

gi | 161076460 | ref | NP_001097242.1 | ...MNVESQLKTPPHIRNLVKHVNKRNFNESSEQINQVKEHGL...EADRSSLRHLFVSVINFE-DLVPFVTVVQLQAKLLGIQLERQLHSSSFVSNICYAFD...OFFASNDKSLKPVAVADLVGVQARLIGINKVCECV 131
gi | 158299778 | ref | XP_319808.4 | ...ARLLATELASLNRKPOLVANCFVAVD...NPPF-QOKSLKP-LSNLLAOLSKLSCPTIQETA 59
gi | 94383743 | ref | XP_899766.2 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 109507689 | ref | XP_001060702.1 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 42716275 | ref | NP_057368.3 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 114662880 | ref | XP_511007.2 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 119910031 | ref | XP_613555.3 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 118096204 | ref | XP_414043.2 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 121582322 | ref | NP_001073420.1 | ...MNLDS-LLSLALSQISYLVLDNLTKKNYRASQOEIQHIVNRHGP...EADRHLRLCLFVSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAI 128
gi | 212645813 | ref | NP_498516.2 | ...MHSVSGLAPVFRVBEENHMLRNRNLERPISKKGTITLLSKMPMGFVLNSCSCAYIDNLLAHSIHRVQPHFMQIRLVVTCGRSSPSLNPHAAANILBAFNFC...QTEAPAKKFLSEEDAAALSLFHTILSYSTVQVQINRSG 138
gi | 42561615 | ref | NP_171710.3 | ...MTPSKVAGHTFRLLHSHFDSDVDSTIALQLSQVDFG...VEHSIPVLKTCLCDCTARRSHPNLQLEKVVSLFKFKVLKLNLAATLLPHALNDFELTQESVDDLTIT 106
gi | 115483368 | ref | NP_001065354.1 |



gi | 161076460 | ref | NP_001097242.1 | ...FALALHSSSYTELKHSARNNLKGSLELIDSYLGNKGTGP...ADSGLEIRISFDLLOVLLCCLSEY...VQPPVEAQFLIKLREEFPRQAVPLVLA...PFLYGSTIATAGAGASETDAEAEANTNSNSS 254
gi | 158299778 | ref | XP_319808.4 | ...LSIALLHSEQPEIVRFAEAHLNKLTELIESYIDSDSGSN...VEGSLNDVSEPEFLQOILSLISYGRHTALGLTDTYERFRSOLCRDFPRDRVPLVLA...PLLY...AESSEIIEAELIKLNTHSI 178
gi | 94383743 | ref | XP_899766.2 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 109507689 | ref | XP_001060702.1 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 42716275 | ref | NP_057368.3 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 114662880 | ref | XP_511007.2 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 119910031 | ref | XP_613555.3 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 118096204 | ref | XP_414043.2 | ...FGLALLNSSSPDLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 121582322 | ref | NP_001073420.1 | ...LGLALLNSSNADLRGFAAFQIKOKLPDLLRSYIDADVSGN...QEGGFODIAIEVLHLLLHLLFSGKAGFVGVEQIDAFKTLRRDFPQERCPVVLA...PLLY...PEKRDILMDRILPDSGGV 246
gi | 212645813 | ref | NP_498516.2 | ...LEILGAQRLTSAALCDLIYATKTMDDMVASKLTLHCKKLAGLFDPLVLPFISKLAKSRRIERHLYQLPFLGHCEYTSDWGVSPEGAEIYNOIARGNFETTLLIEIVQ...TFLEKEVKEVLISSTTDPKILVQYLISCSNPND 280
gi | 42561615 | ref | NP_171710.3 | ...FSISENIQFALALTDFERLDAKTTGRNLLLAQIEQLCANTG...ILSSELIHISVLEFLRKSBDLSMHLLDSFLOFLSSAQPRDDFSFALPMLAQVHEAP...VFRSMDFHDSADNLDAILA 225
gi | 115483368 | ref | NP_001065354.1 |



gi | 161076460 | ref | NP_001097242.1 | ...FEADALNEVGIEDIYDHLSELIFFNQCKNNIMDTSWINLILEIGYEFTS...VEECKNHLCSRERERELQSKDVAIVGLMCRHSLLDCNVNLPFPANFWPGQGGGNSSSGSSQTITPQQNPGSSNNNDGSDGNSSDKDK 401
gi | 158299778 | ref | XP_319808.4 | ...LGS...SIMKTSWNLVVEVGYSTFANFDDCRNHLKVGGR...DITPQDVAIVSSMCLTHESLSESSINLPEFAFWP-QSG...DPGQKGDGNGSSAS 273
gi | 94383743 | ref | XP_899766.2 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 109507689 | ref | XP_001060702.1 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 42716275 | ref | NP_057368.3 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 114662880 | ref | XP_511007.2 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 119910031 | ref | XP_613555.3 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 118096204 | ref | XP_414043.2 | ...AKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTAAQVARVLGMMARTHSGLTDG...IPLOSISAP-GSGIWE-DGDKDSEGAQAH 334
gi | 121582322 | ref | NP_001073420.1 | ...NKT...MMESLADFMEVGYGFCASIEECRNIIIMQFVRR...EVTASQVARVLGMMARTHSGLTDG...ISLOTITNVEVGGGIWE-DGDKDSSQA 335
gi | 212645813 | ref | NP_498516.2 | ...EIVQALAFLLYSN...KLLPAGSGGIDMDVQAADITITARLGDKFKQPVKDALDSGRE...ALLRREIYGVSLLSVENFVTELQAPLQKMKVTVNSVANAILYMLQYN...FDMSRDTEVGRQDNSEFFWG 409
gi | 42561615 | ref | NP_171710.3 | ...SID...KEVSVGLMELCGGFADAQCKEILSFAPLG...EATISRIYGVNVRRCADLENDQTTFSFTVALG...SCITELTEPFR 306
gi | 115483368 | ref | NP_001065354.1 |



