

gi | 124494256 | ref | NP_032538.2 | ...MLTPPLLLLLLPLLSALVSG--ATMDAPKTCSPKQFACRDIITCISKGWRCDGERDCPPDGSDEAPEICPOSK-----AORCPFNEHSCLGTELCPVMSRLC 150
gi | 62652278 | ref | XP_243524.3 | ...MLTPPLLLLLLPLLSALVAG--ATMDAPKTCSPKQFACRDIITCISKGWRCDGERDCPPDGSDEAPEICPOSK-----AORCPFNEHSCLGTELCPVMSRLC 150
gi | 126012562 | ref | NP_002323.2 | ...MLTPPLLLLLLPLLSALVA--AAIDAPKTCSPKQFACRDIITCISKGWRCDGERDCPPDGSDEAPEICPOSK-----AORCPFNEHSCLGTELCPVMSRLC 150
gi | 73968460 | ref | XP_538245.2 | ...MLTPPLLLLLLPLLSALAA--AAIDAPKTCSPKQFACRDIITCISKGWRCDGERDCPPDGSDEAPEICPOSK-----AORCPFNEHSCLGTELCPVMSRLC 150
gi | 292627062 | ref | XP_001920591.2 | ...MPSCANMLAVGLLYLGLVLALEVVDPTRAIAPKTCSPKQFVCKDQVTCISKGWRCDGERDCPPDGSDEAPEICPOSK-----AORCPFNEHSCLGTELCPVMSRLC 150
gi | 28573304 | ref | NP_788284.1 | ...MQIVAEIQMIIEWLAACISSEFFLILSDHYSVLYPLAGPCPASVFTICNDGFCIPMRWKCDKADCPDMSDE-GSECAPKCNEGVFRGVSRRHCIPNNWLCDFGFCGKGDIDSDENLCPNGD-----TPKCRAFEGQCR-NGDCELESRFC 150
gi | 158300186 | ref | XP_320185.4 | ...FPVTCISQSQFTICVM-----DGKICIPALWRCDTSADCSGSDVEYCGCKAKACNEGFHFTVSNRCLIPHDWTCDGVDVCGVLEKYDMVDVSDDEPPLICRAHFKCLFETALQS-DGKCLEIDRFIC 150



gi | 124494256 | ref | NP_032538.2 | ...NGIQDCMDGSDGGAHCR-----ELRANC SRMGCQHHCVPTPSGPTCYCNSSFFLQQA-DGKTCCKDFDECSVYGTCSQLCTNTDGSFTCCGVEGYLLQPDNRSCKAKNEPVDPRPVLIIANSONILATYLSGAQVSE----- 300
gi | 62652278 | ref | XP_243524.3 | ...NGIQDCMDGSDGGAHCR-----ELRANC SRMGCQHHCVPTPSGPTCYCNSSFFLQQA-DGKTCCKDFDECSVYGTCSQLCTNTDGSFTCCGVEGYLLQPDNRSCKAKNEPVDPRPVLIIANSONILATYLSGAQVSE----- 300
gi | 126012562 | ref | NP_002323.2 | ...NGVQDCMDGSDGDEGPHCR-----ELQGNCSRLCQHHCVPTLDGPTCYCNSSFFLQQA-DGKTCCKDFDECSVYGTCSQLCTNTDGSFTCCGVEGYLLQPDNRSCKAKNEPVDPRPVLIIANSONILATYLSGAQVSE----- 300
gi | 73968460 | ref | XP_538245.2 | ...NGVQDCMDGSDGDEGPHCR-----ELQGNCSRLCQHHCVPTLDGPTCYCNSSFFLQQA-DGKTCCKDFDECSVYGTCSQLCTNTDGSFTCCGVEGYLLQPDNRSCKAKNEPVDPRPVLIIANSONILATYLSGAQVSE----- 300
gi | 292627062 | ref | XP_001920591.2 | ...DGVDPDCTDGRDEGPHCR-----ELASKCSIMDCQVNCVSTLSSGPKCYCKNGYVGE-DGKTCCKDFNECAVYGTCSQICNTNDSGSIYCSVVEGYLLQPDNRSCKAKNEPVDPRPVLIIANSONIQATYLSGANPTI----- 300
gi | 28573304 | ref | NP_788284.1 | ...DGRWDCDNDDELCDKQ-----NAACAALNCSFNCKLTPQGARCYPKDKQVPSNSSTRVYDECESEPTCDQVCRNTPGSYECSCVSGYAKTK-GNRCRAIVVPTPEPTLILFLSRDGVQSVGNGTEVIGPPGAKDNDKVIDDKDG 300
gi | 158300186 | ref | XP_320185.4 | ...DGAWDCSNDENLCSNSNDIATASAPTACDALKCSVDCRLTSEGARCFCAKDSQP-----NGSVCEDFDEQIQLGLDQCKKIQPGAYQCSCTTGVYVR-----GNICTAVNLPKDEPTSLFFTIFNKVKKVSIENRTSVLGNFPTIN----- 300



gi | 124494256 | ref | NP_032538.2 | ...TIIPFSTRQITAMDFSYANETVCWVHVGDSSAAQTLKCARMPGLKGFVDEHTINISLSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRRNGDTCVILLD--LELYNPKGIALDPAMGKVFVFDYGGIIP-KVERCDMDGQNRITKL 450
gi | 62652278 | ref | XP_243524.3 | ...TIIPFSTRQITAMDFSYANETVCWVHVGDSSAAQTLKCARMPGLKGFVDEHTINISLSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRRNGDTCVILLD--LELYNPKGIALDPAMGKVFVFDYGGIIP-KVERCDMDGQNRITKL 450
gi | 126012562 | ref | NP_002323.2 | ...TIIPFSTRQITAMDFSYANETVCWVHVGDSSAAQTLKCARMPGLKGFVDEHTINISLSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRRNGDTCVILLD--LELYNPKGIALDPAMGKVFVFDYGGIIP-KVERCDMDGQNRITKL 450
gi | 73968460 | ref | XP_538245.2 | ...TIIPFSTRQITAMDFSYANETVCWVHVGDSSAAQTLKCARMPGLKGFVDEHTINISLSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRRNGDTCVILLD--LELYNPKGIALDPAMGKVFVFDYGGIIP-KVERCDMDGQNRITKL 450
gi | 292627062 | ref | XP_001920591.2 | ...TIIN---DKQITIMDFIYAQETVCWVHVGDSSAAQTLKCARMPGLKGFVDEHTINISLSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRRNGDTCVILLD--LELYNPKGIALDPAMGKVFVFDYGGIIP-KVERCDMDGQNRITKL 450
gi | 28573304 | ref | NP_788284.1 | ...VGSSEELLSQPLRFVHAFEVWHRNRITCSLLFSWNP--ELDMRQORVDDARVNWITLFFSFFVQPFTELRGLDWSGNWYLLDQOREIIFVCSQPMVHCAITIVBALSEVLRPRRMLDPTKGLFFSKWGSQVSTERSLLDGTNRITSL 450
gi | 158300186 | ref | XP_320185.4 | ...ETVEEELKQPNPRIRAMEVHRNRITFLARIDG--KSLLECYSDVNRSHSWVWPRPDLFNNLEDIVDRLDWSGNWYLLDQOREIIFVCSQPMVHCAITIVBALSEVLRPRRMLDPTKGLFFSKWGSQVSTERSLLDGTNRITSL 450



gi | 124494256 | ref | NP_032538.2 | ...VDSKIVFPHGIIITLDVSRVLYWADAYLDYIEVVDYEGKGRQTIITQG---ILIEHLYGLTVFENLYATNSDNANTQOKTSVIRVNRNFSYEQVVTVRDGGALHIYHORRQPRVRSACENDQYKPGGCSDIICLLANSHK---ARTC 600
gi | 62652278 | ref | XP_243524.3 | ...VDSKIVFPHGIIITLDVSRVLYWADAYLDYIEVVDYEGKGRQTIITQG---ILIEHLYGLTVFENLYATNSDNANTQOKTSVIRVNRNFSYEQVVTVRDGGALHIYHORRQPRVRSACENDQYKPGGCSDIICLLANSHK---ARTC 600
gi | 126012562 | ref | NP_002323.2 | ...VDSKIVFPHGIIITLDVSRVLYWADAYLDYIEVVDYEGKGRQTIITQG---ILIEHLYGLTVFENLYATNSDNANAQOKTSVIRVNRNFSYEQVVTVRDGGALHIYHORRQPRVRSACENDQYKPGGCSDIICLLANSHK---ARTC 600
gi | 73968460 | ref | XP_538245.2 | ...VDSKIVFPHGIIITLDVSRVLYWADAYLDYIEVVDYEGKGRQTIITQG---ILIEHLYGLTVFENLYATNSDNANAQOKTSVIRVNRNFSYEQVVTVRDGGALHIYHORRQPRVRSACENDQYKPGGCSDIICLLANSHK---ARTC 600
gi | 292627062 | ref | XP_001920591.2 | ...VDSKIVFPNGIITLDLANKLYWADAYLDYIEVVDYEGKGRQTIITQG---LLEHLYGLTVFENLYATNSDNANMQPQTSVIRVNRNFSYEQVVTVRDGGALHIYHORRQPRVRSACALDPFGKPGGCSDIICLLANSHK---ARTC 600
gi | 28573304 | ref | NP_788284.1 | ...VTDQVYHPSSVLLDLANELVYVWIDYKDEVNRYVDEGRNRWTLKRPDLSVPLKTIHAEVFPENSIYLAANMDI-----AIVALDKFSLKTHIQSNVSRGANLRIFHRKQPEVAHPCRDIN-----AGCNQICVQWPKG-FASAKC 600
gi | 158300186 | ref | XP_320185.4 | ...VLNKIITPLDIALDLVWQHVYVVDTHLDIVRVNYDGSGRVFPKRSQFLFNFGMLYALDVFERTIYIASWQNG-----SIVALNGTGEARVTVNAPHAVHLHFVHRKQPEVAHPCRDIN-----GGDQLCFVWKKIGVATAQC 600



