

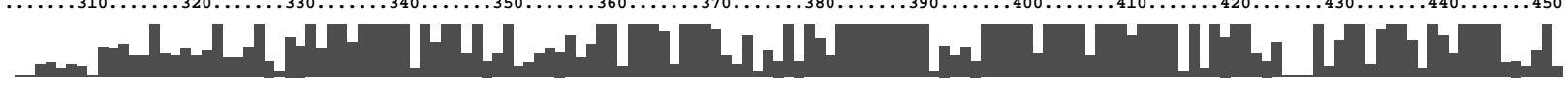
gi | 24583650 | ref | NP_523544.2 | ... MSEYKYLEGGFSGHFSSEDERYPNSLVPVGNSSPQVCPYKLYAEOLSSGSAFAPRTEIMRTWLYRKLPSAAHLFFQPFKGAEY-FEQN- WDEQPPNFNQLRWK 150
gi | 158298465 | ref | XP_318638.4 | ... MPEYQYLSGFGSHFSSEDARFPNALPVGNSPQKCPHGLYAEOLSSGSAFAPRTEIMRTRSWLYRIRPSVHQPFRKFEQVAF-FLRGTG WDEQHPNPNQMRWN 150
gi | 7549763 | ref | NP_038575.1 | ... MAELKYISGFGNECASDDPRCPGSLPKGQNNPQVCPYNLYAEOLSSGSAFAPRNTNKRSLWYRILPVSVSHKPFESIDQG-HVTHN WDEVGPPDNQLRWK 150
gi | 58865860 | ref | NP_001012145.1 | ... MAELKYISGFGNECASDDPRCPGSLPKGQNNPQVCPYNLYAEOLSSGSAFAPRNTNKRSLWYRILPVSVSHKPFESIDQG-HINHN WDEVGPPDNQLRWK 150
gi | 115527117 | ref | NP_000178.2 | ... MAELKYISGFGNECASDDPRCPGSLPEGQNNPQVCPYNLYAEOLSSGSAFAPRSTNKRSLWYRILPVSVSHKPFESIDQG-QVTHN WDEVDPPDNQLRWK 150
gi | 114588728 | ref | XP_516674.2 | ... MAELKYISGFGNECSSDDPRCPGSLPEGQNNPQVCPYNLYAEOLSSGSAFAPRSTNKRSLWYRILPVSVSHKPFESIDEG-HVTHN WDEVDPPDNQLRWK 150
gi | 74002858 | ref | XP_535754.2 | ... --MQYIPGFGNECASDDPRCPGALPEGQNNPQVCPYNLYAEOLSSGSAFAPRSTNKRSLWYRILPVSCHKPFESIDQG-HVTHN WDEVDPPDNQLRWK 150
gi | 50729534 | ref | NP_416553.1 | ... MTSLKYMSSGFGNEHASSDDPRCPGALPEGQNNPQVCPYGLYAEOLSSGSAFAPRATNRRSLWYRILPVSCHKPFPLHEG-HLTHY WDEVEFPDNQLRWK 150
gi | 148298760 | ref | NP_694498.2 | ... MAGLYKMSGFGNEFSDDPRCPGSLPEGQNNPQVCPYGLYAEOLSSGSAFAPRSTNKRSLWYRILPVSVRHKPFTRMSCG-DLTHN WNEVEFPDNQLRWK 150
gi | 17507969 | ref | NP_492433.1 | ... MSEPDELKYLKGFNEHATSDPRVPDALPVGNSPQKSGHGLYAEOLSSGSAFAPRSTNKRSLWYRIRPSVHQPFRKFEQVAF-HWTHN FSSIPPNPNQYRWN 150
gi | 15239545 | ref | NP_200219.1 | ... MBEKKKLELEELKYGSGFNHFSSEA--IAGALPLDQNSPLLCYGLYAEOLSSGSAFAPRSTNKRSLWYRIRPSVHQPFRKFEQVAF-HWTHN FSSIPPNPNQYRWN 150
gi | 115465882 | ref | NP_001056540.1 | MAMATAIPAAQNEQEKGGLEVVYLSGLGNSLSEA--VAGTLPFGQNSPLVCPGLYAEOLSSGSAFAPRANRNLWLYRIRKPSVHQPFRKFEQVAF-HWTHN FSSIPPNPNQYRWN 150
gi | 39974845 | ref | XP_368813.1 | ... MPALTEFEFKERYQNGFDSYLSSEA--VPGALPIAQNPSQKPPHGLYAEOLSSGSAFAPRANRNLWLYRIRKPSVHQPFRKFEQVAF-HWTHN FSSIPPNPNQYRWN 150
gi | 85097536 | ref | XP_960461.1 | ... MPFINDFKERYRYQNGFDSYLSSEA--VSGALPIGHNSPQKPPGLYAEOLSSGSAFAPRHNKQSLWYRILPSCSHPPF VQATPRN GQEPVLER SPARLHYIPNQLRW 150



