

gi | 145616144 | ref | XP_360994.2 | ...MSLLPFAEVTAELGQLEALQPPDAVAVRQAED...HLQNNWVTRPEVLLMGVELIQAQANTTTIRSSAVIFRRIAGKTRKND...KGESVDVYISLAKDAQEIVRQKLLQLASESDRGV 117
gi | 32421379 | ref | XP_331133.1 | ...MSVLPADVTAELSQLLQALQADANNIRSAE...HLQNNWVSSR-PGLLLMGLAQIAGSS-DASVRSFAAVIFRRIILKTRKAP...TSEAATDMFLSLIDNHEAVAVRNKILAEILAEEDRVN 118
gi | 19076002 | ref | NP_588502.1 | ...MSGSFPPEVLVSLNLLVQGLSPPDNTVRNDAEK...SLSSDWNISQR-ADLLNGLLAILAYQSS-DPAVRSFCLVLCRRIISFRITPGD...SELVFSVSISSNESKQSLQSLACFVKEVPTV 115
gi | 50305745 | ref | XP_452833.1 | ...MSVLPDEVNSTLVKLLQVGFASPDNAIRSAE...ALNNNWTPEHIEVLLMFLAQSAISYSD-DLTTAGLSAVLFRKALRAPPSS...KTIITAKNITHIKSKALKQIRDTLLKGFISORPNVI 118
gi | 45200748 | ref | NP_986318.1 | ...MSALSBDVNNLTINLVHGFASPDANNIRAAAE...TLNNQWITEENIHLVLLVFLAQSAFSS-DLTLAGLSAVLFRKALRAPPSS...KAVIITAKNITHIKSKALKQIRDTLLKGFVVSERSGI 118
gi | 6323968 | ref | NP_014039.1 | ...MSALPEEVNRTLQVQAFASPDNQIRSAEK...ALSEEWITENNIEYLTLFLAQSAFSS-QDITVAALSAVLFRKALRAPPSS...KLMIMSKNITHIRKVLQAIRSLLKGLSERADSI 118
gi | 17737759 | ref | NP_524226.1 | ...MAADQAHPQQLLASLLTDNDVRQA...EEAYNNLSR...ELKVTHLGTQNGQQGSEEARQMAAVLLRRL...EEFFDFYKGLIPARSNQKQLQLLVAQOVTFOL 102
gi | 118780654 | ref | XP_310308.5 | ...MAALDQANFQQMLGSLLDNDVTRKA...EEVYNALPC...EIKVPHLLGTQVQMAEDARMLSAVLLRRL...EEFFHYEYLPFRHARQLQKLLILFLQNESGM 103
gi | 24797086 | ref | NP_002262.3 | ...MPEDQVQKLEAIENTISAMAAAAAQQQFYLLGNNLSPDNNVVRKQA...EETVENIPG...OSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTAIKSELLMIIOMEQSSM 123
gi | 73989213 | ref | XP_542647.2 | ...MAAAAAQQQFYLLGNNLSPDNNVVRKQA...EETVENIPG...OSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTAIKSELLMIIOMEQSSM 105
gi | 29789199 | ref | NP_076068.1 | ...MAAAAAQQQFYLLGNNLSPDNNVVRKQA...EETVENIPG...RSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTAIKSELLMIIOMEQSSM 105
gi | 109502015 | ref | XP_224534.4 | ...MAAAAAQQQFYLLGNNLSPDNNVVRKQA...EETVENIPG...RSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTAIKSELLMIIOMEQSSM 105
gi | 114650444 | ref | NP_001140931.1 | ...VMAMRAGVQVYVLLSSGNLLYLIQSKNVNEIVSHDETVENIPG...OSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTAIKSELLMIIOMEQSSM 111
gi | 118084696 | ref | XP_416978.2 | ...MDPESASLE...CETVENIPG...OSKITFLLQAIRNTAAEEARQMAAVLLRRL...SAFDEVYVLPALPSDVYTSLSKTLGILLIQLAQSSM 85
gi | 125802691 | ref | XP_697938.2 | ...MAEQQQFYLLSNNLSPDNTVVRKQA...EEAYDTPG...QTKITFLLQAIRDASAAEVKQMAAVLLRRL...SFEVYVPLNLTVDITAIKTELLLAGIRSEASTNI 101
gi | 17506191 | ref | NP_490715.1 | ...MDVNPQTELITKLQADDIRKQA...EEVYKIEG...FKVAALFEAYTHHTNNSDARSVTLVFLRRLVA...RDNDALWETVRLNSTRKSLKSMLYCIQHEAKSI 100
gi | 15241189 | ref | NP_197483.1 | ...MAEQAQOLQALAMVLSGSAFPELLISHLSSNQRSSA...ESFLNLAQSPDLSLKLALHLQSPHPEG-RAMAAVLLRRL...RDDAYLWVRLNLSSTKSLKSMLYCIQHEAKSI 120
gi | 115472957 | ref | NP_001060077.1 | ...MAAGD...DQAAAAALLGGDPAAPDALLSLTMS...AAAFHRLRSHPEPILALRLASSLSPAPADLRAMAAVLLRRL...SSAAAAPVWPHLSPAGAAALKQHLALSDPPKPT 127
gi | 124506397 | ref | XP_001351796.1 | ...MDKIVVEVIEGLS...ESHIRNECEN...LNYKKNDLNNVLSLILKLLKTRKDSQVRLQCALLRNTRFRVYIKTHVDVVEKEKENEISIGNAEENVWVLLPDNLKNIKSLISNIGTEEDKMW 122



gi | 145616144 | ref | XP_360994.2 | ...R NKISDAVAEVARQCSDNV--SWPDLAALFQLSMA-PDAGKREISFRVFATPGIIEKQHEESVAQAFSAFKDDTVA---VRLAAMEFAAFAFRGMT-KKNQKMFGLPEVNLNLPKIKESQES---DLSKALTALIDLAE 253
gi | 32421379 | ref | XP_331133.1 | ...R NKIGDAVAEVARQYVDNQ--NWPELLQLFLFNLSQA-PDAGKRETAFRIFHATPSIIEKHQDAMAFKAFKATDESVA---VRLAAMEFAAFAFRGLS-KKNQKMFGLPEVNLNLPKIKESQES---DLSQALMALIDLAE 254
gi | 19076002 | ref | NP_588502.1 | ...R NKLCDIAELIARSIVYDQ--EWPELLNINFINAVNS-PDESFRSFRITISLPRLLSSG-DSAVTPLFTGLADPSIR---VRIISAARAYSAVILSEK--STRDQVYIPLLSLMNLPLPQQDRDS---DNLADCLMAIETAE 250
gi | 50305745 | ref | XP_452833.1 | ...R HKLSDAIAECALEELP---EWPELLQLFEALKNK-TDNPRESSFRISFSTPHMLINSIDINALPIFESGTPDSDE---VKIAAVTAFVGYKQFLP-KNWKAGLVLLPILLSLPLKFLDSDKD---EALAAVFEELIELVE 251
gi | 45200748 | ref | NP_986318.1 | ...R HKLSDAIAECAVDLLP---AWPELLRLFEALKNK--GNPNRESSFRISFSTPHMLINAITNAPLPIFAGATDEDD---VKIAAVTAFVGYKQFLP-KMHWAKLVLLPILLSLPLKFLDSDKD---DALAAVFEELIELVE 251
gi | 6323968 | ref | NP_014039.1 | ...R HKLSDAIAECAVDLLP---AWPELLQALLESLSK--GNPNRESSFRILLTVFYLLTAVDINSILRFQSGTDSADN---VKIAAVTAFVGYKQFLP-KSEWSKLVLLPILLSLPLRFLDSDKD---DALAVFEELIELVE 251
gi | 17737759 | ref | NP_524226.1 | ...R RKKICEVVAEVARNLIDEDGNNQWPEILKFLFDSVNS--PTPQLQESALRIFSSVPSIFGNQEAQHLIDLIKQMLAKSMDAG--SDPEVRVQAVRAVGAFLYLDHDKENETAIEKHFADMLPRMIHTGETIEA---QDDQSLKLLIEMTE 245