gi | 161076460 | ref | NP_001097242.1 | ...KETTEATQWPKPDVFOALKEVV...PQLNWKDVCMLDHPPEFLKDRIGLELLLILRLAIGSN...IFPHPECIYRHWANTEGOLSLIANMLKNP-DLFSFADFVFSQPALDVLKTPADANKIESSWKSLLHVEVLLSIADKG 540
gi | 158299778 | ref | XP_319808.4 | ...EVTWKPVEVLVQALKEVV...PALNWKVECVALDHPPEFLKDRAGLSLLLIVKMGQASNMGTTP...VECLYQRWTVNVEGOLSIISLILKNS-DLYSPADHIYTSVSLDLLRPPETDSKEVACWMSLHLDVVDVLLYADHA 410
gi | 94383743 | ref | XP_899766.2 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 109507689 | ref | XP_001060702.1 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 42716275 | ref | NP_057368.3 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 114662880 | ref | XP_511007.2 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 119910031 | ref | XP_613555.3 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 118096204 | ref | XP_414043.2 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 121582322 | ref | NP_001073420.1 | ...TNWVEVLIDVLKELN...PSLNFKVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 464
gi | 212645813 | ref | NP_498516.2 | ...GSNFVIGITRFVBEQQAAVVDMEGFDVDPDINWVEVYELDHPGFQIRDSKGLHNVVYGIQRLGME...VFP-VDFIYRPPWKAEGQLSFIQHSLINP-EVFCFADYPCHTVAVDILKAPPEDDNREIATWKSLLDIESLLRLAEVG 550
gi | 42561615 | ref | NP_171710.3 | ...SWNVDLILDVLIKQLQ...APGISWRKVYENLDHGDGFDIPNMFESFFMRYIKAACKEP...FPDLDAVCGSVKKNMDGQLSFLKHAISAPEVVFVFMHSPRKLVIIDNMHSQEQGLSNHAWLSLDDLVDLQOLAERG 438
gi | 115483368 | ref | NP_001065354.1 |



gi	161076460	ref	NP_001097242.1	-YTTVHLELFKFPANCPDVLFLALLNPPMTARQELFNLVPIFLG-NHPNSNVILASAWSSN--NFQLRNSINMNASWY-LRGNBFDQVLSRILDVAODLKALALLNARSFLFIIDLACLASRREYLKLEKWLTKIREHGEP	685
gi	158299778	ref	XP_319808.4	NLEKVMKIFKVPGLCPDVLFLALLOINPPMTARQELFNLVPIFLG-NHPNAGTILHHAHNSTNVNLRPIILHMSDWY-MVG-EGDOSRLSRILDVAODLKALSNLLNIRTYMFIIDLACLA-----	535
gi	94383743	ref	XP_899766.2	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	109507689	ref	XP_001060702.1	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	42716275	ref	NP_057368.3	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	114662880	ref	XP_511007.2	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	119910031	ref	XP_613555.3	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	118096204	ref	XP_414043.2	-QYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	121582322	ref	NP_001073420.1	-HYEVKQLFSPFIKHCPCDMLVLALLOINTSWHTLRHELISITLMPIFLG-NHPNSAIIILHYAWHGQGGQSPSIRQLIMHMAAEWY-MRGEQYDQAKLSRILDVAODLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTKIREHGEP	611
gi	212645813	ref	NP_498516.2	NGAPKHLAFMVDLAACLAKRDYLNLEKHEIDEDKAKHGAMVAVLQPIQKYOQAQLVAIAIPKQATIPGAPSEPLQVLPVSRKARKPLRQPIFVIVQVMKENSGRSSSSVSSGGHVQSSSGSQPQQQVFGGSSGLPSSGVVVPQQPQ	700
gi	42561615	ref	NP_171710.3	-HAVLVSSLLQVPLTQCPRLILLGMTHIKTAENLIREVVSAILPVIIT--SPQDSGFHNLWQNAELVLWGIIDAHLKADS-----MLRIETICHELKILSVVLESVFPSSSIRLAVLASLRGLLDIENWLNCLYMKDPL	574
gi	115483368	ref	NP_001065354.1610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750	



gi	161076460	ref	NP_001097242.1	FMCAIILVLRRCPOVINAKVPEQDLPKQAQLPETVITMINCLOTICINNCQPEMVEVIMQMTANVAIMANKARAQQQQPGLVPPPPPTILRGHRGMDLPGGVIPPPPQQPFSGNLNAQMFPGMDPLTNMS--NNLAGLNLSCP--	831
gi	158299778	ref	XP_319808.4	-----QLLPFMVDLSNLSIT--ANTIGGLSIGGGGG	562
gi	94383743	ref	XP_899766.2	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	109507689	ref	XP_001060702.1	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	42716275	ref	NP_057368.3	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	114662880	ref	XP_511007.2	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	119910031	ref	XP_613555.3	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	118096204	ref	XP_414043.2	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	121582322	ref	NP_001073420.1	FIOACMTFLKRRCPISILGGLAPEKD-OPKSAQLPAETLATMCLAQACAG-SVSOELSETILTMVANCNSVMNKARQ-----PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMGFFPNLGSFASTPQS	749
gi	212645813	ref	NP_498516.2	QQPPLQQQHSQSLPFPPTISQQQIHWQOSVPGFIQRPAQFAPQPMFPFQAQAQHQMGMGPPSSQNAQPGMN-----LLNMSPFASGNRRDLLKVVQPAPPPPSMSPSPTQMMRSLIPPLTQR-----SNSGWHAAAP	836
gi	42561615	ref	NP_171710.3	FAECLKFKVKN-----VHFSE	591
gi	115483368	ref	NP_001065354.1760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	