gi | 124494256 | ref | NP_032538.2 | ...RCRSFSLGSDGKSCCKPEHELFLVYGKGRPGIIRGMDMG-----AKVPDEHMIP IENLMPRALDFAETGFIFYFADT-----TSYLIQRKIDGTERETILKDGIIHNVGVAVDWMGDNLVYDGGPKKTIISVARLEK 750
gi | 62652278 | ref | XP_243524.3 | ...RCRSFSLGSDGKSCCKPEHELFLVYGKGRPGIIRGMDMG-----AKVPDEHMIP IENLMPRALDFAETGFIFYFADT-----TSYLIQRKIDGTERETILKDGIIHNVGVAVDWMGDNLVYDGGPKKTIISVARLEK 750
gi | 126012562 | ref | NP_002323.2 | ...RCRSFSLGSDGKSCCKPEHELFLVYGKGRPGIIRGMDMG-----AKVPDEHMIP IENLMPRALDFAETGFIFYFADT-----TSYLIQRKIDGTERETILKDGIIHNVGVAVDWMGDNLVYDGGPKKTIISVARLEK 750
gi | 73968460 | ref | XP_538245.2 | ...RCRSFSLGSDGKSCCKPEHELFLVYGKGRPGIIRGMDMG-----AKVPDEHMIP IENLMPRALDFAETGFIFYFADT-----TSYLIQRKIDGTERETILKDGIIHNVGVAVDWMGDNLVYDGGPKKTIISVARLEK 750
gi | 292627062 | ref | XP_001920591.2 | ...RCRSFSLGSDGKSCCKPEHELFLVYGKGRPGIIRGMDMH-----ITVYDEHIVPIENLMPRALDFAETGFIFYFADT-----TSYIIQRKIDGTERETIIVKDGIIHNVGVAVDWMGDNLVYDGGPKKTIISVARLEK 750
gi | 28573304 | ref | NP_788284.1 | ...MCTAGYKLIHN-QTCLLSALDKFLVYSDKHLARISGIPLDLQVVOOLEQVDEQDVMVYVYVSKTALDIVNVRGKAVFVVDVSGASFPFGGEPSCSIRSQSLNGLVSRLLAG-LKRHVHAFVDWINDHLYWIS---HKMKQVAPLRN 750
gi | 158300186 | ref | XP_320185.4 | ...MQSPGVRLKI-KSQCVLTKRFTPLLAKSNPAMIRGFAVG-----IKSQ-EAIVPITDGLPHITFDYHVEDOLIFFSHG-----VIDKPSFRIEAAKLDGICORLLES-FGSDGISYDVLGNNIFWID---SDRNHISVILK 750



gi | 124494256 | ref | NP_032538.2 | AAOTRKTLLIEGKMTHPRAIVVDPPLNGWYWTWDEEDPKDSRRGRLERAWMDGSHRDIFVTT---SKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLNGTDRKIVYEG-PELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVAGAPPTVTI 900
gi | 62652278 | ref | XP_243524.3 | AAOTRKTLLIEGKMTHPRAIVVDPPLNGWYWTWDEEDPKDSRRGRLERAWMDGSHRDIFVTT---SKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLNGTDRKIVYEG-PELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVAGAPPTVTI 900
gi | 126012562 | ref | NP_002323.2 | AAOTRKTLLIEGKMTHPRAIVVDPPLNGWYWTWDEEDPKDSRRGRLERAWMDGSHRDIFVTT---SKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLNGTDRKIVYEG-PELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVAGAPPTVTI 900
gi | 73968460 | ref | XP_538245.2 | AAOTRKTLLIEGKMTHPRAIVVDPPLNGWYWTWDEEDPKDSRRGRLERAWMDGSHRDIFVTT---SKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLNGTDRKIVYEG-PELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVAGAPPTVTI 900
gi | 292627062 | ref | XP_001920591.2 | ASOTRKTLLIEGKMTHPRAIVVDPPLNGWYWTWDEEDPKDSRRGRLERAWMDGSHRDIFVTT---SKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLNGTDRKIVYEG-PELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVAGAPPTVTI 900
gi | 28573304 | ref | NP_788284.1 | LSKVLTFTND--CDAMSELDPTTGLLWYSQWESQ--CEAGIYSSWMDGTHKELLAKGTSMPMOWPRSLDVRRTKELVWCDIRLSTIELMLRDLGTGREVLFK--SDQFHPYSIVQNGLIYWADNKNSTLRFHHAQANLSSSTFS 900
gi | 158300186 | ref | XP_320185.4 | GKRMRYIVLRLVYAPKSIIVVDPKQGMWYSWSVSP---SGRIDRAWMNGQPELLYS--SKERPTEWPTGLSDIMIQKRLVWCDARLSTIESINLDGNSNRVLLFQGRSINQFPVALAVRQLLYFADNVKGHTEKLNLSDFHLETTII 900



gi | 124494256 | ref | NP_032538.2 | LLR--SERPPIFEIRMYDAQQQ--VGTNKRVRNNGCCSSLLCLANPGS--RQCACAEDQV--LDIDGVTCLANPSYVPP---PQCPGPFACANNRICIQRWKCDGNDCLDLSDEAF--ALCHOHTCPSDR-FKCENNRCIPNRWLCDG 1050
gi | 62652278 | ref | XP_243524.3 | LLR--SERPPIFEIRMYDAQQQ--VGTNKRVRNNGCCSSLLCLANPGS--RQCACAEDQV--LDADGVTCLANPSYVPP---PQCPGPFACANNRICIQRWKCDGNDCLDLSDEAF--ALCHOHTCPSDR-FKCENNRCIPNRWLCDG 1050
gi | 126012562 | ref | NP_002323.2 | LLR--SERPPIFEIRMYDAQQQ--VGTNKRVRNNGCCSSLLCLANPGS--RQCACAEDQV--LDADGVTCLANPSYVPP---PQCPGPFACANNRICIQRWKCDGNDCLDLSDEAF--ALCHOHTCPSDR-FKCENNRCIPNRWLCDG 1050
gi | 73968460 | ref | XP_538245.2 | LLR--SERPPIFEIRMYDAQQQ--VGTNKRVRNNGCCSSLLCLANPGS--RQCACAEDQV--LDIDGVTCLANPSYVPP---PQCPGPFACANNRICIQRWKCDGNDCLDLSDEAF--ALCHOHTCPSDR-FKCENNRCIPNRWLCDG 1050
gi | 292627062 | ref | XP_001920591.2 | LLR--NERPPIYIERTYDAQQQQIIISNVCRANNGCCSSLLCLLPTG--RSCACADQI--LDTDNKTCRANPSYVPP---PQCPGPFACANNRICIQRWKCDGNDCLDLSDEAF--ALCHOHTCPSDR-FKCENNRCIPNRWLCDG 1050
gi | 28573304 | ref | NP_788284.1 | STVHLQRTGRAADLRIFDIASQP-LPQTPSACAQSKCPGMCLNTPKG-AICRCPDG---FTLNGTGSHCIP-QLAPSPTRPNCISGYMCRSTRCLDTKDMCDGFEDCEDGIDESSDPKGPQNVNTCDKTHNFVCG--RCYQRSLLCST 1050
gi | 158300186 | ref | XP_320185.4 | ---IEKPOVLGLKIFDNLITQY--GGNGRNACEID--CPGICLNIPVAVASCKEDGQVLSLS--EGKPVACVFPFLQHSLS--CNSSTHFLCRNKIDCIEIKVTCDDGDRDCEGSDDEETTPDGPDPN--CDLERNFKCDEQRCSRSVHCDG 1050