gi | 118780654 | ref | XP_310308.5 | ...R RKKICEVVAEVARCLIDDDGNNWPEFLQFLFHCNS--ANVQLQEAALRIFASVPGIFGNQQAHLPLIKQMLKYLEPT--SDQEVRFQAVRAVGAFLYLDHDKEDD--VQRFADLLPQITIMTAEISIEL---GDPQNLMLQDLDMAE 244
gi | 24797086 | ref | NP_002262.3 | ...R KKKVCDIAAELARNLIDEDGNNQWPEGLKFLFDSVSS--QNVGLREAAALHIFWNPFGIFGNQOQHYLDVIRKMLVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGFLQAVNDSQYQ---NDD-SVLKSLVEIAD 263
gi | 73989213 | ref | XP_542647.2 | ...R KKKICDIAAELARNLIDEDGNNQWPEGLKFLFDSVSS--QNMGLREAAALHIFWNPFGIFGNQOQHYLDVIRKMLVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGFLQAVNDSQYQ---NDD-SVLKSLVEIAD 245
gi | 29789199 | ref | NP_076068.1 | ...R KKKICDIAAELARNLIDEDGNNQWPEGLKFLFDSVSS--QNMGLREAAALHIFWNPFGIFGNQOQHYLDVIRKMLVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGFLQAVNDSQYQ---NDD-SVLKSLVEIAD 245
gi | 109502015 | ref | XP_224534.4 | ...R KKKICDIAAELARNLIDEDGNNQWPEGLKFLFDSVSS--QNMGLREAAALHIFWNPFGIFGNQOQHYLDVIRKMLVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGFLQAVNDSQYQ---NDD-SVLKSLVEIAD 245
gi | 114650444 | ref | NP_001140931.1 | ...R KKKVCDIAAELARNLIDEDGNNQWPEGLKFLFDSVSS--QNVGLREAAALHIFWNPFGIFGNQOQHYLDVIRKMLVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGFLQAVNDSQYQ---NDD-SVLKSLVEIAD 251
gi | 118084696 | ref | XP_416978.2 | ...R KKKICDIAAELARNLIDEDGNNQWPEILKFLFDSVNS--QNVGLREAAALHIFWNPFGIFGNQOQHYLEVIKRMVQCMQDQ--EHPISIRTLASARATAAFILAN--EHNVALFKHFADLLPGILQAVNDSQYQ---NDD-SVLKSLVEIAD 225
gi | 125802691 | ref | XP_697938.2 | ...R KKKICDIAAELARNLIDDDGNNQWPEILKFLFDSVNS--QDVGLEAAALHIFWNPFGIFGNQOQHYMEVIKRMVQCMQDQ--ENPQIRTLASARAAAFFILSN--EGNTALLKHFSDLLPGILQAVNDSQYQ---GDD-SVLKSLVEIAD 241
gi | 17506191 | ref | NP_490715.1 | ...R KKKIADLISEIASNLIDSDGDMTGGVLELDMDHCLKS--EDLTGNYIALLILRGCPIFGNRLAHLFPLKLVVLEKCMATP--DLQTKAAAVRAVIAFAVDN--DEEKDRVRLMTSLVNVLVQCNTEISDE---DPSDGLGEFAELAS 240
gi | 15241189 | ref | NP_197483.1 | ...R SKKICDIAEELASGILPENG---WPELLPFVQCQVTS--VTPKLQESAFLLIQLSQYVGETLTPHIKELHGVFLQCLSSNSASSDVKIAALNAVISFVQCLANSTRDRFQDVLPAIRLFTLSLNNNE---ATAQEALEELLBLAG 261
gi | 115472957 | ref | NP_001060077.1 | ...R AKKVCDAISELAALLPENNA---WABELLPFLRAASGPEAPNLQESALLIFARLADYIAESLLDHLMTIHNLLASALAH--TSPDRIAALSAAVNLVQCLFPAADKDKQDILLPAMRALTDCLNSQEE---ASAQEALELLBLAG 268