gi	161076460	ref	NP_001097242.1	--NGAFNENMLTSPSRIMTPGANPYPLNLMQMP-QAPPPNVGNLGRMLPGGP-----QQQPTPTPTAP-----NPNVMDLQIPVSKVEDEVNSYFORIYNHQPNPILSDEVDLILQRFKESNRRQEVFLCMLRNLFEFY	967
gi	158299778	ref	XP_319808.4	GNSAFSENNIATPPSRILLSSSPFMMPLPPGAAAAQAQLSRLQOTFN-----DKLGAASAAAGIPTQALAPFADAPLPSKVEVEDEANSYFORIYNLPPHPLSDEVDLMLQRYKDSNRRHENDVYQCLRNLFEFY	704
gi	94383743	ref	XP_899766.2	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNNDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	898
gi	109507689	ref	XP_001060702.1	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNSDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	899
gi	42716275	ref	NP_057368.3	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNNDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	899
gi	114662880	ref	XP_511007.2	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNNDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	899
gi	119910031	ref	XP_613555.3	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNSDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	899
gi	118096204	ref	XP_414043.2	PAKAFPPPLSTPNQITAFSGIGGLSSQLP-CGLGTGSLTGIGTGALGLPAVNNDFVORLGTSGLNQPTFOOSKMKPDLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	899
gi	121582322	ref	NP_001073420.1	PAKAFSNLNPSTAFFGINPLSSQLQ-GPLST-SLSIGSG-LGMPVSSDVFSARKMSIFGLNPPPTQ-----DLSSQVWPEANQHFKEIDDEANSYFORIYNHPPHPTMSVDEVLEMLQRFKDSIKRREVFNCMLRNLFEFY	891
gi	212645813	ref	NP_498516.2	FORPSPPPPOQMDERQIQEFAPQGFQOLQRSVTVGRSMGIVGQKTSNFSVSG-----APIPGSAAATAAANVQPMNEDFQSMFAEDIQBEANSYFEKIVSVNN--AMSVENLIDLKRFVSNDRRERVLACVVKNLFEFY	979
gi	42561615	ref	NP_171710.3	DDFRAKIFHPSDPLSDLHLEATFSLKLVKAHDNAITSQVVEIEKVN-----AAILDCNPKLQNGEAKDSSAPNAYGDDVBAEANAAYFHQM-----SHLQVDAMVQMLSRYESLVPREKLIFCMLNLFEEY	719
gi	115483368	ref	NP_001065354.1910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050	9



gi	161076460	ref	NP_001097242.1	RFFCQYPEKELQITAQFLGGIIDRNLVPTFVALGSLRCVLDALRKPDGSKLYYFVGTALDRFTRLHTYNYKCEHRSIPHSDFPPHLIIOYVEYGMH-----GOEPPPKLIG--LNSNIPSAISS-----	1088
gi	158299778	ref	XP_319808.4	KFFPQYDPEKELQITAQFLGGMVERNLIITFVALGALRCVLDALRKPEGKMYFYGITALDRFKNKHLHPKYCEYVHSIAHFSFPFPHLIEYIEYGSQ-----GOEPPNKTILGPGPLPPIIQFMPSGAAGRG-----	833
gi	94383743	ref	XP_899766.2	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1025
gi	109507689	ref	XP_001060702.1	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1026
gi	42716275	ref	NP_057368.3	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1026
gi	114662880	ref	XP_511007.2	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1026
gi	119910031	ref	XP_613555.3	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1026
gi	118096204	ref	XP_414043.2	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1026
gi	121582322	ref	NP_001073420.1	RFFPQYDPEKELHIACLFGGIIIEKGLV-FYMALGLALRYVLEALRKPFSGKMYFYGIAALDRFKNRLKDYPOYQHLASISHFMQFPHLQYIEYGOQ-----SRDPFVKMOGSIITPGSIALAQAAQAV-----	1017
gi	212645813	ref	NP_498516.2	RFFHEYPERELRTAAVYGGIITREDII-SNVQFAAVRKVIESLSADPNMLNTFQIVALQHCRSKLCAYPKVQCMIVSSENFARFPQLLKDYYVITAGVK-----GELPPEG-----GRH-----	1087
gi	42561615	ref	NP_171710.3	RFFPKYPEROLKIASILFGSVIKHQLI-SSLILGMALRLVLDLRLKPADSKMFLFGSKALEQFVNRVLDYPOYCNHILQISHLRSHPHELVTVIEQALSRTSSGNLSDAS--VSHFGPSQSFPGNGELSGS---GIGQPALQLSPLQL	863
gi	115483368	ref	NP_001065354.1	KFFPKYDPTQLKLAALVMSLKHQVL-AHLGLGIALRSVLDALRKSIDSKMFMTTALQEFMDRLLEWPOYCNHILQISHLRAHAEVLAIVLAKISSQNFVNGSMLSDAQHGSSSIGNMEASEASWQLINPPTQLERHQ	158
			1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200	