gi | 124494256 | ref | NP_032538.2 | DNDCGNS EDESNAI CSART CPPNQFSCA--SGRCIPISWTCDLDDDCGDRSDESAS CAYPTCFPLTQFTCNNGRCININWRCDNDNDCGNSDEAGCSHSCSSTQFKCNSGRCIPEHWTCDGNDCCGYSDETHANCTINQATRPFGGCHSD 1200
gi | 62652278 | ref | XP_243524.3 | DNDCGNS EDESNAI CSART CPPNQFSCA--SGRCIPISWTCDLDDDCGDRSDESAS CAYPTCFPLTQFTCNNGRCININWRCDNDNDCGNSDEAGCSHSCSSTQFKCNSGRCIPEHWTCDGNDCCGYSDETHANCTINQATRPFGGCHSD 1200
gi | 126012562 | ref | NP_002323.2 | DNDCGNS EDESNAI CSART CPPNQFSCA--SGRCIPISWTCDLDDDCGDRSDESAS CAYPTCFPLTQFTCNNGRCININWRCDNDNDCGNSDEAGCSHSCSSTQFKCNSGRCIPEHWTCDGNDCCGYSDETHANCTINQATRPFGGCHSD 1200
gi | 73968460 | ref | XP_538245.2 | DNDCGNS EDESNAI CSART CPPNQFSCA--SGRCIPISWTCDLDDDCGDRSDESAS CAYPTCFPLTQFTCNNGRCININWRCDNEKPCDGGSDKKTQPEPA-----AATRPFGGCHSD 1200
gi | 292627062 | ref | XP_001920591.2 | DNDCGND EDESNSI CLART CPSNOYPCA--SGRCIPVSWMCDLDDDCGDRSDEPASCAYPTCFPLTQFTCANNGRCININWRCDNDNDCGNSDEAGCSHSCSSTQFKCNSGRCIPEHWTCDGNDCCGYSDETHANCTINQATRPFGGCHSD 1200
gi | 28573304 | ref | NP_788284.1 | IPYCSGTDG--ANCHQNTGNSNEFTCHKRSGRCIQHTVWVNDGVVDCGPDSSDTESETIFASKCPEFDCNRRQRQFADVCDGIDNCGNADEMECEQCEHGEKYCRPTGCGYEMHMCDDGIHDCDFSDRANCNQIKSDNHPVT 1200
gi | 158300186 | ref | XP_320185.4 | SVYCIDESDEDIYCNPKTCESEFFQCEVSHRCIPNTVWVCRHLDCGPNSSD---EPHECHKCEPECKSACVPEFLCDGVNCGDKSDSQCDDVCGVNEFFSPHGICDRSLMCDPKLNCLNFAHFCDDLKAGSNG----- 1200



gi | 124494256 | ref | NP_032538.2 | EFOCRLDGLCIPLRWRCDGTDICMDSSDEKSCGEGVTHVCDPNVFKGCKDS-----ARCIKAWVCDGSDCEPNSDEENCEALACRPPSHPCANNTSVCLPDKLDCGKDDCGDSDGEGELDCQCSLNNNG-GCS 1350
gi | 62652278 | ref | XP_243524.3 | EFOCRLDGLCIPLRWRCDGTDICMDSSDEKSCGEGVTHVCDPNVFKGCKDS-----ARCIKAWVCDGSDCEPNSDEENCEALACRPPSHPCANNTSVCLPDKLDCGKDDCGDSDGEGELDCQCSLNNNG-GCS 1350
gi | 126012562 | ref | NP_002323.2 | EFOCRLDGLCIPLRWRCDGTDICMDSSDEKSCGEGVTHVCDPNVFKGCKDS-----ARCIKAWVCDGSDCEPNSDEENCEALACRPPSHPCANNTSVCLPDKLDCGKDDCGDSDGEGELDCQCSLNNNG-GCS 1350
gi | 73968460 | ref | XP_538245.2 | EFOCRLDGLCIPLRWRCDGTDICMDSSDEKSCGEGVTHVCDPNVFKGCKDSGKKKDGREGLGOYGOKEIVLTRCIKAWVCDGSDCEPNSDEENCEALACRPPSHPCANNTSVCLPDKLDCGKDDCGDSDGEGELDCQCSLNNNG-GCS 1350
gi | 292627062 | ref | XP_001920591.2 | EFOCRMDGLCIPMRWRCDGTDICMDLSDKSNCEGVTMCDPAVKFAKDS-----ARCIKAWVCDGSDCEPNSDEENCEALECKLSHHVCASNDIICLPEPKLDCGKDDCFDADE-KLNLCTVENG-GCS 1350
gi | 28573304 | ref | NP_788284.1 | ---EWKELGECAPLEFACMFPEFCIP--DFLRCDGISHCDFRDTDFENCTHI-----NTFRDMNEVVICHEPDRLCG--FKQCVTVDQLCDGKDCEDTDEGFLCADKLCBRGHECS 1350
gi | 158300186 | ref | XP_320185.4 | ---ITQSSVPRSEPELKDILRQ--DLRIVCGLDKQCEENVRVCRM-----EFAPF--NEIMVCHHPDRLCR--VINQCIVTLCNGRTDQFDEGDFRCAEKLCDAPNDCS 1350



gi | 124494256 | ref | NP_032538.2 | HNCVAPGEGIVCSPLGMEGLSDNHTCQIQSYCAKHLKCSQKCDONKFSVVKCSYEGWVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDYSVLVPLRLNTIALDFHLSOSA---LWTDVVEDKIVRGKLLDNGALTSFEVVIQ 1500
gi | 62652278 | ref | XP_243524.3 | HNCVAPGEGIVCSPLGMEGLSDNHTCQIQSYCAKHLKCSQKCDONKFSVVKCSYEGWVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDYSVLVPLRLNTIALDFHLSOSA---LWTDVVEDKIVRGKLLDNGALTSFEVVIQ 1500
gi | 126012562 | ref | NP_002323.2 | HNCVAPGEGIVCSPLGMEGLSDNHTCQIQSYCAKHLKCSQKCDONKFSVVKCSYEGWVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDYSVLVPLRLNTIALDFHLSOSA---LWTDVVEDKIVRGKLLDNGALTSFEVVIQ 1500
gi | 73968460 | ref | XP_538245.2 | HNCVAPGEGIVCSPLGMEGLSDNHTCQIQSYCAKHLKCSQKCDONKFSVVKCSYEGWVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDYSVLVPLRLNTIALDFHLSOSA---LWTDVVEDKIVRGKLLDNGALTSFEVVIQ 1500
gi | 292627062 | ref | XP_001920591.2 | HNCVAPGEGIVCSPLGMEGLSDNHTCQIQSYCAKHLKCSQKCDONKFSVVKCSYEGWVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDYSVLVPLRLNTIALDFHLSOSA---LWTDVVEDKIVRGKLLDNGALTSFEVVIQ 1500
gi | 28573304 | ref | NP_788284.1 | HRCHNTP--EGVICSPDHLVLOPNGKRCSSMACHDHWDTCSQVCESSGKGYDCRCLDGLDFDRFTCKSTAPDEPVVIFINRQDIKGLNLTLMVNGVNFSSLRNIALDFLNNSNVEIWFVDVVDKIVRGHVLG--DFLNVAVVH 1500
gi | 158300186 | ref | XP_320185.4 | HACHNAP--EGLIICSFAHLFLOPNRDCDHACDNWTCISQITKAGVHYRCCGVEGYTLMDYKFCRSNNGDSPVIFSNRQELIYGLDNLTVLGRSFFYLSRLNTIALDFLNNSNVEIWFVDVVDKIVRGHVLG--DFLNVAVVH 1500