gi | 124506397 | ref | XP_001351796.1 | ...R SNICNNLIDLSKLLLN---WPELLSVTFEFCNS--NVVDLVISGYKLLGILLSIPDLDELDGKQETIISICKMGLNS--NVQVRGECINLISICVDENS--SSLVKSVMHCIPILLIQSLSLMAKNSSDIAVLEKEALVQIGKMDI 265



gi | 145616144 | ref | XP_360994.2 | ...ISPKMFRQQFNHLVQFISVIOQK---ELDDICRONALELMAFADY---APSMCKRDPNYNDMILQCLSLMTDLGEDDDD---AAEWLSEELDQDESQPCGRRAMYGYVQQ---AGRPNFRPD---LQLAASHDA 380
gi | 32421379 | ref | XP_331133.1 | ...ISPKMFKTVFSTLVGFSISVIOQK---ELTDLICRONALELMAFADY---APSMCKKDASYIKDMIQCLSLMTDLGEDDDD---AAEWLSCDDLDTDESNSHVAGEQCLDRLANK---LGGAAILSPFIFGLPSSMMNSPAWRDR 388
gi | 19076002 | ref | NP_588502.1 | ...VFPKLFKPIFESVIAFGLGIKIK---ELDNSARQAALLVCFSEG---APAMCKRNSDYLDQVLQCLLMTDVLGDDDEEALEQLWELNTDLDQDESANHVAGEQAMDRLERK---LGGKILPFPFTWLPRLIISQKWSER 388
gi | 50305745 | ref | XP_452833.1 | ...LAPKLFKDMFDQIIFADMVIKKN---DLEBSARTALELLVTFSEC---APQMCKSSNYQSVVLDLVMVMTVEVSIIDDQ---AIEWQNSDVEEDNEENTVDMARQALDRVALK---LNGKYLAPLFLQDMVTSSEWRER 385
gi | 45200748 | ref | NP_986318.1 | ...LAPKLFKSMFDQIIFDMVIKKN---DLETSARTALELLVTFSEC---APQMCKSNPNYAQSLLMDLMLMTEVSIIDDQ---AIEWQNSDVEEDDEETAHDNARQALDRVALK---LNGKYLAPLFLQDMVTSSEWRER 385
gi | 6323968 | ref | NP_014039.1 | ...LAPKLFKDMFDQIIFDMVIKKN---DLEBPARTALELLVTFSEN---APQMCKSNQNYQTLVMVFLMTEVSIIDDQ---AAEWLSEDDT--DEEVEVTDHARQALDRVALK---LGGEYLAPLFLQDMVTSSEWRER 384
gi | 17737759 | ref | NP_524226.1 | ...NPKPFLRPQLEFIEVCMKVFSSQ---DFEDSBRHLVLEVMVSLAEN---APSMIRKRADKYIVALIPLILHMTDLDLDDENWST---ADVDDD--DHSDDNVIAESSLDRLACC---LGGKIVLPVLMVNLVGLHADWKKR 376
gi | 118780654 | ref | XP_310308.5 | ...GVPKFRRPQLEFIEPFCMKVFSSTV---DMEDNLRLEALEMMVSLAEN---APAMVRKRAAKVYVALVPLILQMMTDLDEDDWSV---SDKITED--DTSDDNVIAESSALDRACC---LGGKILPILPHVNNIPNMLSPDWKQR 375
gi | 24797086 | ref | NP_002262.3 | ...TVPKYLRPHLEATLQLSLKLCGDT---SLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 393
gi | 73989213 | ref | XP_542647.2 | ...TVPKYLRPHLEATLQLSLKLCGDT---NLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 375
gi | 29789199 | ref | NP_076068.1 | ...TVPKYLRPHLEATLQLSLKLCGDT---NLNNMQRQALAEVIVTLSET---AAAMLRKHTN-LIAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 375