gi | 161076460 | ref | NP_001097242.1 | -----GPGTEPIVRSNLSMLGN---MPAATPGS--GPKSNAAVSHATRMK-----SIANA^{*****}NID^{*****}LLLVANQ^{*****}--E^{*****}EKV^{*****}IV^{*****}VP^{*****}PE^{*****}VD^{*****}K^{*****}TAF^{*****}IF^{*****}FN^{*****}LS^{*****}QL^{*****}NI^{*****}PK^{*****}Q^{*****}DE^{*****}BI^{*****}KE^{*****}IM^{*****}TK^{*****}E-----YV 1186
gi | 158299778 | ref | XP_319808.4 | -----GPVGNPLVRSN^{*****}SV^{*****}IG^{*****}TN^{*****}LAG^{*****}V^{*****}ST^{*****}IG^{*****}NS^{*****}GG^{*****}T^{*****}GG^{*****}S^{*****}GG^{*****}Q^{*****}PP^{*****}RVK-----SIANA^{*****}NID^{*****}LLVLA^{*****}QDREK^{*****}II^{*****}APP^{*****}DAI^{*****}Q^{*****}DK^{*****}TAF^{*****}IF^{*****}FN^{*****}LS^{*****}QL^{*****}NI^{*****}Q^{*****}Q^{*****}CE^{*****}BI^{*****}KE^{*****}IL^{*****}Q^{*****}K-----YV 939
gi | 94383743 | ref | XP_899766.2 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1126
gi | 109507689 | ref | XP_001060702.1 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1127
gi | 42716275 | ref | NP_057368.3 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1127
gi | 114662880 | ref | XP_511007.2 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1127
gi | 119910031 | ref | XP_613555.3 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1127
gi | 118096204 | ref | XP_414043.2 | -----PAKAPLAGOVNTMVTTS-----TTTTVAKT^{*****}IV^{*****}TR^{*****}PG^{*****}VS^{*****}FK^{*****}KD^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1127
gi | 121582322 | ref | NP_001073420.1 | -----PPKAPQPGQASTLV^{*****}VTAT-----TTTTAAKT^{*****}IT^{*****}TR^{*****}PA^{*****}V^{*****}AV^{*****}GP^{*****}PK^{*****}D^{*****}VP-----PSINT^{*****}TN^{*****}ID^{*****}LLVLA^{*****}D^{*****}Q^{*****}TER^{*****}IV^{*****}EP^{*****}PE^{*****}NI^{*****}Q^{*****}E^{*****}K^{*****}I^{*****}AF^{*****}IF^{*****}N^{*****}LS^{*****}Q^{*****}SN^{*****}MT^{*****}Q^{*****}K^{*****}V^{*****}EL^{*****}KE^{*****}IV^{*****}KE-----FM 1119
gi | 212645813 | ref | NP_498516.2 | -----TPVGSAAQGSASST^{*****}PTAAAP^{*****}TN^{*****}NG^{*****}AV^{*****}AR^{*****}AS^{*****}V^{*****}PK^{*****}NS^{*****}LPAN^{*****}RTG-----NVL^{*****}SY^{*****}IN^{*****}VD^{*****}IL^{*****}VA^{*****}M^{*****}AK^{*****}GD^{*****}AE^{*****}IA^{*****}PA^{*****}EA^{*****}VD^{*****}K^{*****}IS^{*****}FL^{*****}FN^{*****}LS^{*****}Q^{*****}SN^{*****}LT^{*****}L^{*****}KK^{*****}DE^{*****}IV^{*****}EM^{*****}IS^{*****}DH^{*****}GD^{*****}AF^{*****}T 1196
gi | 42561615 | ref | NP_171710.3 | -----NEVPSVPSNEAK^{*****}PL^{*****}LS-----L^{*****}ST^{*****}VS^{*****}V^{*****}DV^{*****}SV^{*****}PN^{*****}KG^{*****}IP^{*****}TSS^{*****}-----ST^{*****}GF^{*****}VR^{*****}PAR^{*****}AT^{*****}-----R^{*****}FG^{*****}SAL^{*****}NI^{*****}ET^{*****}VAA^{*****}AER^{*****}RE^{*****}NA^{*****}E^{*****}APP^{*****}SD^{*****}VD^{*****}K^{*****}VS^{*****}FI^{*****}IN^{*****}IST^{*****}NI^{*****}ES^{*****}KG^{*****}EF^{*****}AIL^{*****}PS^{*****}-----YV 981
gi | 115483368 | ref | NP_001065354.1 | -----RH^{*****}GF^{*****}L^{*****}GR^{*****}SK^{*****}GS^{*****}TN^{*****}IT^{*****}IA^{*****}KN^{*****}IL^{*****}SS^{*****}Q^{*****}MP^{*****}LA^{*****}SS^{*****}PD^{*****}L^{*****}AV^{*****}N^{*****}L^{*****}KA^{*****}AT^{*****}PS^{*****}Q^{*****}AS^{*****}PH^{*****}ST^{*****}VS^{*****}AL^{*****}PL^{*****}QT^{*****}GL^{*****}RS^{*****}SS^{*****}AP^{*****}GI^{*****}R^{*****}QP^{*****}FT^{*****}-----G^{*****}FG^{*****}AAL^{*****}NI^{*****}ET^{*****}VAA^{*****}AER^{*****}RD^{*****}TP^{*****}E^{*****}APP^{*****}SE^{*****}VD^{*****}K^{*****}IF^{*****}FM^{*****}IN^{*****}IST^{*****}NI^{*****}ES^{*****}MA^{*****}KA^{*****}RE^{*****}FN^{*****}VL^{*****}Q^{*****}CE^{*****}-----YV 305
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 161076460 | ref | NP_001097242.1 | -----PWLAAQYL^{*****}V^{*****}L^{*****}K^{*****}RA^{*****}S^{*****}ME^{*****}FN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}AL^{*****}K^{*****}GE^{*****}IN^{*****}RF^{*****}V^{*****}KE^{*****}TL^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}RS^{*****}DK-----G^{*****}VI^{*****}NF^{*****}SD^{*****}RS^{*****}LL^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}GR^{*****}NP^{*****}IL^{*****}Q^{*****}LD^{*****}DL^{*****}DK^{*****}S^{*****}LL^{*****}EA^{*****}Y^{*****}HK^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}IL^{*****}ES^{*****}AK^{*****}ER^{*****}IF^{*****}RS^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1333
gi | 158299778 | ref | XP_319808.4 | -----TWLAAQYL^{*****}V^{*****}L^{*****}K^{*****}RA^{*****}S^{*****}IE^{*****}V^{*****}N^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}AL^{*****}K^{*****}PI^{*****}EN^{*****}RL^{*****}V^{*****}KE^{*****}TF^{*****}RN^{*****}IK^{*****}V^{*****}LL^{*****}RS^{*****}DK-----G^{*****}IAN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}GR^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}CA^{*****}KS^{*****}V^{*****}K^{*****}VP^{*****}KN^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1086
gi | 94383743 | ref | XP_899766.2 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1273
gi | 109507689 | ref | XP_001060702.1 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1274
gi | 42716275 | ref | NP_057368.3 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1274
gi | 114662880 | ref | XP_511007.2 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1274
gi | 119910031 | ref | XP_613555.3 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1274
gi | 118096204 | ref | XP_414043.2 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1274
gi | 121582322 | ref | NP_001073420.1 | -----PWV^{*****}SQ^{*****}YL^{*****}V^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}SL^{*****}Y^{*****}N^{*****}FD^{*****}L^{*****}L^{*****}KN^{*****}PE^{*****}FN^{*****}K^{*****}ML^{*****}NE^{*****}TY^{*****}RI^{*****}K^{*****}V^{*****}LL^{*****}TS^{*****}DK-----AA^{*****}AN^{*****}FS^{*****}DR^{*****}SL^{*****}L^{*****}K^{*****}N^{*****}L^{*****}GH^{*****}WL^{*****}GM^{*****}TL^{*****}AK^{*****}NP^{*****}IL^{*****}HD^{*****}LV^{*****}K^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1266
gi | 212645813 | ref | NP_498516.2 | -----LWLA^{*****}Q^{*****}Y^{*****}IV^{*****}M^{*****}K^{*****}RV^{*****}S^{*****}IE^{*****}Q^{*****}N^{*****}F^{*****}Q^{*****}PL^{*****}Y^{*****}N^{*****}Q^{*****}F^{*****}NA^{*****}LE^{*****}ND^{*****}CL^{*****}CK^{*****}RE^{*****}TF^{*****}RN^{*****}IR^{*****}IL^{*****}RT^{*****}DK^{*****}RT^{*****}LV^{*****}AS^{*****}Y^{*****}SD^{*****}R^{*****}Q^{*****}LL^{*****}K^{*****}NG^{*****}SW^{*****}LG^{*****}AI^{*****}T^{*****}ARN^{*****}K^{*****}PI^{*****}LL^{*****}ND^{*****}L^{*****}DK^{*****}S^{*****}LL^{*****}EA^{*****}V^{*****}Y^{*****}NG^{*****}GO^{*****}ELL^{*****}V^{*****}VP^{*****}VF^{*****}V^{*****}AK^{*****}V^{*****}LES^{*****}IR^{*****}SL^{*****}VF^{*****}RP^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}VA^{*****}EL^{*****}HQ^{*****}EP^{*****}D 1346
gi | 42561615 | ref | NP_171710.3 | -----PWFA^{*****}Q^{*****}Y^{*****}VM^{*****}M^{*****}K^{*****}RA^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}DL^{*****}YL^{*****}KL^{*****}FD^{*****}VD^{*****}SK^{*****}LL^{*****}KE^{*****}IL^{*****}Q^{*****}EN^{*****}CK^{*****}VL^{*****}GS^{*****}EL^{*****}IK-----SS^{*****}EE^{*****}RS^{*****}LL^{*****}K^{*****}N^{*****}L^{*****}GS^{*****}WL^{*****}GR^{*****}IT^{*****}GR^{*****}NY^{*****}VL^{*****}RA^{*****}RE^{*****}ID^{*****}PK^{*****}SL^{*****}IV^{*****}EA^{*****}Y^{*****}KE^{*****}RG-----L^{*****}M^{*****}IA^{*****}IV^{*****}PF^{*****}SK^{*****}VL^{*****}EP^{*****}CQ^{*****}SI^{*****}AV^{*****}Q^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}GL^{*****}LA^{*****}EL^{*****}IV^{*****}SM^{*****}PN 1126
gi | 115483368 | ref | NP_001065354.1 | -----PWFA^{*****}Q^{*****}Y^{*****}VM^{*****}M^{*****}K^{*****}RA^{*****}S^{*****}IE^{*****}PN^{*****}F^{*****}H^{*****}DL^{*****}YL^{*****}KL^{*****}FD^{*****}VD^{*****}SK^{*****}LL^{*****}KE^{*****}IL^{*****}Q^{*****}EN^{*****}CK^{*****}VL^{*****}GS^{*****}DL^{*****}IK-----SS^{*****}EE^{*****}RS^{*****}LL^{*****}K^{*****}N^{*****}L^{*****}GS^{*****}WL^{*****}GR^{*****}IT^{*****}GR^{*****}NY^{*****}VL^{*****}RA^{*****}RE^{*****}ID^{*****}PK^{*****}SL^{*****}IV^{*****}EA^{*****}Y^{*****}KE^{*****}RG-----L^{*****}M^{*****}IA^{*****}IV^{*****}PF^{*****}SK^{*****}VL^{*****}EP^{*****}CQ^{*****}SI^{*****}AV^{*****}Q^{*****}PN^{*****}WT^{*****}IM^{*****}VL^{*****}GL^{*****}LA^{*****}EL^{*****}IV^{*****}SM^{*****}PN 450
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi | 161076460 | ref | NP_001097242.1 | -----L^{*****}KL^{*****}N^{*****}L^{*****}K^{*****}FE^{*****}IV^{*****}EL^{*****}VC^{*****}KN^{*****}L^{*****}N^{*****}LE^{*****}L^{*****}AK^{*****}L^{*****}QR^{*****}VI^{*****}YL^{*****}DK^{*****}PN^{*****}RI^{*****}EE^{*****}Q^{*****}MS^{*****}Q^{*****}PK^{*****}PK^{*****}Q^{*****}LE^{*****}P^{*****}V^{*****}AS^{*****}AP^{*****}AL^{*****}PRE^{*****}Q^{*****}Q^{*****}SP^{*****}AP<

