

gi | 189531926 | ref | XP_699686.3 |-ITGSKTYITIVSVVNIQPEAPRFKPAVKVITISBESTVILNKVITNVAADISDTMLIATNVRVYAKGGDNDNLIDIEKADIRLNKIPDYESVFL 750
gi | 125832294 | ref | XP_688512.2 | GSGGGGAGSGAAGGAGAMGGAS-----GSGGGTGAESWSSGVLVNVNIVKVNQEPGPKFPPTKAIPISE-GKAFDSTELIARYPAIDTDTGKEATNVKVIKSSDPDNWLTIDEKTAIRMNKAPDRESKYL 750
gi | 189533450 | ref | XP_001919999.1 | GAIAGAGQSGSSGASGQSGASG-----AGSOLMPFGSSNPGFNVS-----KLLKSLVNVNKNKPDAPKMPKVKPISE-NKINSIPRVIDTYTATBEDTGRPAENVKYAKGYDDPNWISIDVDTAETKLNKAPDRESFPV 750
gi | 189533588 | ref | XP_699916.3 | AGMDAGGDVGLKPGVNPAGKPGPSLGVKPGPKPGKPGTKPGTSPSGKPVSDPDKKPAKGGVYKIVISVNNLDPGPGFSPVKVDFPVSE-DPNEDEFPVLTGTFALDGDGTGEPANVRYAKGDDPNWITIDEETAEIKLNKAPDRESKYL 750
gi | 116534898 | ref | NP_001934.2 | -----KYKPTPIPIKVKVKNVKEGIHFKSSVISIYVSEMDRSSKGOIIGNFOAFDEDTG-LPAHARYVKLEDRDNWISVDSVTSSEIKLAKLPDFESRYV 750
gi | 114672785 | ref | XP_512079.2 | -----KYKPTPIPIKVKVKNVKEGIHFKSSVISIYVSEMDRSSKGOIIGNFOAFDEDTG-LPAHARYVKLEDRDNWISVDSVTSSEIKLAKLPDFESRYV 750
gi | 73961765 | ref | XP_547622.2 | -----KYKPTPIPIKVKVKNVKEGIHFKSSVISIYVSEMDRSSKGOIIGNFOAFDEDTG-QAARVYKAKLEDIDNWNISVDSVTSSEIKLAKLPDFESRYV 750
gi | 114672785 | ref | XP_512079.2 | -----KYKATPIPIITVKVKNVVEGIHFKSSVVSFRASEAMDSSLSRIGKFOVDFEETG-QAAKVTYVKVQDIDNWNISVDSVTSSEIKLVKIPDFESRYV 750
gi | 109506355 | ref | XP_226112.4 | -----KYKATPIPIITVKVKNVVEGIHFKSSVVSFRASEAMDSSLSRIGKFOVDFEETG-KAADVTYVKVQDIDNWNISVDSVTSSEIKLVKIPDFESRYV 750
gi | 194678057 | ref | XP_584890.4 | -----KYKPTPIPIKVKVKNVKEGIHFKSSVISIYVSEMDRSSKGOIIGNFOAFDEDTG-KVPNVKYAKFEDIDNWNISVDSVTSSEIKLVKIPDFESRYV 750
gi | 118086934 | ref | XP_426083.2 | -----SYKAQTPIPIRIHVIVDVRGPGVPGGKTIIEASEVVR-VNVOVIGQVQAIQDDETKGAHVHKKYIKGRDPAWNIINANSIETQLAKNLIDYESVFL 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 189531926 | ref | XP_699686.3 | KNYTYAHILCIINETPAKTATGTIAIQVKDFNDHCPVLIHQSQKLCYEHVVFVVAEDKDHFPNAHPPFGKVNTK--HMKESWSVEHNDAAAFRSQETLWPGVYHLSVDVWDDQGRKVC-AOLLVVEVCMGAEKVCLPVTV---- 900
gi | 125832294 | ref | XP_688512.2 | VNGTYAKVLSITQDPLSKTATGTIAIQVEDFNDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 189533450 | ref | XP_001919999.1 | VNGTYAKVLSITQDPLSKTATGTIAIQVEDFNDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 189533588 | ref | XP_699916.3 | VNGTYFAKIIICMTQDVPKATATGTIAIKVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 116534898 | ref | NP_001934.2 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 114672785 | ref | XP_512079.2 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 73961765 | ref | XP_547622.2 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 114672785 | ref | XP_512079.2 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 73961765 | ref | XP_547622.2 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 109506355 | ref | XP_226112.4 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 194678057 | ref | XP_584890.4 | QNGTYTVKIVVAISVDYPRKTIITGTIVLINVEDINDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