gi | 124494256 | ref | NP_032538.2 | YGLAIPPEGLAVDWIAGNIYVWVENLDOI EAVKLDGTLRITLLAGDIEHPRAIALDPRDGILFWTDWASLPRIEAAASMSGAGRRITIHRETGS-GGWPNGLVDVYLEKRLIWLWDARSDAIYSARYDGS GHMVEVLRGHEFLSHPPFAVILYGG 1650
gi | 62652278 | ref | XP_243524.3 | YGLAIPPEGLAVDWIAGNIYVWVENLDOI EAVKLDGTLRITLLAGDIEHPRAIALDPRDGILFWTDWASLPRIEAAASMSGAGRRITIHRETGS-GGWPNGLVDVYLEKRLIWLWDARSDAIYSARYDGS GHMVEVLRGHEFLSHPPFAVILYGG 1650
gi | 126012562 | ref | NP_002323.2 | YGLAIPPEGLAVDWIAGNIYVWVENLDOI EAVKLDGTLRITLLAGDIEHPRAIALDPRDGILFWTDWASLPRIEAAASMSGAGRRITIHRETGS-GGWPNGLVDVYLEKRLIWLWDARSDAIYSARYDGS GHMVEVLRGHEFLSHPPFAVILYGG 1650
gi | 73968460 | ref | XP_538245.2 | YGLAIPPEGLAVDWIAGNIYVWVENLDOI EAVKLDGTLRITLLAGDIEHPRAIALDPRDGILFWTDWASLPRIEAAASMSGAGRRITIHRETGS-GGWPNGLVDVYLEKRLIWLWDARSDAIYSARYDGS GHMVEVLRGHEFLSHPPFAVILYGG 1650
gi | 292627062 | ref | XP_001920591.2 | YGLAIPPEGLAVDWIAGNIYVWVENLDOI EAVKLDGTLRITLLAGDIEHPRAIALDPRDGILFWTDWASLPRIEAAASMSGAGRRITIHRETGS-GGWPNGLVDVYLEKRLIWLWDARSDAIYSARYDGS GHMVEVLRGHEFLSHPPFAVILYGG 1650
gi | 28573304 | ref | NP_788284.1 | SGLSLTEGLAVDWVWKNLYWIDSNLDOI EAVKLNQSFRRITLIVAGDMVNPRAIALDPMEGVLFWTDWEGSPRLERCIIMAGENRTVTKYVGS-DGWPNGLIADYIPRRVYWDARS DSITITTYDQDHLVLDQGVLAHPFSITVFDN 1650
gi | 158300186 | ref | XP_320185.4 |1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 124494256 | ref | NP_032538.2 | EYVYWDWRITNLAKANKWTGHNVTVVORINTQPFDLQVYHPSRQPMAP-NPCEANGGRGPCSHLCLINYNRIVSCACPHLMKLNKHN-TTCYEFKFKFLLYAROMIEIRGVLDAPYNYIISFTVPE-DIDNVTVLDYDAREQRVWVSDVRIT 1800
gi | 62652278 | ref | XP_243524.3 | EYVYWDWRITNLAKANKWTGHNVTVVORINTQPFDLQVYHPSRQPMAP-NPCEANGGRGPCSHLCLINYNRIVSCACPHLMKLNKHN-TTCYEFKFKFLLYAROMIEIRGVLDAPYNYIISFTVPE-DIDNVTVLDYDAREQRVWVSDVRIT 1800
gi | 126012562 | ref | NP_002323.2 | EYVYWDWRITNLAKANKWTGHNVTVVORINTQPFDLQVYHPSRQPMAP-NPCEANGGRGPCSHLCLINYNRIVSCACPHLMKLNKHN-TTCYEFKFKFLLYAROMIEIRGVLDAPYNYIISFTVPE-DIDNVTVLDYDAREQRVWVSDVRIT 1800
gi | 73968460 | ref | XP_538245.2 | EYVYWDWRITNLAKANKWTGHNVTVVORINTQPFDLQVYHPSRQPMAP-NPCEANGGRGPCSHLCLINYNRIVSCACPHLMKLNKHN-TTCYEFKFKFLLYAROMIEIRGVLDAPYNYIISFTVPE-DIDNVTVLDYDAREQRVWVSDVRIT 1800
gi | 292627062 | ref | XP_001920591.2 | EYVYWDWRITNLAKANKWTGHNVTVVORINTQPFDLQVYHPSRQPMAP-NPCEANGGRGPCSHLCLINYNRIVSCACPHLMKLNKHN-TTCYEFKFKFLLYAROMIEIRGVLDAPYNYIISFTVPE-DIDNVTVLDYDAREQRVWVSDVRIT 1800
gi | 28573304 | ref | NP_788284.1 | YVYWDWRITSVIRANKWNGSDVQVLRITQSPFFGIQVLSRSRQPMWDR-NPCGEGNNGG--CSHLCLLSGRGTFCCECPVVMRLDPANERNCPVNEQVLLFMVDEIRGIDLHQPHHTIPIRQS----PRRIDFLVDSRIFWSDIQ 1800
gi | 158300186 | ref | XP_320185.4 | YVYWDWRITSVIRANKWNGSDVQVLRITQSPFFGIQVLSRSRQPMWDR-NPCGEGNNGG--CSHLCLLSGRGTFCCECPVVMRLDPANERNCPVNEQVLLFMVDEIRGIDLHQPHHTIPIRQS----PRRIDFLVDSRIFWSDIQ 1800
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



gi | 124494256 | ref | NP_032538.2 | QAIKRAFINGTGVETVVSADLPNAHGLAVDWVSRNLFWTSYDITNKKQINVARLDGSEFKNAVVOG--LEQPHGLVHVPLRGLKLYWTDGDN-----ISMANMDGSRNLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDSGLSE 1950
gi | 62652278 | ref | XP_243524.3 | QAIKRAFINGTGVETVVSADLPNAHGLAVDWVSRNLFWTSYDITNKKQINVARLDGSEFKNAVVOG--LEQPHGLVHVPLRGLKLYWTDGDN-----ISMANMDGSRNLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDSGLSE 1950
gi | 126012562 | ref | NP_002323.2 | QAIKRAFINGTGVETVVSADLPNAHGLAVDWVSRNLFWTSYDITNKKQINVARLDGSEFKNAVVOG--LEQPHGLVHVPLRGLKLYWTDGDN-----ISMANMDGSRNLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDSGLSE 1950
gi | 73968460 | ref | XP_538245.2 | QAIKRAFINGTGVETVVSADLPNAHGLAVDWVSRNLFWTSYDITNKKQINVARLDGSEFKNAVVOG--LEQPHGLVHVPLRGLKLYWTDGDN-----ISMANMDGSRNLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDSGLSE 1950
gi | 292627062 | ref | XP_001920591.2 | QAIKRAFINGTGVETVVSADLPNAHGLAVDWVSRNLFWTSYDITNKKQINVARLDGSEFKNAVVOG--LEQPHGLVHVPLRGLKLYWTDGDN-----ISMANMDGSRNLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDSGLSE 1950
gi | 28573304 | ref | NP_788284.1 | NEITSAGISGLIPIINTINIEKPNLQFVADWIANRMYSSG-QIKCNILASNLKGEFASIIHED--LNMVDSIVLDPANGKWRMIHSAASDGSMSQLESNLDGSRSLIYQHENN-LQSLTMDFDQSRLYAYDNS-GIAYYDIPRNETR 1950
gi | 158300186 | ref | XP_320185.4 | NEITSAGISGLIPIINTINIEKPNLQFVADWIANRMYSSG-QIKCNILASNLKGEFASIIHED--LNMVDSIVLDPANGKWRMIHSAASDGSMSQLESNLDGSRSLIYQHENN-LQSLTMDFDQSRLYAYDNS-GIAYYDIPRNETR 1950
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950



gi | 124494256 | ref | NP_032538.2 | VIDTMRSQLGKATALAIMGDKLWADQVSEKMGTCNKADGSGSVVLRNSTLVMHMKVYDESIOLEHEGTPNCSVNN--GDCSOLCLPTSETTRSCMCTAGYSLRSGQQA-CEGVGSFLLYSVHEGIRGIPLDPNDK-----SDALVP 2100
gi | 62652278 | ref | XP_243524.3 | VIDTMRSQLGKATALAIMGDKLWADQVSEKMGTCNKADGSGSVVLRNSTLVMHMKVYDESIOLEHEGTPNCSVNN--GDCSOLCLPTSETTRSCMCTAGYSLRSGQQA-CEGVGSFLLYSVHEGIRGIPLDPNDK-----SDALVP 2100
gi | 126012562 | ref | NP_002323.2 | VIDTMRSQLGKATALAIMGDKLWADQVSEKMGTCNKADGSGSVVLRNSTLVMHMKVYDESIOLEHEGTPNCSVNN--GDCSOLCLPTSETTRSCMCTAGYSLRSGQQA-CEGVGSFLLYSVHEGIRGIPLDPNDK-----SDALVP 2100
gi | 73968460 | ref | XP_538245.2 | VIDTMRSQLGKATALAIMGDKLWADQVSEKMGTCNKADGSGSVVLRNSTLVMHMKVYDESIOLEHEGTPNCSVNN--GDCSOLCLPTSETTRSCMCTAGYSLRSGQQA-CEGVGSFLLYSVHEGIRGIPLDPNDK-----SDALVP 2100
gi | 292627062 | ref | XP_001920591.2 | VIESVKGKLTKATALAIMGDKLWADQSDIDQIGTCDKSDGGNKVLRYHTSPMMHKNVNESVH--QIGTNLCSKNN--GDCSOLCLPTSPSTRACMCTAGYSLKSGQQA-CEGVGSFLLYSVHEGIRGIPLDPNDK-----SDALVP 2100
gi | 28573304 | ref | NP_788284.1 | KVLVASPIHS-ISSLTYNNGTLFPEPNIQSVIMQCEKEACNMSYLRVNIKSIQSMKMFYADAQGSNTCAEWAVR--GGCQLCLARSSIDHVCRCALGYDEFPNPPCQVPRAEFIFYSI-DVLQGVEMIDPSEQDFP-----SPALVP 2100
gi | 158300186 | ref | XP_320185.4 | QVLAAPHEDNHPISITITVRSIYYDDNHPGRMRCKNLCQNVSVSRNNSGLNATRMYHPGASGNTSCQKRNKDSAGTCEHLCLIPVSAQSHVCRCAIGYRDPDRNPWRICGLDDILVYVSGQLKGIALLSSDDETSGLRNRSLG 2100
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100



gi | 124494256 | ref | NP_032538.2 | VSGTSLAVGIDFHAENDTIYVWDMGLSTISRAKRDOVWREDDVVTNGIGRVEG-----IAVDWIAGNIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
gi | 62652278 | ref | XP_243524.3 | VSGTSLAVGIDFHAENDTIYVWDMGLSTISRAKRDOVWREDDVVTNGIGRVEG-----IAVDWIAGNIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
gi | 126012562 | ref | NP_002323.2 | VSGTSLAVGIDFHAENDTIYVWDMGLSTISRAKRDOVWREDDVVTNGIGRVEG-----IAVDWIAGNIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
gi | 73968460 | ref | XP_538245.2 | VSGTSLAVGIDFHAENDTIYVWDMGLSTISRAKRDOVWREDDVVTNGIGRVEG-----IAVDWIAGNIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
gi | 292627062 | ref | XP_001920591.2 | VSGTSLAVGIDFHAENDTIYVWDMGLSTISRAKRDOVWREDDVVTNGIGRVEG-----IAVDWIAGNIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
gi | 28573304 | ref | NP_788284.1 | ISRVVSAFIDYLANITLVYWDNELGSTRVSKRDGTQREITILEALN-LVGYKQDMLGGIAIDVAVGANIYWSDTKRNIIIEVARLDGSRHYVVVSN-LKSPALAVDPLQGLLFYVQOIGRVS-----LDGSQFVLLVQRANWAGSL 2250
gi | 158300186 | ref | XP_320185.4 | LQOISLAISIDFDVAHYVVIADIDRGSITRIKRDGSAVREIISNFFQVVDGSTLMDLGGIAIDVAVGANIYWTQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPPEKGYLFWTEWGHYPRRIERSRLDGETRVVLVNVV--ISWPNGI 2250
.....2110.....2120.....2130.....2140.....2150.....2160.....2170.....2180.....2190.....2200.....2210.....2220.....2230.....2240.....2250