gi | 24583650 | ref | NP_523544.2 | ... PFDLPPKDGKNNVFEVGLHIVCGAGDPRSRHGLAIHIYSCNGSMDNS-AFYNSDGGDFLIVPQGVLDITTEFGNMSVAPNEICVIPCGRFAVNVDD--SPRGYILEVVDHDFVLPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 158298465 | ref | XP_318638.4 | ... PFDLP-AAGSEVDFVAGLHIVCGAGDVRANGLAVHVLANCSMKT-AFYNSDGGDFLIVPQGVLDITTEFGNMSVAPNEICVIPCGRFAVNVDD--SPRGYILEVVDHDFVLPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 7549763 | ref | NP_038575.1 | ... PFEIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 58865860 | ref | NP_001012145.1 | ... PFEIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 115527117 | ref | NP_000178.2 | ... PFEIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 114588728 | ref | XP_516674.2 | ... PFEIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 74002858 | ref | XP_535754.2 | ... PFEIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 50729534 | ref | NP_416553.1 | ... PFEIPKASONKLDVFSGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 148298760 | ref | NP_694498.2 | ... PFNIPKASEKKVDFVSLGLHILCGAGDIRSNNGLAVHIFLNCNSMENR-CFYNSDGGDFLIVPQKGLLIYTEFGKMLVQNEICVIOGRMRFSVDVF--EETRGIYILEVYGVHFFELPDLGPIGANGLANPRDFLIPVAWFD 300
gi | 17507969 | ref | NP_492433.1 | ... PFDLP--HKEGVTFVNDLYIVCGGGDVIISRTGLAIHQFSCNASMEHT-AMYNDDGDFLIVPQGALEITTEFGRLNVPQIAVPIQGRFVAVR--GPRGYILEVYGVHFFELPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 15239545 | ref | NP_200219.1 | ... PFDLP--DSEIDFVDGLFVICGAGSSFLRHGFAIHMVAVNTGMKDS-AFCNADGDFLIVPQKGLLIYTECGKLLVPPGIEVVIQGRFVAVR--GPRGYILEVYGVHFFELPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 115465882 | ref | NP_001056540.1 | ... PADVPP-HHPPDFIDGLYIVCGAGSSFLRHGFAIHMVAVNTGMKDS-AFCNADGDFLIVPQKGLLIYTECGKLLVPPGIEVVIQGRFVAVR--GPRGYILEVYGVHFFELPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 39974845 | ref | XP_368813.1 | ... PFDHD--POSDFVSLGLHILGAGPPTLKHGIGMVFVYAAAGKSMSTSAFYNSADGDLIVASGVLDIRTEGLNLLVRLPQIAVPIQGRFVAVR--GPRGYILEVYGVHFFELPDLGPIGANGLANPRDFEIPVAWFD 300
gi | 85097536 | ref | XP_960461.1 | ... PFDHE--SDTDFVSLGLRIVAGAPPTLKHGIGMVFVYAAAGKSMSTSAFYNSADGDLIVASGVLDIRTEGLNLLVRLPQIAVPIQGRFVAVR--GPRGYILEVYGVHFFELPDLGPIGANGLANPRDFEIPVAWFD 300



gi | 24583650 | ref | NP_523544.2 | ... ---RDVKD-FQVLSKFGRLVFAKQNHIVFDVVAWHGNYVPKYDLKSKFMVINSVDFDHCDSIFTVLTCPSLRAGTAIADFVIFPPRWSVQEHFRPPYIYHRCMSEFMGLILGKYEAKEDG--FAAGGATLHSMTPHGPVCKFEK 450