gi | 118086934 | ref | XP_426083.2 | VNGTYTFTMLGVITDLEPKTIITGTIVVHILQDENDHCPVLIHNSVQTLCTDKDAVLVIAKDEDAAPPAGPFDNFVSE--GTAGKWTVEYMNDTIAFRTRHEKRLWPGHELMVEVTDQGLKCPPEKLVVDVCTCKNQGDDRATGDAKK 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi | 189531926 | ref | XP_699686.3 | VSRFGGSGVLLMLLGLLLLLLPLLLLLFLCAGAAAG-DFKAIPTFAKEHLIAYNTEGQGEDKGMALLHMSKDENTR--LNVGTV-----GGAQKQDGDGDGAVTAGGSHWSFYHYDQFNNAAYHHHRDRIDGDF 1050
gi | 125832294 | ref | XP_688512.2 | GSRLLGPAIGLGLLLGLLALLLPLLLLLLCTCGMT--G-AFDMDFEAKVHLISSNTEGQGEDKDRVPLMCPSSVNDGGMFTKDYM-----AVGAMHSAGLGLGVGAVGAAGFLESSTMGGRGYN---EMELDY 1050
gi | 189533450 | ref | XP_001919999.1 | PLMWPPNL----- 1050
gi | 189533588 | ref | XP_699916.3 | PLKIKGPAIGLGLLGAALLLLVPLLLLLCQCCTV--N-EFTDLPFAKEYLIPIYHTEGIGE----- 1050
gi | 116534898 | ref | NP_001934.2 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGKGA--GFTPIPG-TIEMLPWNNEGAPPEDKVVPSFLPVDQGGSLVGRNG-----VGGMAKEAMKGGSSASIVKGOHEMSEMDGRWEHRSLLSGRATQFTGAGAIMTTE 1050
gi | 114672785 | ref | XP_512079.2 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGKGA--GFTPIPG-TIEMLPWNNEGAPPEDKVVPSFLPVDQGGSLVGRNG-----VGGMAKEAMKGGSSASIVKGOHEMSEMDGRWEHRSLLSGRATQFTGAGAIMTTE 1050
gi | 73961765 | ref | XP_547622.2 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGEGAK--GFTPIPG-TIEMLPWNNEGAPPEDKVVPLHLTADHGESVAADR-----LGVVTTKETTKESSA-LIKDHHEMSEMDGRWEHRSLLSGGVTVGTGANTGAEA 1050
gi | 22779879 | ref | NP_031909.1 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGGGAK--GFTPIPG-TIEMLPWNNEGAPPEDKVVPSLLVADHAESSAVRGG-----VGGAMKREGMKGGSSASIVKGOHEMSEMDGRWEHRSLLSGRATQFTGAGAIMTTE 1050
gi | 109506355 | ref | XP_226112.4 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGEGAK--GFTPIPG-TIEMLPWNNEGAPPEDKVVPSLLVTDHVENSGVRGGGGGGGGVGVKLEKGVN--SSASITKGOHELIEVDGRWEHRSLLSGLTHHVAAGSIAAND 1050
gi | 194678057 | ref | XP_584890.4 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGKGA--GFTPIPG-TIEMLPWNNEGAPPEDKVVPLPGLADVRDGAAVGAGAG-----GGVTAKEAIVKGGSSASIVKGOHEMSEMDGRWEHRSLLSGGATQFTGAGAIMTTE 1050
gi | 118086934 | ref | XP_426083.2 | VVGLGPAAIALMILAFLLLLLPLLLLLCHCGSGAK--KGFATIPDCSEITLRKWNSEGAVPEEKAAT-----GRAEGMISEGNVVGGGVAMESIG----- 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 189531926 | ref | XP_699686.3 | MYAQ-RKDEHSRFENYNAFDGLALSDAFLGNYSQKSSHVAQKQ--ALGDNLVVVEYEQESRAGSFEDICSLMHEEDLAFDNLDMKFKTLAELICSGSTIQRES----INVSKKTESKDLVSVQETSNLQSQEKKSTILAGSV 1200
gi | 125832294 | ref | XP_688512.2 | MNSIGRNNAYSRDMAGDFDGMALSDGYLCEYSQKSRVVDGF--GK-DDPMVVDYEGKSPVSGVGC--CSLLEDNDLEFLNDLGPKFTLADICGGKKEIAPAPAPLPPPPKPVDRSEVSVSTNINLNG--NIATNRVNTVN 1200