gi|124494256|ref|NP_032538.2| SVDYQGGKLYWCDARMDKI ERIDLE TGENREVVLSNNMDFSVSVFEDFIYWSDRTHANGS IKRCKGKDNATD SVPLRTGIGVO -LKD IKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400
gi|62652278|ref|XP_243524.3| SVDYQGGKLYWCDARMDKI ERIDLE TGENREVVLSNNMDFSVSVFEDFIYWSDRTHANGS IKRCKGKDNATD SVPLRTGIGVO -LKD IKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400
gi|126012562|ref|NP_002323.2| SVDYQGGKLYWCDARMDKI ERIDLE TGENREVVLSNNMDFSVSVFEDFIYWSDRTHANGS IKRCKGKDNATD SVPLRTGIGVO -LKD IKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400
gi|73968460|ref|XP_538245.2| SVDYQGGKLYWCDARMDKI ERIDLE TGENREVVLSNNMDFSVSVFEDFIYWSDRTHANGS IKRCKGKDNATD SVPLRTGIGVO -LKD IKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400
gi|292627062|ref|XP_001920591.2| SIDYQEGLLYWCARDARTDKI ERINLE TGENRELVLSNNMDFSVSVFEDFIYWSDRTHANGS IKRCKGKDNATD SVPLRTGIGVO -LKD IKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400
gi|28573304|ref|NP_788284.1| VLDI EATKVYWCERYPDALMKVYD -GNLREQLLNESLNNPVALAKMDLYWAENKYNNEGIIRVAPLANLSQK -VVLQEQDAIRDLDKINSKHLORGSNPAHNSNGACEOLCLFNG-TSVAACAHSLAS-DGYSCEPFYENFLIFY 2400
gi|158300186|ref|XP_320185.4| ALDLLNQVYVCEI S D TIWKVDYD -GNLKRLLNGTSHNPKSLDLFGDSIYNAD --SRGNITYEAGLSNIFNYSRVEALEVYS LKDKIKVFNRRDRKGTNVCAVANGGCOOLCLYRGGGORACACAHG-MLAEDGASCREYAGYLLYSE 2400



gi|124494256|ref|NP_032538.2| RTILKSIHLSDERNLNAPVPPFEDPEHMKNVIALAFDYRAGTSPTGNRIFFSDIHFGNIQIINDGSGRTIIVENVGSVEGLAYHRGWDLYWTSYTTSTITRHTVDQTR---PGAFAERETVITMSGDDHPRAFVLDECONLMFWTN 2550
gi|62652278|ref|XP_243524.3| RTILKSIHLSDERNLNAPVPPFEDPEHMKNVIALAFDYRAGTSPTGNRIFFSDIHFGNIQIINDGSGRTIIVENVGSVEGLAYHRGWDLYWTSYTTSTITRHTVDQTR---PGAFAERETVITMSGDDHPRAFVLDECONLMFWTN 2550
gi|126012562|ref|NP_002323.2| RTILKSIHLSDERNLNAPVPPFEDPEHMKNVIALAFDYRAGTSPTGNRIFFSDIHFGNIQIINDGSGRTIIVENVGSVEGLAYHRGWDLYWTSYTTSTITRHTVDQTR---PGAFAERETVITMSGDDHPRAFVLDECONLMFWTN 2550
gi|73968460|ref|XP_538245.2| RTILKSIHLSDERNLNAPVPPFEDPEHMKNVIALAFDYRAGTSPTGNRIFFSDIHFGNIQIINDGSGRTIIVENVGSVEGLAYHRGWDLYWTSYTTSTITRHTVDQTR---PGAFAERETVITMSGDDHPRAFVLDECONLMFWTN 2550
gi|292627062|ref|XP_001920591.2| RTILKSIHLSDETNLNAPVPPFEDPEHMKNVIALAFDYRAGTSPTGNRIFFSDIHFGNIQIINDGSGRTIIVENVGSVEGLAYHRGWDLYWTSYTTSTITRHTVDQSR---SGAFDRDVTVITMSGDDHPRAFVLDECONLMFWTN 2550
gi|28573304|ref|NP_788284.1| RSNIESIHMTDHADKNWPVQMSNTSLMRNVIAITVYEE-----QLVYSDVQLSTINQVHFNQGHRRVLLBQQQRVEGLAYDIVNEQLFWTSNNNAIRSVLELRHLSEHADQNVVHVKKVLSLREDDKPRGIAPVPCLGMIYVWTR 2550
gi|158300186|ref|XP_320185.4| QSATESIHMTDANNINGPIPEIKNSSYLKNLTALSYDYEQ-----QLIFYSDDIDHSTINCVFNGNHRRIIVTKQLVVEGLAFNVLRVLFWTSNNNAIRSLDLNKAASLTPAANAELVQVYIKLRATDKPRGIAPVPCLAMVYVWTR 2550



gi|124494256|ref|NP_032538.2| WNEQHPSIMRAALSGANVLLIEKDIRTPNGLAIDHRAEKLYFSDANLDKIERCEYDGSRRVVLKSEFVHPFGLAVYGEHIFWTDWVRRVAVQRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700
gi|62652278|ref|XP_243524.3| WNEQHPSIMRAALSGANVLLIEKDIRTPNGLAIDHRAEKLYFSDANLDKIERCEYDGSRRVVLKSEFVHPFGLAVYGEHIFWTDWVRRVAVQRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700
gi|126012562|ref|NP_002323.2| WNEQHPSIMRAALSGANVLLIEKDIRTPNGLAIDHRAEKLYFSDANLDKIERCEYDGSRRVVLKSEFVHPFGLAVYGEHIFWTDWVRRVAVQRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700
gi|73968460|ref|XP_538245.2| WNEQHPSIMRAALSGANVLLIEKDIRTPNGLAIDHRAEKLYFSDANLDKIERCEYDGSRRVVLKSEFVHPFGLAVYGEHIFWTDWVRRVAVQRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700
gi|292627062|ref|XP_001920591.2| WNEQSPS IMRASLSGANVLLIENIRTPNGLAIDHRAEKLYFSDANLDKIERCEYDGSRRVVLKSEFVHPFGLAVYGEHIFWTDWVRRVAVRADKYG-RDMKVLRADIPQPMGLIAVAKDINSCEFSPLINNGCCDLCLLHSEGR 2700
gi|28573304|ref|NP_788284.1| WNEGSPCTQRSYLYGTEVVIKTDIKMPNALTLBLEQKLYWADARLDKIERINVDGSRVVLVLAHSTPKHAFAMAVYDGLLEWVAVRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700
gi|158300186|ref|XP_320185.4| WNEHAASIQRAYPSEYGLEIITSDIOMPNALTLBYQARKLYWADALLDKVERTDYDGRVRLVLAHSTPKHAFALAVFDGLLEWVAVRANKVVGSDMKLLRVDIPQPMGLIAVANDTNSCELSPCRIINNGCCDLCLLTHQGH 2700



gi|124494256|ref|NP_032538.2| VNCS CRGGRILQEDFTCRAVNSS CRAQDEFECANGECISFSLT CDGVSHCKDKSDEKPSYCNRRCKKTFRCNNGRCVSNMLWCNGVDDCGDGSDEIPCNKTACG-----VGEFRCDGSCIGNSSRCNQFVDCEDASD 2850
gi|62652278|ref|XP_243524.3| VNCS CRGGRILQEDFTCRAMNSS CRAQDEFECANGECISFSLT CDGVSHCKDKSDEKPSYCNRRCKKTFRCNNGRCVSNMLWCNGVDDCGDGSDEIPCNKTACG-----VGEFRCDGSCIGNSSRCNQFVDCEDASD 2850
gi|126012562|ref|NP_002323.2| VNCS CRGGRILQEDFTCRAVNSS CRAQDEFECANGECINFLSLT CDGVPHCKDKSDEKPSYCNRRCKKTFRCNNGRCVSNMLWCNGADDCGDGSDEIPCNKTACG-----VGEFRCDGTCIGNSSRCNQFVDCEDASD 2850
gi|73968460|ref|XP_538245.2| VNCS CRGGRILQEDFTCRAVNSS CRAQDEFECANGECINFLSLT CDGVSHCKDKSDEKPSYCNRRCKKTFRCNNGRCVSNMLWCNGADDCGDGSDEIPCNKTACG-----VGEFRCDGTCIGNSSRCNQFVDCEDASD 2850
gi|292627062|ref|XP_001920591.2| VNCS CRGERKLLGNTCVAENTT CNSVDEFECANGDCIDYSLT CDSLAKCKDKSDEKQAYCANRMCKKGYRRCINGRICIKHSWCSTLDDCGDGSDELPCNMTLCS-----AAEFCKDGS CITNSSRCNQFVDCEDASD 2850
gi|28573304|ref|NP_788284.1| ATCHCTQVLAADGRRICIAVNVN SCLSLSYNCHSGECIPLELT CDNVTHCADGSDEFRRYCFIFRCPEHFMCQNHRCIPKHKCDGEQCGDGSDEIPLLCKCQSEDDMHP SNNNTKEMPMFRCSGSECIPKFLCSLKDCKRFED 2850
gi|158300186|ref|XP_320185.4| VECHCTQVLAADGRRICIPKSVNCS SSESFECS TNGNCIPFHLT CDGVKNGLDSDDELVTFCAHRPCDGFRCNARRCIPKNGQCNHINQNGDGSDEVGCSCNN-----ATHFRCTDGCITVKS SMCRCYEPDCKDVED 2850