gi | 161076460 | ref | NP_001097242.1 | ELVCAFIQKSAEKAAAEIDRRRLSDFEPRKRIAR...EGNRFVDAQILTYQERLPEAVRIKVGAAATLAVVSEFARISIPGFOQMSDR-DIALFVFPKFDLELQPNVFANDDSMVV 1723
gi | 158299778 | ref | XP_319808.4 | ELVAFIQKTAIEKVAIEMDKILAEFDQLRKHAR...EGRRYWDAAVLSYHAERMPERIKLVGGVSPSLAVYEEFARNIPGFLPITER-DAAQFAPKMAEMLFFVATPELIGAIY 1431
gi | 94383743 | ref | XP_899766.2 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1611
gi | 109507689 | ref | XP_001060702.1 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1612
gi | 42716275 | ref | NP_057368.3 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1612
gi | 114662880 | ref | XP_511007.2 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1612
gi | 119910031 | ref | XP_613555.3 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1612
gi | 118096204 | ref | XP_414043.2 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1612
gi | 121582322 | ref | NP_001073420.1 | ELACCFIQKTAIEKAGPEMDKRLATEFELRKHAR...EGRRYCDPVVLTQAEARMPEQIRLKVGGVDPKOLAVYEEFARNVPGFLPTNDLSQPTGFLAQPMMK---QAWATDDVAQIY 1611
gi | 212645813 | ref | NP_498516.2 | ELSTNFIIVKTAACEKATQDIKRLKLEADYQKRIAAK...AMSPYRDEIATAAHTAH-LPKAATVYVPTDKALMGIYDQSSRICGFKANSGE-DPVSAAEPGGSAIPVQVQSKMELVVC 1720
gi | 42561615 | ref | NP_171710.3 | DLGCAATECAATEKATQITIDADTAQQLLRKRRKRDGAGSSFFDPNLLSONSVSEFIPESLRPKP-GHLSLS...QRVYEDFVQHPWQKSTQTSHGLSAASSSSGDVALGSGYGPVSGKVASEFLSNAGNARMMDVSRPDISVDGFE-SSPV 1544
gi | 115483368 | ref | NP_001065354.1 | DLGICALITVATRKAEMIDGELKQPFPSQLRQKELLGSAAYDAPFYTQGLKRVDPALRPPKPGHLSAAARRVYEDFIT-VVHSS...SSQAGG-SATATAMAVAPSNSSVPRVPSNSALTSSSSFSHFFASASQTELVEESDRNAHL 870
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950