gi | 109502015 | ref | XP_224534.4 | ...TVPKYLRPHLEATLQLSLKLCGDT---NLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 375
gi | 114650444 | ref | NP_001140931.1 | ...TVPKYLRPHLEATLQLSLKLCGDT---SLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 381
gi | 118084696 | ref | XP_416978.2 | ...TVPKYLRPHLEATLQLSLKLCAET---NLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQIPQMLAMMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKLVLPMIKEHIMQMLQNPDWKQR 355
gi | 125802691 | ref | XP_697938.2 | ...TAPKYLRLPNEATLQLSLKLCAET---NLNNMQRQALAEVIVTLSET---AAAMLRKHTN-IVAQSVQMLMVMVDLEEDEDWAN---ADELEDD--DFDSNAVAGESALDRMAGC---LGGKILPILPMIKOHIQMLQNPDWKQR 371
gi | 17506191 | ref | NP_490715.1 | ...SLPKCLNTHSQVLQVLAIAAGNK---EKNEMVRQNAIEVICSMES--APKGLKKYAPGALGPILLETLLSCMTEMDDDVNLNEM---LNEIEEEDYEDIPITAEASADRACC---INGKVMFLVFLPVEKLLTSEDWKMK 372
gi | 15241189 | ref | NP_197483.1 | ...EPRFLRRQLVDIVGSMQLQAEAD---SLEESTRHIAEFLVLAEBARERAPGMRRKLPQFDRLFAVLMKMLLEDIEDPAWIS---ARTEDEAGETSINYSMGCECLDRLAIS---LGGNIVFVYQFSAFLAASEWOKH 395
gi | 115472957 | ref | NP_001060077.1 | ...AEPFLRRQIADVVGMQLQAEAA---QLEDSTRHLAEFVTLAEBARERAPGMRRRPFQVGRIFAVLMKMLLEDIEDPAWIT---ARTEDEAGEGNNYVGAQCECLDRLAIS---LGGNIVFVYASLELLPOLYLAASEWOKH 402
gi | 124506397 | ref | XP_001351796.1 | ...YNAKFFTKHTISLDCILFESICMKDENELNYDFNSLSLSIALVLTIPER---RPKMALSVPHFVDKILHLSMLFMDLNNDCFNEW---MNSIKGKDDSQELMDIGEEELDRVQKAFSELEEEAFIHLFNKVSFELMKNTEWEH 406



Table with 4 columns: gi, ref, XP accession, and protein sequence. The sequence is color-coded by amino acid type. Reference IDs include XP_360994.2, XP_331133.1, NP_588502.1, etc. The sequence ends with a line of dot scores from 460 to 600.



Table with 4 columns: gi, ref, XP accession, and protein sequence. The sequence is color-coded by amino acid type. Reference IDs include XP_360994.2, XP_331133.1, NP_588502.1, etc. The sequence ends with a line of dot scores from 610 to 750.



Table with 4 columns: gi, ref, XP accession, and protein sequence. The sequence is color-coded by amino acid type. Reference IDs include XP_360994.2, XP_331133.1, NP_588502.1, etc. The sequence ends with a line of dot scores from 760 to 900.