gi|124494256|ref|NP_032538.2| EMNCSATDCSSYFRLGVKGVLFOPCERTSLCYAPSWVCDGANDCGDYS DERDCPGVKRPRCPLNYFACPSGRCPIMSWTCDKEDDCENGE-----DETHCN-----KFCSEAOFECQNHRCISKQWLCDGSDDCGDGSDEAAHCEGKTCG 3000
gi|62652278|ref|XP_243524.3| EMNCSATDCSSYFRLGVKGVLFOPCERTSLCYAPSWVCDGANDCGDYS DERDCPGVKRPRCPLNYFACPSGRCPIMSWTCDKEDDCENGE-----DETHCN-----KFCSEAOFECQNHRCISKQWLCDGSDDCGDGSDEAAHCEGKTCG 3000
gi|126012562|ref|NP_002323.2| EMNCSATDCSSYFRLGVKGVLFOPCERTSLCYAPSWVCDGANDCGDYS DERDCPGVKRPRCPLNYFACPSGRCPIMSWTCDKEDDCENGE-----DETHCN-----KFCSEAOFECQNHRCISKQWLCDGSDDCGDGSDEAAHCEGKTCG 3000
gi|73968460|ref|XP_538245.2| EMNCSATDCSSYFRLGVKGVLFOPCERTSLCYAPSWVCDGANDCGDYS DERDCPGVKRPRCPLNYFACPSGRCPIMSWTCDKEDDCENGE-----DETHCN-----KFCSEAOFECQNHRCISKQWLCDGSDDCGDGSDEAAHCEGKTCG 3000
gi|292627062|ref|XP_001920591.2| EMNCSPTDCSSYLLGVKGMTFERCETLFCFAPSWRCDGSDNDCEFTSDERNCPKRRQKCSSENFACPSGRCPIMSWTCDKEDDCENGE-----DEAHCEKFFQFCASNQFECQNHRCIFKFTWVCDGSDDCGDGTDDESRCKAKTCG 3000
gi|28573304|ref|NP_788284.1| EKMCAPIP-CEKNDM-----TFVHCNASTICLMPWRWCDGDPDPTDRLD CANSTSLSCDPCGFRCLASNCIAGSWHCDGKEDDCDGS-----DEINRC-----TECRHNOFACDKT-----CIFASWQCDGSDGSDGSDGEPQPNRPR 3000
gi|158300186|ref|XP_320185.4| FICGPMRNCIEG-----FVNCANTIGCYMPWRWCDGSDNDCEFTSDERNCPKRRQKCSSENFACPSGRCPIMSWTCDKEDDCENGE-----DEAHCEKFFQFCASNQFECQNHRCIFKFTWVCDGSDDCGDGTDDESRCKAKTCG 3000



gi | 124494256 | ref | NP_032538.2 | PSSFSCPETHVCPERWLCDDGKDCADG--ADESVTAG----CLYNSTCDDREFMCONRLCIPKHFVCDHRRDCADGSDSEPECEYPTCGPNE-----FRCANGRCLSSRQWECGDGENDCHDHSDEAPKNPHCTSPHE 3150
gi | 62652278 | ref | XP_243524.3 | PSSFSCPETHVCPERWLCDDGKDCADG--ADESISAG----CLYNSTCDDREFMCONRLCIPKHFVCDHRRDCADGSDSEPECEYPTCGPNE-----FRCANGRCLSSRQWECGDGENDCHDHSDEAPKNPHCTSPHE 3150
gi | 126012562 | ref | NP_002323.2 | PSSFSCPETHVCPERWLCDDGKDCADG--ADESISAG----CLYNSTCDDREFMCONRLCIPKHFVCDHRRDCADGSDSEPECEYPTCGPNE-----FRCANGRCLSSRQWECGDGENDCHDHSDEAPKNPHCTSPHE 3150
gi | 73968460 | ref | XP_538245.2 | PSSFSCPETHVCPERWLCDDGKDCADG--ADESVTAG----CLYNSTCDDREFMCONRLCIPKHFVCDHRRDCADGSDSEPECEYPTCGPNE-----FRCANGRCLSSRQWECGDGENDCHDHSDEAPKNPHCTSPHE 3150
gi | 292627062 | ref | XP_001920591.2 | PDSFCQPGSHVCIILQRWVCDGDKDCPDG--GDEGLKAG----CVFVKTCDTTFEQONSCCIPKHFVCDHRRDCADGSDSEPECEYPTCGPND-----FHCANGCQLCKQKNWACDGFDRQDSEAPKNLQCDTSES 3150
gi | 28573304 | ref | NP_788284.1 | PHLFQCKSSGRICIPKQWVCDGKDCPSGLDGSDEDEGPGCGVAHIPCPPPAHLCTSGLCIDSHYVCDGEDPCGGDDEYEGCVPAFPQHPSCPGGE-----LMHQODGLCIFKN--QTCDGKPCDGDGSDETS--LCAHTRG 3150
gi | 158300186 | ref | XP_320185.4 | EEFQCPITNRCIPKQWVCDGVEVDCGATDDEMGDCDE----MMVNECDKTSFCKNGECISLHVCDGEQDCVDSDEPLYCKEGDGDYDEEGAGVDHLCVPEDFRCNNGRCIERN--LTCNVNDCADGSDEDI--LCRNTTL 3150
.....3010.....3020.....3030.....3040.....3050.....3060.....3070.....3080.....3090.....3100.....3110.....3120.....3130.....3140.....3150



gi | 124494256 | ref | NP_032538.2 | KCNASSQFLCSSGRCAVEALLCNGQDDCGDSDERGCHEVNECLARKLSGCSQDCEDLKIIGFKRCRPGFRLLK--DDGRTCADVDECSSTFP--CSQLCINTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 62652278 | ref | XP_243524.3 | KCNASSQFLCSSGRCAVEALLCNGQDDCGDSDERGCHEVNECLARKLSGCSQDCEDLKIIGFKRCRPGFRLLK--DDGRTCADVDECSSTFP--CSQLCINTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 126012562 | ref | NP_002323.2 | KCNASSQFLCSSGRCAVEALLCNGQDDCGDSDERGCHEVNECLARKLSGCSQDCEDLKIIGFKRCRPGFRLLK--DDGRTCADVDECSSTFP--CSQRCINTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 73968460 | ref | XP_538245.2 | KCNASSQFLCSSGRCAVEALLCNGQDDCGDSDERACHVNECLARKLSGCSQDCEDLKIIGFKRCRPGFRLLK--DDGRTCADVDECSSTFP--CSQRCINTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 292627062 | ref | XP_001920591.2 | RCNDT-AFLCSSGRCAVEALLCNGQDDCGDSDENNCVNECLNSKLSGCSQDCEDLKIIGFKRCRPGFRLLK--DDGRTCADVDECSSTFP--CSQRCINTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 28573304 | ref | NP_788284.1 | --CNGDDFRCKNGACIHADLLCDRRNDCAFDSDELGNVNEC--LIPDI CEHECEDKVVYQCHCRPGYKVLKPSPHLCIDIDECEQQP--CSQTCINTYGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
gi | 158300186 | ref | XP_320185.4 | IAGFDLFRCESSGACIISNMLCDGANDCGDWDEKSCQVNECE--MIPDLCAHECEDRPPVGVVGVCRKGRFRVNVNKKHLVDVDECEEQPRPCTGTCVNTHGSYKCLVGEYAPRGGDPHSCKAVTD--EEFFLIFANRYLRLKLNLDGS 3300
.....3160.....3170.....3180.....3190.....3200.....3210.....3220.....3230.....3240.....3250.....3260.....3270.....3280.....3290.....3300