gi | 189533450 | ref | XP_001919999.1 | -----DNKGGCEMSN-----GHLR-MVSAAMSKIIVDTMGLASS-----NQAVHTS-----SKMDGIVQESFEGGYIDDDVECTGRFQELE 1200
gi | 189533588 | ref | XP_699916.3 | -----DKKASAAANP-----PLADGLLVVEYVQGGSPAGSLG--CSLLEDNDLEFLNDLGSKFKTLAELICSGSTIQRES----INVSKKTESKDLVSVQETSNLQSQEKKSTILAGSV 1200
gi | 116534898 | ref | NP_001934.2 | TK-TARATGASRDMAGAAQAAVALNVEEFLRNVTDKAASYTEEDENHTAKDCLLVYSQDETESLNASIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 114672785 | ref | XP_512079.2 | TK-TARATGASRDMAGAAQAAVALNVEEFLRNVTDKAASYTEEDENHTAKDCLLVYSQDETESLNASIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 73961765 | ref | XP_547622.2 | LR-IKATGASRDLGAAQAAVALNVEEFLRSYFTEKAASYTEEDDIHTGKDCLLVYSQEDTASLHGSIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 22779879 | ref | NP_031909.1 | VR--FRATGASRDMAGAAQAAVALNVEEFLRSYFTEKAASYTEEDDIHTGKDCLLVYSQEDTASLHGSIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 109506355 | ref | XP_226112.4 | IRTTRATGASRDMAGAAQAAVALNVEEFLRSYFTEKAASYTEEDDIHTGKDCLLVYSQEDTASLHGSIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 194678057 | ref | XP_584890.4 | FR-TTRATGAAREVAGARAGAVAVNVEEFLRSYFTEKAASYTEEDDIHTGKDCLLVYSQEDTASLHGSIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
gi | 118086934 | ref | XP_426083.2 | -----AMNEEFLRVDYDKAVSYFAEEDAQAARDCLLVYSQEDTASLHGSIG--CSFIEGELDDFLDDLGLKFKTLAELVCLGKIDINMEIBOROKPATETSMNASHSLYEGTMVNSENTYSSGSPFPVK 1200
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



| | | | | | |
|----|-----------|-----|----------------|---|------|
| gi | 189531926 | ref | XP_699686.3 | QSSNMQQTSQEKKSTIIAGSI-----NQSSSLQHASTGVVLOEQVML-----PNTILLVQQPALYY-----APAAPVYVVEP-----HPTVLVASC---QVLG---HOENQK-----RPKNAKH | 1350 |
| gi | 125832294 | ref | XP_688512.2 | VASNMATASSRVENVLVLDNR-----PTMITSVQAPATLLVQPPMYVMVEQPPSTVLVAERPAMTGMVVLNSGPVABGMVVQGGN---LAANTLIRGERMVLVDRGGPAQALNNGMLHTSNLSCGQLLLVDGGATSGQVLQGTIQRG | 1350 |
| gi | 189533450 | ref | XP_001919999.1 | VSQNAILQD-----YLMQKSRV-----ISLDDSPGEAITSYDVEG-----NGSIAGSIGSCSYRPGG---YFVSMSTMGMNFVSMPT-----QVATQVNNNSQVLVN-----A | 1350 |
| gi | 189533588 | ref | XP_699916.3 | LAPQVQVQS-----SVTKVETV-----NTFATLPTASQVYVVEQQPLFYFVVEEQMPNISFVESPTQGL---FVINGNHGMEGLILQDG-----KISORQQQAMVLVNG-----AA | 1350 |
| gi | 116534898 | ref | NP_001934.2 | SLQEANAQKVTQEIIVTERSVSS-RQAKVATPLPDPMASRNVIAETSYVTGSTMPPPTIVILGSPSQPSLIVTERVYAPASTLVDC-----PYANEGTVVVTERVIOPHGGGNSPLEGTOHLQDVPVVMVRERESFLAPSSGVQPTLAMPN | 1350 |
| gi | 114672785 | ref | XP_512079.2 | SLQEANAQKVTQEIIVTERSVSS-RQAKVATPLPDPMASRNVIAETSYVTGSTMPPPTIVILGSPSQPSLIVTERVYAPASTLVDC-----PYANEGTVVVTERVIOPHGGGNSPLEGTOHLQDAPVVMVRERESFLAPSSGVQPTLAMPN | 1350 |