gi		145616144		ref		XP_360994.2		DRVNRQAEADKEGVTAEDAEDLAEDILMAIEDDQTLISDMNKAFHVVFKYHGSSFLRHWELRMLPTVESFLKSSERORQWGLCIMDDVLEYCGADSIHYANVIEQPILLDGCGRQNAAIRQAAAYIGVAAH--KCGAAWAQFLGGALEVY	936
gi		32421379		ref		XP_331133.1		DRAAAREEQG---GEDGDESSEMMAIEDDQTLISDMNKAFHVVFKYHGSAFLSAWRLRLLPTVYSSFLSND--RORQWGLCIMDDVLEYCGAESIHYAYIIEPILLDGCQDASPAIRQAAAYIGVAAH--HGGQAWAPLVGQAVEVY	955
gi		19076002		ref		NP_588502.1		SRVQOREEBAK---NGDIDIIEEDDMTILAVENDQNLNINEINKRFVSVLKIKHTAFPCFFWERLLPYMDGFSLGND--TVAKQWALCMMDDLETFEFPDSWYNKDHFLPLVLAEGIQSSPEIRQAAAYIGVAAH--HGGELLYAEICSSALPAL	955
gi		50305745		ref		XP_452833.1		ERTKSRVDDDD---EYNEVDVDDLDLDEDE--LLDEINKSLAAVFKSAGVSYLQQQFTLWPIIHSVLQETE--VFILLFALTAIADMIEYTGDNAPFKHFVQKIKKELTFPEPSIRQGTAYLLGVCAH--YAPNTYSDICLGLSELT	949
gi		45200748		ref		NP_986318.1		ERVRRQRHGED---EYNEVDVEEYEDFTDED--LLDDINKSLAAVQFTNGVYLLTHFQSVWPLIHMVLQDSE--VILTFLFALVAISDMVHYCGDNAMFKDSFAGKMKDLVLFPEPSIRQAAAYIGVCAH--YAPNTYFGEVCMASLDL	949
gi		6323968		ref		NP_014039.1		ERMQRHGGD---EYNEVDDEE--EDFTDED--LLDEINKSLAAVFKTNGHYLKNLGNINWPMINTFLDNE--PILVIFALVVIQDGLIQYGGEQASMKNAFIPKVECLISPDARIRQAAAYIGVCAH--YAPSTYADVCIPFLDL	946
gi		17737759		ref		NP_524226.1		ERADKR--LAARNBEDDDGVEBELAEQDDTVYLLKIVDITHALQFNKAQFLPQVAVPHVFKLLESRVAVDRQWGLCVDFDLEIFCGPACAPYQIFIPALVQVVCDAPEVRQAAAYGCGVLGQ--FAGEQFAHTCAQIIPLL	952
gi		118780654		ref		XP_310308.5		EKEEKR--AQARKBEDYDDGVEBELQAEEDDDADIVYLLKRSIDILHSIFSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	950
gi		24797086		ref		NP_002262.3		KNQELR--QVKRODEDYDEQVEESLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	969
gi		73989213		ref		XP_542647.2		KNQELR--QVKRODEDYDEQVEESLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	951
gi		29789199		ref		NP_076068.1		KNQELR--QVKRODEDYDEQVEESLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	951
gi		109502015		ref		XP_224534.4		KNQELR--QVKRODEDYDEQVEESLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	951
gi		114650444		ref		XP_001140931.1		KNQELR--QVKRODEDYDEQVEESLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	957
gi		118084696		ref		XP_416978.2		KNQELR--QVKRODEDYDEQVEESLQDE-----CPORPWPDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	840
gi		125802691		ref		XP_697938.2		KNQEVV--QAKRODEDYDEQVEETLQDEDDNDVYLLKRVSDILHSIFSSYKKEVLPWFQQLLPLIVNLLICPHRPWDRQWGLCIFDDVLEIHCSPASFKAIEYFLRPMLOVVCNDSPEVRQAAAYGLGVMAH--YGGDNIRFPFCTEALPLL	947