gi | 124494256 | ref | NP_032538.2 | NYTLKQGLNNAVALDFDYREOMIYWDVTTQGSMIRRMHLN--GSNVQLHRTGLSNPDGLAVDWGGNLYWCDKGRDITIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLWTDWGDHSLIGRIGMDGSGRSIIIVDTKITWPNGL 3450
gi | 62652278 | ref | XP_243524.3 | NYTLKQGLNNAVALDFDYREOMIYWDVTTQGSMIRRMHLN--GSNVQLHRTGLSNPDGLAVDWGGNLYWCDKGRDITIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLWTDWGDHSLIGRIGMDGSGRSIIIVDTKITWPNGL 3450
gi | 126012562 | ref | NP_002323.2 | NYTLKQGLNNAVALDFDYREOMIYWDVTTQGSMIRRMHLN--GSNVQLHRTGLSNPDGLAVDWGGNLYWCDKGRDITIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLWTDWGDHSLIGRIGMDGSGRSIIIVDTKITWPNGL 3450
gi | 73968460 | ref | XP_538245.2 | NYTLKQGLNNAVALDFDYREOMIYWDVTTQGSMIRRMHLN--GSNVQLHRTGLSNPDGLAVDWGGNLYWCDKGRDITIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLWTDWGDHSLIGRIGMDGSGRSIIIVDTKITWPNGL 3450
gi | 292627062 | ref | XP_001920591.2 | NYTLKQGLNNAVALDYHVAEOMIYWDVTTQGSMIRRMHLN--GSNVQLHRTGLSNPDGLAVDWGGNLYWCDKGRDITIEVSKLNGAYRSVLVNSGLREPRAVAVDVRNGYLWTDWGDVPHIGRIGMDGSDRQIIIQDKITWPNGL 3450
gi | 28573304 | ref | NP_788284.1 | NGSILLINELSNVALDYDWDSCLYVSDVTVTGVTKRKYC--KENK-TTTLHOAMLNKPDGLAVDWVAKNLYWCDKGLDITIEVSKLNGAYRVLVSSGLREPRALVVDVQNGYLWTDWGDSPHIGRIGMDGSGRSIIIVDTKITWPNGL 3450
gi | 158300186 | ref | XP_320185.4 | GMTILAHNLNATITLDFDWDKDECYVNSDVTTRVTIVKRMCESEENRPFVEIHRITNLKPEGLAVDWGRNLYWCDKGLDITIEVSKLNGAYRVLVSSGLREPRALVVDVQNGYLWTDWGDSPHIGRIGMDGSGRSIIIVDTKITWPNGL 3450
.....3310.....3320.....3330.....3340.....3350.....3360.....3370.....3380.....3390.....3400.....3410.....3420.....3430.....3440.....3450



gi | 124494256 | ref | NP_032538.2 | TVDVYTERIYWADAREDYIEFASLDGNSNRHVLS-----QDIPHIFALTLFEDYVYWDWETKSIINRAHKTGTGANKTLLISTLHRPMDLHVHFHALRQPD--VPNHPCQVNNGGCSNLCLLSPG--GGHKACPTNFYLGSDGRTCVSNCTA 3600
gi | 62652278 | ref | XP_243524.3 | TVDVYTERIYWADAREDYIEFASLDGNSNRHVLS-----QDIPHIFALTLFEDYVYWDWETKSIINRAHKTGTGANKTLLISTLHRPMDLHVHFHALRQPD--VPNHPCQVNNGGCSNLCLLSPG--GGHKACPTNFYLGSDGRTCVSNCTA 3600
gi | 126012562 | ref | NP_002323.2 | TVDVYTERIYWADAREDYIEFASLDGNSNRHVLS-----QDIPHIFALTLFEDYVYWDWETKSIINRAHKTGTGANKTLLISTLHRPMDLHVHFHALRQPD--VPNHPCQVNNGGCSNLCLLSPG--GGHKACPTNFYLGSDGRTCVSNCTA 3600
gi | 73968460 | ref | XP_538245.2 | TVDVYTERIYWADAREDYIEFASLDGNSNRHVLS-----QDIPHIFALTLFEDYVYWDWETKSIINRAHKTGTGANKTLLISTLHRPMDLHVHFHALRQPD--VPNHPCQVNNGGCSNLCLLSPG--GGHKACPTNFYLGSDGRTCVSNCTA 3600
gi | 292627062 | ref | XP_001920591.2 | TLDVFINDRIYWADAREDYIAFASLDGNSNRHTVNLN--HDIPHIFAMILFEEFYIYWDWETKSIINRAHKTGTGANKTLLISTLHRPMDIHFHFPSRQPE--VSGHPQEDNNGCSNLCLLSPG--GGYKACPTNFYLAADGKQCLSNCTA 3600
gi | 28573304 | ref | NP_788284.1 | TISFEIQLFWDAREDTISVSDLDGNHTRLLLARSLINPLNLNHHIFAIYAVWEGHYIYWDWETKSIIEYCSIFNGQNCETLITLTHRPMDLHVHFHYRQPPMSGNPCLAA--CSTLCVLSPEEFPYKCMCPNFILADDGRTCRANCTA 3600
gi | 158300186 | ref | XP_320185.4 | TISFEINLFWGDAREDYIAVSDLDGQVRIILSRARQPLNHLHHVFAIYAVWEDRIYSDLDKSIIEYCHFRGDDCGGLINLTHRPMDIRVFHYRQPPMSGNPCLAA--CSTLCVLSPEEFPYKCMCPNFILADDGRTCRANCTA 3600
.....3460.....3470.....3480.....3490.....3500.....3510.....3520.....3530.....3540.....3550.....3560.....3570.....3580.....3590.....3600



gi | 124494256 | ref | NP_032538.2 | SQFVCKND--KCIPIFWKCDTEDDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----NTNRCIPGIFRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
gi | 62652278 | ref | XP_243524.3 | SQFVCKND--KCIPIFWKCDTEDDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----NTNRCIPGIFRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
gi | 126012562 | ref | NP_002323.2 | SQFVCKND--KCIPIFWKCDTEDDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----NTNRCIPGIFRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
gi | 73968460 | ref | XP_538245.2 | SQFVCKND--KCIPIFWKCDTEDDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----NTNRCIPGIFRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
gi | 292627062 | ref | XP_001920591.2 | SQFVCKND--KCIPIFWKCDTEDDCGDSDDEPDCPEFKCRPGQFCSTGLCTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----HPSRCIPGILLRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
gi | 28573304 | ref | NP_788284.1 | AHFEQVNTYKCIPIFYWRCDTEDDCGDSDDEPDCPEFKCRPGQFCSTGLCTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----ATAA--SFAFCVNVKRCQGVKDCPGEDESACTEPVCKKDFQCGNN--RCMPFVWCDGIDIC 3750
gi | 158300186 | ref | XP_320185.4 | AHFCRTTFKCIPIFYWRCDTEDDCGDSDDEPDCPEFKCRPGQFCSTGLCTNPAFICDGDNDQDSDNDEANCDIHVCLPSQFKC-----HPSRCIPGILLRCNGQDNCDDGDEDERDCPEVTCAPNOFQCSITKRCIPRVVWCDRDND 3750
.....3610.....3620.....3630.....3640.....3650.....3660.....3670.....3680.....3690.....3700.....3710.....3720.....3730.....3740.....3750



gi |124494256|ref|NP_032538.2|
gi |62652278|ref|XP_243524.3|
gi |126012562|ref|NP_002323.2|
gi |73968460|ref|XP_538245.2|
gi |292627062|ref|XP_001920591.2|
gi |28573304|ref|NP_788284.1|
gi |158300186|ref|XP_320185.4|

-----PVCTCP-----NGKRLDNGTCVVPVSPPT-----PPPDAPRPGTCTLQCFNNGSCFLNARR--PKRCOPRYTGDKCGLDCEWYC 4650
-----PVCTCP-----NGKRLDNGTCVVPVSPPT-----PPPDAPRPGTCTLQCFNNGSCFLNARR--PKRCOPRYTGDKCGLDCEWYC 4650
-----PVCTCP-----NGKRLDNGTCVVPVSPPT-----PPPDAPRPGTCTLQCFNNGSCFLNARR--PKRCOPRYTGDKCGLDCEWYC 4650
-----PVCTCP-----NGKRLDNGTCVVPVSPPT-----PPPDAPRPGTCTLQCFNNGSCFLNARR--PKRCOPRYTGDKCGLDCEWYC 4650
-----PVCTCP-----NDHVPDNGTCVKVQPPD-----QPFPSF---TCDLQCFNNGSCFLNARR--PKRCOPRYTGDKCGLDCEWYC 4650
AEG---VVMDDGVCKAHADIP---DYCPLQCNLGTCKI-VDHVPKICQPFEGELCEHYRCSGYCQNYGVCVAPALPGSQEPPPLKCTCHAGWSGARCETSMACQSRCHNGGCLISETEG--MKSCPKMFTGEOCEHCRLNIT-C 4650
PDAARPRIVFDERGEVKECLDLPAQAPECKLHCNNGTCFTIDGQKQKCSASFDGVCYCHYICSGYCKNKGFCELVNGEP-----DCTCLPQWTKRCKDISTNKCQRYCHNGGNCILVQRDGGSLSCSPVGYTGEQCEHCNLR-C 4650
.....4510.....4520.....4530.....4540.....4550.....4560.....4570.....4580.....4590.....4600.....4610.....4620.....4630.....4640.....4650



gi |124494256|ref|NP_032538.2|
gi |62652278|ref|XP_243524.3|
gi |126012562|ref|NP_002323.2|
gi |73968460|ref|XP_538245.2|
gi |292627062|ref|XP_001920591.2|
gi |28573304|ref|NP_788284.1|
gi |158300186|ref|XP_320185.4|