gi | 161076460 | ref | NP_001097242.1 | GELASKMEAFMNTAIGVPTLQIQASKMHMLLNALIAITRR...LRQESAFNLLTRAVEGLTEGLVNM---HENMSEQMKMYQNIHLRITGLLNNS 1811
gi | 158299778 | ref | XP_319808.4 | DELASKMDFLKTIRLVPIQLQHNMEQLLECLLHAHR...SLDNLGCTLLNKAVEGLEGLINLI---PQIEHVKLYRDIHLRVMRLMOH 1519
gi | 94383743 | ref | XP_899766.2 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1697
gi | 109507689 | ref | XP_001060702.1 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1698
gi | 42716275 | ref | NP_057368.3 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1698
gi | 114662880 | ref | XP_511007.2 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1698
gi | 119910031 | ref | XP_613555.3 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1698
gi | 118096204 | ref | XP_414043.2 | DKCITELQHLHAIPPLAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADADLLRYRECHLLVLKALODG 1698
gi | 121582322 | ref | NP_001073420.1 | EKCSIDLEQHLHAIPPALAMNPPQAALRLLLEVVLSRN...SRDAIAALGLLQKAVEGLLDATS---GADPELLLSYRECHLLVLKALODG 1697
gi | 212645813 | ref | NP_498516.2 | QQQLVIKREVDQITQAQPHLSNSAFQIVCLMRELQNVIS...TKDANHLMLLVKRSIEHLLHAYRLEG---PPKNLLDVEWARRLDFIIGLMLLQNY 1815
gi | 42561615 | ref | NP_171710.3 | SLLSNCVDPAGDSSSLQFVKSPLISELNLSAESSDAAKETGSLQTLISAAIMERLGASN---ITQPSLTRDALDKCQIVTKMELVANNAGDIEICAVISEVPEIILRCISRDEAAFAVAQKAFKALYENASNLVSVANLAILVA 1690
gi | 115483368 | ref | NP_001065354.1 | SLLSKIG-ASDITSTQVIGITNVAISVFPFPMVNDLPVGEPTITTKDKLVTSAPLSPITAVDRMGSVFVPELNL...SDALEMIVQVQSKLDLTLAKGDDBIEIVIAEVVDILLRCVSRDEAALATAQVRFSLVDNANSSVWTLALVA 1019
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100



gi | 161076460 | ref | NP_001097242.1 | --FGAPNTERAVTKCFDFIDREVEVRYNVEAARALITSHFVNLNCPDGMRLMDCNGNMYVAISFGALLERLIMDDRIVNIVDNEFMAVVELLGLRTOHR-HRYFPCIVNAIDVLLGCFNFS--SDYSPFNENDRVLGSGASHYIHSQMHHV 1958
gi | 158299778 | ref | XP_319808.4 | RLFQPMWTKAITRYMLRECEELRYNVEAVDILLITSNFVNMCPDMMVLVLMDDNGNMYVAVFAMQLLQFPFIDRHNSAITENDLACHIEMLRLTAH--FRAPBEGTLHIEMLRHDHPN---FLMDRAIVGPTSYIHAGVAJA 1661
gi | 94383743 | ref | XP_899766.2 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHITADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1838
gi | 109507689 | ref | XP_001060702.1 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHITADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1839
gi | 42716275 | ref | NP_057368.3 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHVTEADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1839
gi | 114662880 | ref | XP_511007.2 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHVTEADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1839
gi | 119910031 | ref | XP_613555.3 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHVTEADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1839
gi | 118096204 | ref | XP_414043.2 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHVTEADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1839
gi | 121582322 | ref | NP_001073420.1 | RAYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMCOQYDLHLAQSMEGLNMYAVAFAMQLVKILLVDRSVAHITADLFHTIETLMRINAHSRGNAPEGLPOLMEVVRSNY-----EAMIDRAHGGPNFMHSGISQA 1838
gi | 212645813 | ref | NP_498516.2 | --FPLVELSRRIITAIMGIRSDYKVMMEGIEILFQNLLOQVLDNDQHLASMDNGNMEAVLFAQKFRVRSICGDMRIFQFLKRFPLICBQLTKLHQLSATRTBGMNANMNGAGNAHHHAGLQPPVALPMEAAPMPQASADAMA 1963
gi | 42561615 | ref | NP_171710.3 | IRDVCKRVRKELTSWVIYSEEDRKNKDIITIGLIRELLSAGVNVHMAKHLDDGRNKLAIDFAISLLOSLVTEBSVITELHSLVDALAKLASKSSSESLLQQLIDITRNVTNTAGLSDS--GNDNDRQKDKVACN--TNTNEES 1838
gi | 115483368 | ref | NP_001065354.1 | IRDVCRLVVKELTSWVIYSEEDRKNKDIITIGLIRELLSAGVNVHMAKHLDDGRNKLAIDFAISLLOSLVTEBSVITELHSLVDALAKLASKSSSESLLQQLIDITRNVTNTAGLSDS--GNDNDRQKDKVACN--TNTNEES 1838
.....2110.....2120.....2130.....2140.....2150.....2160.....2170.....2180.....2190.....2200.....2210.....2220.....2230.....2240.....2250