gi		17506191		ref		NP_490715.1		KRMSDR--PVE--DEDDDDAAEAKEELDYFMELRASCGLAISDLTHSLMKFEKGTIFEGMINVFNCAIQLESGQVFERQWGMCLLDDAIEFGVGHMPTRFPKLIFIMYKLLGDEYPEVRQAAAYGFGVMAH--YHGISDMRNEILSCLPEL	942
gi		15241189		ref		NP_197483.1		SRKRER--GERAHAEDFAEGELIKKEENEQEEEIFDQVGEILCTLVKTFKASFLPFDFELSYLTPMWRGDKTAEERRIAICIFDDVABQCREAAFKYVDYLPFLVLEACNDESPEVRQAAAYGLGVMAH--YGGVFKFLIGEALSRL	970
gi		115472957		ref		NP_001060077.1		TKKRER--SERSKAEDFDAEGELIKKEENEQEEEIFDQVGEILCTLVKTFKASFLPFDFELSYLTPMWRGDKTAEERRIAICIFDDVABQCREAAFKYVDYLPFLVLEACNDESPEVRQAAAYGLGVMAH--YGGVFKFLIGEALSRL	976
gi		124506397		ref		XP_001351796.1		DRRVVY--NQKKNNDVDEDELLIIDREELRQNYRNLLDILGLVLIKYPTQFLNCCLELCIGFINNVMNSPNSPSEVVALALVCDLLELFLQEKSVNLWDFFMNPLLLNINHADDKVQAAACYGVIOATK-----IEAFKLYANTAVELV	975



gi		145616144		ref		XP_360994.2		FQAAQVPEP-RSEEN-VYATENACAATAIKILHFNSSSTVONADGIIAQWLGLTLPVTNDEEAPF-----QHPAVIS--QPKDFVIYTAAGLESDDTLTGOTA---IRVVAAMYAVFPTQCKQVCTREYADTRDKRLLSESR	1063
gi		32421379		ref		XP_331133.1		FKATQIPDA-RNEDN-VYATENACAATAIKILHFNSSSTVONADGIIAQWLGLTLPVTNDEEAPF-----QHPAVIS--QPKDFVIYTAAGLESDDTLTGOTA---IRVVAAMYAVFPTQCKQVCTREYADTRDKRLLSESR	1075
gi		19076002		ref		NP_588502.1		FKMLRDPDA-RDEEQ-IYATENICVAICKICRFCSQRVQDLKVVYTWINLTLPTVHDEDDAPYATFLAELMEOVNHVAVAS--QMPTEIILAEFTFASGVLRGRTL---TRLEASKVLARFP---ADQV	1076
gi		50305745		ref		XP_452833.1		QIVQVMPFS-RSEEN-VNNSSENASCAIAKILSSYGSSIPNPEQYTNLWLTFFVVIDECCAAFNVRMLAQLLIDHNSPVIOG---NTAEIVDVIYQALHQSISGGKVA---TAVVEAKLLSIFP---QBEA	1070
gi		45200748		ref		NP_986318.1		FLITITIPDA-RSEEN-ISAENITAAAVAKILHSFGANIPFTFTVYVNWLSFPILQDEAAAFNRMLFGLHLDNSNPTVDEKE--KLGETVYVYVQALHQSISGGKVA---TAVVDSIKLLSAVF---QBEA	1072
gi		6323968		ref		NP_014039.1		VOIVDFPQS-KLEEN-RSSSENASAAIAKILYXNSNIPNVDYTNANWFKLPTFITDKAAEFNQCFLSOLLENNSPVCAQS--NISAVVDVVIQALNERSITREK---QTVISVKKLLGFLP---SSDA	1069
gi		17737759		ref		NP_524226.1		VQVINDPKA-REIEN-ISPTENASISAFAKILKYNNSALSVDLELIGVWFVSWLPSVSEDEEAHIVGLYCDLIEGNHPVILGANNGNLPRIVSIASFSFCTKVVEAESA---TQTRMLTIVKQVESNPE	1077
gi		118780654		ref		XP_310308.5		VEVIMAPDS-REPEN-VNPENENASISAVTKILKYNNTAITNPDEIIALWFVWLPGVEDEDEAVVYVGLYCDLIEGNHPVILGANNGNLPRIVSIASFSFCTKVVEAESA---TQTRMLTIVKQVESNPE	1075
gi		24797086		ref		NP_002262.3		VRVIQSADS-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1093
gi		73989213		ref		XP_542647.2		VRVIQSADS-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1075
gi		29789199		ref		NP_076068.1		VRVIQAPEA-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1075