HNNGTCAASP*GMP*TCRCPTGFTGPKCTAQV*GAGYCSNNS*CTVNOGNQ*PQCRCLPGFLGDRCOYR*CSGFCE*FGT*QMAADGSR*CRCT*YFEG*PRCEV*NKCSRL-----GACV*VNK*ITGD 4800
HNNGTCAASP*GMP*TCRCPTGFTGPKCTAQV*GAGYCANNS*CTVNOGNQ*PQCRCLPGFLGDRCOYR*CSGFCE*FGT*QMAADGSR*CRCT*YFEG*PRCEV*NKCSRL-----GACV*VNK*ITGD 4800
RNNGTCAASP*GMP*TCRCPTGFTGPKCTAQV*GAGYCANNS*CTVNOGNQ*PQCRCLPGFLGDRCOYR*CSGFCE*FGT*QMAADGSR*CRCT*YFEG*PRCEV*NKCSRL-----EGACV*VNK*ITGD 4800
RNNGTCAASP*GMP*TCRCPTGFTGPKCTAQV*GAGYCANNS*CTVNOGNQ*PQCRCLPGFLGDRCOYR*CSGFCE*FGT*QMAADGSR*CRCT*YFEG*PRCEV*NKCSRL-----DGACV*VNK*ITGD 4800
QNRG*CS*PSR*GAP*TCRC*Q*GFT*GPK*CNLYI*ENY*Q*NGNC*AV*SL*NO*PT*CR*CP*PG*FL*GD*Q*COYR*CED*FCK*ID*GO*CLE*LN*NG*TK*HC*Q*SD*K*FF*GP*Q*CE*LD*K*EY*CG-----TGK*CEK*-L*ITG 4800
ENGGICRE*TL*G*TP*Q*CE*PD*G*FT*G*K*RC*E*ID*E*CA*DF*CK*NG*G*CV*IS*TK*GR*Q*CR*CP*SG*Y*F*GE*HC*ES*NS*CR*DF*CR*NG*G*CS*ER*-GG*RL*SC*TP*PR*Y*IG*ES*CE*SD*LC*TK*ES*--P*HF*CD*NT*IK*V*PR-----D*P*CL*ML*TI*Q*NA*G*TC*HI*IK*GV 4800
ENGGVCR*KT*IT*DR*SQ*CL*CA*EG*Y*V*GR*N*CE*KN*V*CT*EF*CE*NG*GE*CT*IER*-GA*AK*CS*CP*EN*TY*G*ER*CO*LR*Q*CAD*LR*NG*GD*CV*P*--G*ER*PY*CK*CR*Q*G*Y*EG*PY*CE*HD*LC*EL*PE*GI*RP*SY*CS*TI*IR*PT*TE*PE*AH*PF*SS*SS*CG*SY*SC*NN*GG*H*CL*EV*RG*K 4800
.....4660.....4670.....4680.....4690.....4700.....4710.....4720.....4730.....4740.....4750.....4760.....4770.....4780.....4790.....4800



gi |124494256|ref|NP_032538.2|
gi |62652278|ref|XP_243524.3|
gi |126012562|ref|NP_002323.2|
gi |73968460|ref|XP_538245.2|
gi |292627062|ref|XP_001920591.2|
gi |28573304|ref|NP_788284.1|
gi |158300186|ref|XP_320185.4|

V*TCNCTDGRV*AP*SL*CL*-----C*ID*H*CS*NG*G*SC*TM*NS*-----K*MM*PE*CC*P*P*H*MT*G*PR*CE*EQ*-----V*VS*Q*Q*Q*P*--G*H*MA*S*IL*IP*-L*LL*LL*LL*LL*LV*AG*V*V*F*W*Y*K*RR*V*RG*AK*GF 4950
V*TCNCTDGRV*AP*SL*CL*-----C*ID*H*CS*NG*G*SC*TM*NS*-----K*MM*PE*CC*P*P*H*MT*G*PR*CE*EQ*-----V*VS*Q*Q*Q*P*--G*H*MA*S*IL*IP*-L*LL*LL*LL*LL*LV*AG*V*V*F*W*Y*K*RR*V*RG*AK*GF 4950
V*TCNCTDGRV*AP*SL*CL*-----C*V*G*H*CS*NG*G*SC*TM*NS*-----K*MM*PE*CC*P*P*H*MT*G*PR*CE*EQ*-----V*VS*Q*Q*Q*P*--G*H*MA*S*IL*IP*-L*LL*LL*LL*LL*LV*AG*V*V*F*W*Y*K*RR*V*RG*AK*GF 4950
V*TCNCTDGRV*AP*SL*CL*-----C*V*G*H*CS*NG*G*SC*TM*NS*-----K*MM*PE*CC*P*P*H*MT*G*PR*CE*EQ*-----V*VS*Q*Q*Q*P*--G*H*MA*S*IL*IP*-L*LL*LL*LL*LL*LV*AG*V*V*F*W*Y*K*RR*V*RG*AK*GF 4950
I*TC*KA*DN*TK*RP*CY*-----C*DD*F*CI*EG*Q*CS*VD*TY*-----T*NL*P*Q*CR*CH*TW*G*FR*CE*LN*-----V*AP*V*NS*DS*GN*IP*SV*V*IP*V*ML*LL*LL*LL*LV*VA*IL*W*Y*K*RR*MR*G*AK*GF 4950
A*LC*NC*TD*Q*W*NG*DL*CT*LP*V*DD*NP*CA*RY*CA*NG*GV*CH*LD*-----Y*RL*P*HC*SI*GE*W*Q*NA*CE*MP*PH*CV*G*G*EC*V*CR*P*G*SS*IN*EC*LC*EN*NR*V*-V*P*CL*SD*SA*DA*LK*KE*Q*E*PT*ES*GG*V*F*SV*V*LV*LV*AV*LL*V*F*AL*F*AG*AV*Y*FL*KK*H*RI*AO*PF 4950
P*IC*NC*IT*MQ*YA*GE*HC*EN*V*MY*LP*CN*RY*CM*NN*GI*QL*DL*G*FF*SS*NV*TY*IP*SC*V*IG*EW*TK*HK*CD*LP*PR*CV*G*EC*GT*CI*EG*SS*IN*EC*LC*DD*NP*V*P*V*P*CO*Q*VV*LS*EL*ER*ME*SN*DS*SY*TL*SV*LA*IA*LF*V*IL*VA*AG*FG*CT*TY*GL*RR*RT*G*OP*F 4950
.....4810.....4820.....4830.....4840.....4850.....4860.....4870.....4880.....4890.....4900.....4910.....4920.....4930.....4940.....4950



gi |124494256|ref|NP_032538.2|
gi |62652278|ref|XP_243524.3|
gi |126012562|ref|NP_002323.2|
gi |73968460|ref|XP_538245.2|
gi |292627062|ref|XP_001920591.2|
gi |28573304|ref|NP_788284.1|
gi |158300186|ref|XP_320185.4|

Q*H*OR*MT*G*AM*N*VE*IG*N*P*TY*K*MY*EG*GE*P*DD*V*G*LL*DA*F*AL*DP*DK*PT*NF*TN*PV*YA*TL*Y*MG*G*HG*G*-----R*H*SL*AS*TD*EK*RE*LL*GR*GP*E*DE*IG*DP*LA 5056
Q*H*OR*MT*G*AM*N*VE*IG*N*P*TY*K*MY*EG*GE*P*DD*V*G*LL*DA*F*AL*DP*DK*PT*NF*TN*PV*YA*TL*Y*MG*G*HG*G*-----R*H*SL*AS*TD*EK*RE*LL*GR*GP*E*DE*IG*DP*LA 5056
Q*H*OR*MT*G*AM*N*VE*IG*N*P*TY*K*MY*EG*GE*P*DD*V*G*LL*DA*F*AL*DP*DK*PT*NF*TN*PV*YA*TL*Y*MG*G*HG*G*-----R*H*SL*AS*TD*EK*RE*LL*GR*GP*E*DE*IG*DP*LA 5056
Q*H*OR*MT*G*AM*N*VE*IG*N*P*TY*K*MY*EG*GE*P*DD*V*G*LL*DA*F*AL*DP*DK*PT*NF*TN*PV*YA*TL*Y*MG*G*HG*G*-----R*H*SL*AS*TD*EK*RE*LL*GR*GP*E*DE*IG*DP*LA 5056
Q*H*OR*MT*G*AM*N*VE*IG*N*P*AY*K*I*Y*EG*GE*P*DD*AG*LL*DS*FT*LD*P*DK*PT*NF*TN*PV*YA*TL*Y*MG*G*AN*NS*-----R*NS*LA*ST*DE*KK*EL*LS*AG*-D*DD*MG*DP*LA 5056
S*H*AR*LT*D*---N*VE*IM*L*-T*NA*MY*RG*DA*DE*-----A*PT*FA*SE*DD*DK*-G*NF*AN*PV*VE*SM*Y*AD*AI*PE*P*V*ST*-----E*TI*HS*AP*DE*KK*GL*LL*Q*HT*D*EN*TP*DP*IL 5056
L*H*AR*LT*D*---N*VE*IT*---N*PM*Y*LG*DA*DE*-----G*PA*F*V*H*ED*DK*-V*H*FG*NP*V*VE*Q*MY*AG*SV*NV*H*ED*SS*TI*AG*NS*AH*PL*LT*TS*SA*PE*KK*GL*LL*Q*H*P*ED*TA*AD*LL 5056
.....4960.....4970.....4980.....4990.....5000.....5010.....5020.....5030.....5040.....5050

