMYPNVICLAC	589
gi	18397852	ref	NP_566299.1	DQQ-----QKTDESEV-----LKKINVSPTDKVSSGMMEMMLBPCPEKSVASISIEYDKGFLHIDYPPDANQGFDP--SALISIFPDHSHALDFQELSNLPLSLKREK-----SLVRSYTVLVLPLTPTDFSMYPNVICLAC	554
gi	50302957	ref	XP_451416.1	SDDPE-----LTLDS-----VVKSTFVSPARDRERPTHLEERAMITPPNT--AFATVQFDKSLKLYAEYPPDANHGFEIETAAVAVLP--PER-----YEARTSLLLSLSTPTDFSMYPNVICLAC	581
gi	45188206	ref	NP_984429.1	TDDN-----LSIND-----VIKSTVYLPARDRERPTHLEVMQVIPANT--TFALTYQFDKSLLOVAEYPPDANHGFEIETAAVAVLP--PER-----YEARTSLLLSLSTPTDFSMYPNVICLAC	592
gi	6321982	ref	NP_012058.1	TTSPP-----LQEND-----IILDKYVLOAADRKRPGHLEFIMLIPANT--DIVMITYQFDKSLLOVAEYPPDANHGFEIETAAVAVLP--PER-----YEARTSLLLSLSTPTDFSMYPNVICLAC	557
gi	39943496	ref	XP_361285.1	ADSELD--RGSLV--SAGQAQAKGDKK--VIQELYRPAALDRARSGQVEVRMRVPPAS--TVFVLYDFEKSILRYIEYPPDANRGFEDVASAVV--LILNSQSSST--SSRNA-----NLR--TASVLLSLSTPTDFSMYPNVICLAC	561
gi	32410037	ref	XP_325499.1	DG-----QPKADS-----LIQEVYVYRPAVDRARGTQLEVRMTVPPAS--TVFVLYDFEKSILRYIEYPPDANRGFEDVASAVV--LILNRDNKSGG-----NCRNSRFAAVNLR--TTL--CNL--LSTPTDFSMYPNVICLAC	568



gi	18857981	ref	NP_572475.1	* .. : * : : : : TVVALAFGPIHNSVATKMIIVGR--TSAKPNFVKKIFNQLFRRGKATDE--AAEGEGLPAAGAAATGVA--SGRAAISPGSPSGDQPLLEDLDESEEBEQD	633
gi	158293278	ref	XP_314651.3	TVVALAFGPIHNSVATKMIIVGR--TSAKPNFVKKIFNQLFRRGKATDE--AAEGEGLPAAGAAATGVA--SGRAAISPGSPSGDQPLLEDLDESEEBEQD	574
gi	76633701	ref	XP_870165.1	TVVAVCYGSFYNLLTRTFQIE--EPKRGGLVKRLANLIRRARGVPPL	578
gi	73992513	ref	XP_534436.2	TVVAVCYGSFYNLLTRTFHIE--EPSTGGGLAKRLANLIRRARGVPPL	579
gi	120587021	ref	NP_598540.2	TVVAVCYGSFYNLLTRTFHIE--EPKSGGLAKRLANLIRRARGVPPL	582
gi	34860689	ref	XP_215919.2	TVVAVCYGSFYNLLTRTFHIE--EPKSGGLAKRLANLIRRARGVPPL	580
gi	23397653	ref	NP_057021.2	TVVAVCYGSFYNLLTRTFHIE--EPRTGGGLAKRLANLIRRARGVPPL	578
gi	114682189	ref	XP_001155968.1	TVVAVCYGSFYNLLTRTFHIE--EPRTGGGLAKRLANLIRRARGVPPL	578
gi	118100578	ref	XP_417358.2	TVVAVCYGSFYNLLTRTFHVE--EFSRGLGLAKRLANLIRRARGVPPL	571
gi	68401542	ref	XP_684608.1	TVVAVCYGSFYNLLTRTFQVD--EFSPP--LAKRLANLIRRARGVPPL	634
gi	18397852	ref	NP_566299.1	TIFALYFGLLNLVRRRIGEE--ERFLKSOAGKKGGLKQLLSRTAKIRGRPIEAPSS--SEAE--SSVL--SKLLIKLITLIVAGAAAAGVFS--DE	644
gi	50302957	ref	XP_451416.1	IVMGLAF--GTLFNLISKQLITL--EADKILAST--GPRAKLLRVKAKIVNMLQGNKNI--IKS--VE--	643
gi	45188206	ref	NP_984429.1	IVMGLIF--GTLFNLVKKITL--VEADKHMCHSGLRARARSIKQNLDFDKLGSQK--LKKD--	648
gi	6321982	ref	NP_012058.1	TIMGLIF--GMLVNLVKKRMV--VEADKITLQSGLK--KLLKLEKFLGK--KTKTD--	610
gi	39943496	ref	XP_361285.1	TAIALGFGGLFNILVRRFVGADEG--PRPGLANLARLQKIKGKFGANKTPGDDAP--TLA--SAGDQ--GADG--KQQAALT	636
gi	32410037	ref	XP_325499.1	TAIALAF--GGMFNILVRRFVAANEG--PESGLKGVNKLKAKVAGFLKKGK--KES--APAVAAEEEEKME--	632