gi | 161076460 | ref | NP_001097242.1 | R-SCDIDDPGLQKTEFLLLKDWVALYQQNQSTRDARNFGAFVQKMNTYGLLKKDDLLTRFFRQAHTICIDVYR-MFAEPLS---PINQAKNIFQWIDAFVHLIAMLVHSGEAGNPTKINLLNKVLGIVGLTLKDHMRGV 2102
gi | 158299778 | ref | XP_319808.4 | RVSSDIDDPGLQKTEFLLLKDWVALYQQNQSTRDARNFGAFVQKMNTYGLLKKDDLLTRFFRQAHTICIDVYR-MFAEPLS---PINQAKNIFQWIDAFVHLIAMLVHSGEAGNPTKINLLNKVLGIVGLTLKDHMRGV 1800
gi | 94383743 | ref | XP_899766.2 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1983
gi | 109507689 | ref | XP_001060702.1 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1984
gi | 42716275 | ref | NP_057368.3 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1984
gi | 114662880 | ref | XP_511007.2 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1984
gi | 119910031 | ref | XP_613555.3 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1984
gi | 118096204 | ref | XP_414043.2 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1984
gi | 121582322 | ref | NP_001073420.1 | S---EYDDPPGLRKAAYLLREWVNLVYHSA--AGRDS TKAFSAFVGMHQGILKDDLLTRFFRCLTEMCVETSYR-AQAEQOHNPAANPMIRAKCYHNLDAFVRLIALLVKHSGEATNVTKINLLNKVLGIVGVLLQDHDVROSE 1982
gi | 212645813 | ref | NP_498516.2 | QRG---YDDQEMTAKVBIIMREWIGLCYSP--GQRSPOQESLAQMIQLMHEHGVLA--DDKITQFFRCLVENCVETSYR-VMKSEQLANGLPTLILRHRCYVYTLDAFVKLMAIMLRHS--DNGQKQNKINLLKLLNIVGVLLHMDHEVRKQD 2107
gi | 42561615 | ref | NP_171710.3 | SLDVYESDPAGFQNRVSLFKFNWYQICELPQ---ANETACSQVVLHLHGTLGLKDDLLTESFFRILLLEVAHSSVSEVAVPAGGISQPPSPFLIIDMYAKLVFSILKYFFEQESE--SRLFLISEIMADTVRFQKDAEDKKS 1981
gi | 115483368 | ref | NP_001065354.1 | ANDVAFTDAVGFQEKVAVSEWCNLCIDHPT---MGDSAYTHYIVKLODGLLKGDDLLDRFYHILLTELAHSSVSEVAVPAGGISQPPSPFLIIDMYAKLVFSILKYFFEQESE--SRLFLISEIMADTVRFQKDAEDKKS 1305
.....2260.....2270.....2280.....2290.....2300.....2310.....2320.....2330.....2340.....2350.....2360.....2370.....2380.....2390.....2400



gi | 161076460 | ref | NP_001097242.1 | FQOVGYHRFFMMLFPELCT--TADVILESLMHSIVSAFAYTVHLLNPSVAPGFCFAWLELISHRVFLGRILVQI-----PGQKGWPLYAQLLQDLFKYLAPFLRNTELKQVPLLYKGLRVLVLLVLLHDFPEFLCDYHFGCDIIPPNCV 2244
gi | 158299778 | ref | XP_319808.4 | FQOVGYHRIFAMLFLELT--TDPILLENISISVITAFCHTFPHILRPSAAGPGFCYSWLELIAHRVFIGRVLQAI-----POQKGWHMYSQLLIDLFKYLAPFLRNAELAKPVOHLKGTLRVLLVLLHDFPEFLCDYHFAFCVDVIPNCCI 1942
gi | 94383743 | ref | XP_899766.2 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2125
gi | 109507689 | ref | XP_001060702.1 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2126
gi | 42716275 | ref | NP_057368.3 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2126
gi | 114662880 | ref | XP_511007.2 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2126
gi | 119910031 | ref | XP_613555.3 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2126
gi | 118096204 | ref | XP_414043.2 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2126
gi | 121582322 | ref | NP_001073420.1 | FOQLPYHRIFIMLLLELN--APEHVLETINFOTLAFACNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT-----POQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGLRVLVLLVLLHDFPEFLCDYHFGCDVIPNCCI 2124
gi | 212645813 | ref | NP_498516.2 | FNAMPYHRILISLNFNEITGDDPKLLEPFAWSILFAFGQTFALQPRRMPGFAFAWLDIVGHRNVIGRLLANTGIAETVDAVKTAATYVQLIISHLKFLAPFLRNITQPKSIAILYKGLRVLVLLVLLHDFPEFLCEFHVIICDIIPPNCV 2257
gi | 42561615 | ref | NP_171710.3 | LNSKPYFRILFNWLLDLC--SLDPGDDGANFQVLLAFANAFHQLPKIPAFSFAWLELISHRSFMPKLLLVN-----GQKGWVYVQRLLVDLFLKFMPEYVLRNABELGQPIHLLYKGLRVLVLLVLLHDFPEFLCDYHFTFCVDVIPSSCI 2122
gi | 115483368 | ref | NP_001065354.1 | FNRPYFRILFNWLLDLC--TSDLHSDSANFQVLLAFANAFHVLQPLRVPAWFAWLELISHRSFMPKLLLCN-----AQKGWPFQRLVLDLFLKFMPEYVLRNABELGQPIHLLYKGLRVLVLLVLLHDFPEFLCDYHFSFCVDVIPSSCI 1446
.....2410.....2420.....2430.....2440.....2450.....2460.....2470.....2480.....2490.....2500.....2510.....2520.....2530.....2540.....2550