| gi | 73961765 | ref | XP_547622.2 | PLDEANAQKVTQEIIVTERSVSS-RQGHKVALLLPDLASGNVIVTETSYSYGTGSTMPPSTVVLGPGQSSALIVTERVYAPAPLVEG-----RYANDTNVMVTETIIQPNGGFPGLPGLTQHLPCRIVVVRERESFLAPSSGAQPTLAMPN | 1350 |
| gi | 22779879 | ref | NP_031909.1 | PLREVTQKVTQEIIVTERSVSS-RQSKVVPVPP-FDPVVASGNIIVTETSYSYAKGSAVPPSTVLLAPRQPSLIVTERVYAPASTLVDC-----HYANEKVLVTERVIOPNGGIPKPLEVTOHLKDAQVVMVRERESILAPSSGVQPTLAMPN | 1350 |
| gi | 109506355 | ref | XP_226112.4 | PLHGAHTEKVTQEVVTERSVSS-RQSKVVPVPP-PNPVASGNIIVTETSYSYAKGSAVPPSTVLLAPRQPSLIVTERVYAPASTLVDC-----HYANEKVLVTERVIOPNGGIPKPLEVTOHLNDAQVVMVRERESILAPSSGVQPTLAMPN | 1350 |
| gi | 194678057 | ref | XP_584890.4 | PLHGAHTEKVTQEVVTERSVSS-RQSKVVPVPP-PNPVASGNIIVTETSYSYAKGSAVPPSTVLLAPRQPSLIVTERVYAPASTLVDC-----HYANEKVLVTERVIOPNGGIPKPLEVTOHLNDAQVVMVRERESILAPSSGVQPTLAMPN | 1350 |
| gi | 118086934 | ref | XP_426083.2 | AGGAVGSEAVSDEVIMET-TSSLQSGCHDARTLTPPETNVTMTET-VSGGGPTCSAASFLLDPQFKENIVVTERVLAPASGLREMVETIPLSPSGKNMVTTERMLTSEGPGVG-TMAVQDLPNSKVVVVRERERVLVPSST-EDGSLSFPT | 1350 |
| | | | |1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350 | |



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|----|-----------|-----|----------------|---|------|
| gi | 189531926 | ref | XP_699686.3 | ETHYQSLVYVEEQ--QPLRESQGS-ISGAVHMVNIEIMQSTEGHGVR-----ETRPARRVMEEVREVERVDSLHLRVPMSL--- | 1448 |
| gi | 125832294 | ref | XP_688512.2 | VAGSQCLMFVDGQGGQVIQGSINNGISTEGGSQNVFYVENKGGSSVVQGLQMGKASTAGSLIGDVGIGGSVKIITQNPSSHKVVVQERKVVITQSVK | 1448 |
| gi | 189533450 | ref | XP_001919999.1 | LGSN---ILSREGGECRLANGPFFVEGPPAS-----GGNLWVS-----GPGQYFVSLGAGTPNLLE--- | 1448 |
| gi | 189533588 | ref | XP_699916.3 | VAANQPIQFQTEGQEQEGLGFLSLSLSSPIGSHKGVVLMQTHFQGKAVQG-----DAGRSPAKLEKQNKKLLSLSLKS--- | 1448 |
| gi | 116534898 | ref | NP_001934.2 | IAVG-QNVTVTERVLAPASTLQSSYQIPENEMTARNITVSGAGVPGPLPDFGLEESGHSN-----SITITSSSTRVTKHSTVQHSYS--- | 1448 |
| gi | 114672785 | ref | XP_512079.2 | IAVG-QNVTVTERVLAPASTLQSSYQIPENEMKARNITVSGAGVPGPLPDFGLEESGHSN-----SITITSSSTRVTKHSTVQHSYS--- | 1448 |
| gi | 73961765 | ref | XP_547622.2 | VAVG-QNMTVTERVQTPAS---SYWIPACTVMARKTEVSGAGVGRPLPNCLEESGHSNEMLIGHNSNTLTAASSTRVSKHSIVQHSYS--- | 1448 |
| gi | 22779879 | ref | NP_031909.1 | VAAAGGNVTVTERILTFASTLQSSYQIPSETITARNITVLSVSGSIGPLPNLDLEESDRPN-----SITITSSSTRVTKHSTMQHSYS--- | 1448 |
| gi | 109506355 | ref | XP_226112.4 | VAAAGGNVTVTERVLTFASTLQSSYQIPSEASIKARKITVLSVSGGMGPLPNLDLEESGPPN-----SITITSSSTRVTKHSTVQHSYS--- | 1448 |
| gi | 194678057 | ref | XP_584890.4 | VALG-QNVTVTERVLTFASTLQSSYQIPSETVMSRKITVLSAAGVPGSLPDSGLEESSHSN-----YITITSSSTRVSKQSTVQHSYS--- | 1448 |
| gi | 118086934 | ref | XP_426083.2 | LEFG-QSMVVNENDLTASAGPRAEQVLLITDLSLSC---SGSAMEGAPPAS-----SITLKSRS-RVTKYSTVQYSRS--- | 1448 |
| | | | |1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440..... | |