gi		109502015		ref		XP_224534.4		VRVIQSADS-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1075
gi		114650444		ref		XP_001140931.1		VRVIQSADS-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1081
gi		118084696		ref		XP_416978.2		VRVIQSPDA-KTKEN-VNAENENCISAVGKIMFKFPDCVN--VEEVLPHWLWVPLPHEDKKEAVQTFNYLCLDLESNHPVILGNPNTNLPKIFSIIAEGEMHEAIKHEDP---CAKRLANVVRQVOTSGG	1094
gi		125802691		ref		XP_697938.2		VGVISQADS-RAKEN-VNAENENCISAVAKVMKIRPECVN-VTEILPHWLWVPLNEDKKEAVHTFNYLCLDLESNHPVILGNPNTNLPKIFAIADGVANESVKGEDG---CSKRLANVIRQVOTSGG	1071
gi		17506191		ref		NP_490715.1		AAMIQREDA-RATESVVAENASISAFAKITGNVPLPAEAVGKVVEMFLSWLPTYSDEESPYITCLAEFLDKQDAALFGPNQNLPRIFLVCLLSIANDAFNDDSGNQTQRIVTILKQIYAFPP	1071
gi		15241189		ref		NP_197483.1		NVVIIQLNA-ROSEN-AMAYDNASVAVGKICQFHRDSD--SSVLPWLNCLPISNDVLEAKRVVDDQLCSMVRRQDWDLLGPNQNLPRILVFAEVLVTKGVDVTE---TAGRMINILRQLQHLPP	1095
gi		115472957		ref		NP_001060077.1		NNVITHPEA-KHADN-IMAYDNASVAVGKICQFHRDSD--AAQVIPAWLQCLPIKDDKTEAKRVVDDQLCSMVRRQDWDLLGPHSQYLKPIVIFAEVLCNGETLATDE---TTKRMVLLRRFQHLPP	1102
gi		124506397		ref		XP_001351796.1		LKLVHVESTNKKPKKEYISAIDNAIAALGDVVLHMTSKFNAAEDLTKVNLNHLPIKEDDAGRRVVKNLNLDLVSQNHPLLPKDNSTAKIIEIFLTIETEDFSPTDCN---KKISLILNSLDKSYLN	1099



gi		145616144		ref		XP_360994.2		RVVRIILLPPPPRPLPVARIIRLAIIDNHPVFPSSPHLLGTSPPWLQITDSSAVVITQAPLDEEPTAVRRILRAPEGTGRG	1144
gi		32421379		ref		XP_331133.1		DPVLQQFGPESQLIRERFS	1096
gi		19076002		ref		NP_588502.1		NSVIATLSVDNQRALSAPF	1095
gi		50305745		ref		XP_452833.1		SALLQRVPPPEIMQIHKWFA	1090
gi		45200748		ref		NP_986318.1		LRYFQRVPSIMQDITWFA	1092
gi		6323968		ref		NP_014039.1		MAIFNRYPADIMEKVHKWFA	1089
gi		17737759		ref		NP_524226.1		AACASTLSPEQQALQDAYRELNAVAPA	1105
gi		118780654		ref		XP_310308.5		QACINTLTAEQKAALEGAVRAAAAVTAAAGVYIQ	1109
gi		24797086		ref		NP_002262.3		TECIAQLSPEQAAIQELLNSA	1115
gi		73989213		ref		XP_542647.2		TECIAQLSPEQAAIQELLNSA	1097
gi		29789199		ref		NP_076068.1		TECIAQLSPEQAAIQELLNSA	1097
gi		109502015		ref		XP_224534.4		TECIAQLSPEQAAIQELLNSA	1097
gi		114650444		ref		XP_001140931.1		TECIAQLSPEQAAIQELLNSA	1103
gi		118084696		ref		XP_416978.2		TECISQLNADQAAIQELLNSA	986
gi		125802691		ref		XP_697938.2		TQCVSALNETQKAIODLLNTA	1093
gi		17506191		ref		NP_490715.1		AQ-QDGIDEHLTSVLQCLLNGQ	1092
gi		15241189		ref		NP_197483.1		ASTWSTLKPEQALALQSLSS	1116
gi		115472957		ref		NP_001060077.1		ASTFSSLQPOQQLLQSLSS	1123
gi		124506397		ref		XP_001351796.1		NLASSTLSHKAKKLNILNPNRK	1123