gi | 161076460 | ref | NP_001097242.1 | QMRNLIILSAFPRNMLPDPFPTNLK--VDMLSDSSNAPKVLSSVIMNIQPANFKKDLDSYLKA-RAPVIFLSELGRHLOVT-----SEPGTRYNMLMNAVLVMYVGTQAIALIRNKNFVPTNS-----NIAHSAHMDIFONLAVDLDI 2379
gi | 158299778 | ref | XP_319808.4 | QMRNLIILSPYPRNMLPDPFPTNLK--VDMLNDIGSSPRISINASSIQPVSFKKDLDSYLKA-RAPVIFLSELGRHLOVT-----NEVGSRYNMLMNAVLVYVGTQAIHNRKNGLPTMS-----TIHSAHMDIFONLAVDLDI 2077
gi | 94383743 | ref | XP_899766.2 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2259
gi | 109507689 | ref | XP_001060702.1 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2260
gi | 42716275 | ref | NP_057368.3 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2260
gi | 114662880 | ref | XP_511007.2 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2260
gi | 119910031 | ref | XP_613555.3 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2260
gi | 118096204 | ref | XP_414043.2 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2260
gi | 121582322 | ref | NP_001073420.1 | QLRNLIILSAFPRNMLPDPFPTNLK--VDMLSEINIAPRILNFTG--VMPPQFKKDLDSYLK--RSPVIFLSDLRNLOVS-----NEPGNRYNLQINLALVYVGTQAIHNRKNGSTPMS-----TIHSAHMDIFONLAVDLDI 2258
gi | 212645813 | ref | NP_498516.2 | QMRNLIILSAYPRQMRPDPFPTNLK--VDIPEMAVEPKSNLNMAT--IIPDNIRIPLDEVLAN--RISVDLFLNPLPILLOIQ-----NQAGTKYNTVMNALVLYVGTQAIHNRKNGSTPMS-----NIAHTSYMDIFONLAVDLDI 2392
gi | 42561615 | ref | NP_171710.3 | QMRNLIILSSFRNMLPDPFPTNLK--IDLPLSIVAPCMLSEVDAALKAKOMKNDVDEYLRQNS--FLSELKTLKLLSSSEASSAGTSVPLINSLVLYVGTQAIHNRKNGSTPMS-----VVALQMKYLSMELDI 2257
gi | 115483368 | ref | NP_001065354.1 | QMRNLIILSAFPRNMLPDPFPTNLK--IDLLEAISIPPRKIDVDGALKKQKMTQVDEYLRK--RDPGFLDLKQKLLLPQNEANLAGTRYNVPLVNSLVLYVGTQAIHNRKNGSTPMS-----VVALQMKYLSMELDI 1593
.....2560.....2570.....2580.....2590.....2600.....2610.....2620.....2630.....2640.....2650.....2660.....2670.....2680.....2690.....2700



gi | 161076460 | ref | NP_001097242.1 | EGRYLFLNAIANQLRYPNSTHYFSCAVLHLFAEANSBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPI--YKFWDDDFVH-----CAPETIKLFSVARSGLAKS 2483
gi | 158299778 | ref | XP_319808.4 | EGRYLFLNAIANQLRYPNSTHYFSCCILYLFABEANSBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPI--YKFWDDDFVH-----CAPIERLFSVARSQMVTS 2181
gi | 94383743 | ref | XP_899766.2 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2363
gi | 109507689 | ref | XP_001060702.1 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2364
gi | 42716275 | ref | NP_057368.3 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2364
gi | 114662880 | ref | XP_511007.2 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2364
gi | 119910031 | ref | XP_613555.3 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2364
gi | 118096204 | ref | XP_414043.2 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2364
gi | 121582322 | ref | NP_001073420.1 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPA--FKFWNHEFVH-----CAPETIKLFSVAOCCMGOK 2362
gi | 212645813 | ref | NP_498516.2 | EGRYLFLNGIANQLRYPNSTHYFSCVFLYLFKFNITNDIQEQITRILFERLIVNRPHPWGLLIIFIELIKNPI--YKFWDDDFVH-----CAPETIKLFSVARSGLAKS 2496
gi | 42561615 | ref | NP_171710.3 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPI--YKFWDDDFVH-----CAPETIKLFSVARSGLAKS 2358
gi | 115483368 | ref | NP_001065354.1 | EGRYLFLNAIANQLRYPNSTHYFSCMLYLFAEANTEBAIQEQITRVLLERLIVNRPHPWGLLIIFIELIKNPI--YKFWDDDFVH-----CAPETIKLFSVARSGLAKS 1743
.....2710.....2720.....2730.....2740.....2750.....2760.....2770.....2780.....2790.....2800.....2810.....2820.....2830.....2840.....2850



gi | 161076460 | ref | NP_001097242.1 | NVTQQLNMPVVDGEGQEVANIN----- 2505
gi | 158299778 | ref | XP_319808.4 | KBOOQIQN--VEPDITECS----- 2198
gi | 94383743 | ref | XP_899766.2 | QAQQVMEGTGAS----- 2375
gi | 109507689 | ref | XP_001060702.1 | QAQQVMEGTGAS----- 2376
gi | 42716275 | ref | NP_057368.3 | QAQQVMEGTGAS----- 2376
gi | 114662880 | ref | XP_511007.2 | QAQQVMEGTGAS----- 2376
gi | 119910031 | ref | XP_613555.3 | QAQQVMEGTGAS----- 2376
gi | 118096204 | ref | XP_414043.2 | QAQQVMEGTGAS----- 2376
gi | 121582322 | ref | NP_001073420.1 | QAQQVMEGTGAS----- 2374
gi | 212645813 | ref | NP_498516.2 | GSPQQAQPDGAPGPGNNITGAANQOONPNTN 2527
gi | 42561615 | ref | NP_171710.3 | GLKPVDGEMVSG---GWVDDNSH----- 2378
gi | 115483368 | ref | NP_001065354.1 | GAAALCDGAVAWRRRRGGVEAAAWRGG--- 1770
.....2860.....2870.....2880