gi | 158298465 | ref | XP_318638.4 | ... ---RSVEG-YRIVSKFGCALFVATQHSFPDVAWHGNYVPKYDLARFMVINSVDFDHCDSIFTVLTCPSNRPGTAIADFVIFPPRWSVQEHFRPPYIYHRCMSEFMGLIFGRYEAKEGG--FMPGGASLHSMTPHGDHRCFEK 450
gi | 7549763 | ref | NP_038575.1 | ... ---RRVPGGYIVINKFGKLFACKQDVSPFNVTWGHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIKGHYEAKEGG--FLPGGGSLHSMTPHGPADCFEK 450
gi | 58865860 | ref | NP_001012145.1 | ... ---RQVPGGYIVINKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIKGHYEAKEGG--FLPGGGSLHSMTPHGPADCFEK 450
gi | 115527117 | ref | NP_000178.2 | ... ---RQVPGGYIVINKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIRGHYEAKEGG--FLPGGGSLHSMTPHGPADCFEK 450
gi | 114588728 | ref | XP_516674.2 | ... ---RQAPGGYIVINKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIRGHYEAKEGG--FLPGGGSLHSMTPHGPADCFEK 450
gi | 74002858 | ref | XP_535754.2 | ... ---RQVPGGYIVINKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIKGHYEAKEGG--FLPGGGSLHSMTPHGPADCFEK 450
gi | 50729534 | ref | NP_416553.1 | ... ---RKIPGGYIVISKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIKGHYEAKEGG--FQPGGASLHSMTPHGPADCFEK 450
gi | 148298760 | ref | NP_694498.2 | ... ---RTIATGYIVINKYQKLFASKQDVSPFNVAWHGNYTPYKYNLENFMVINAVAFDHADPSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLIKGHYEAKEGG--FQPGGASLHSMTPHGPADCFEK 450
gi | 17507969 | ref | NP_492433.1 | ... ---LDVE--FTIINKYQGSWFQAKQHSFPDVAWHGNYVPKYDLKSKFMVINTVDFDHCDSIFTVLTAKSLRPGVAIADFVIFPPRWGVADKFRPPYIYHRCMSEFMGLITGCEYEAKEGG--FKFPGGSLHSMTPHGPDFNCFEM 450
gi | 15239545 | ref | NP_200219.1 | ... ---GLRPE-YIIVQKFGGELFATQDFSPFNVAWHGNYVPKYDLKSKFCPNTVLEFDHADPSVNTVLTAPTDKPGVALLDFVIFPPRWVLAHFRPPYIYHRCMSEFMGLIYGAYEAKEGG--FLPGGASLHSMTPHGPDTTYEA 450
gi | 115465882 | ref | NP_001056540.1 | ... ---VHRPG-YIIVQKFGGELFATQDFSPFNVAWHGNYVPKYDLKSKFCPNTVLEFDHADPSVNTVLTAPTDKPGVALLDFVIFPPRWVLAHFRPPYIYHRCMSEFMGLIYGAYEAKEGG--FLPGGASLHSMTPHGPDTTYEA 450
gi | 39974845 | ref | XP_368813.1 | ... AGPSAPRDCYEVAKFNNTLFAIRCAHTPFDVVAWHGNYVPKYDLGRFNIGSISFDHDDPSIFTVLTAKSLRPGVAIADFVIFPPRWVLAHFRPPYIYHRCMSEFMGLITGDAYDAKGGKGGFVPGGASLHSMTPHGPDAASYEG 450
gi | 85097536 | ref | XP_960461.1 | ... -GPNSS--YIIVAKFNNTLFAIRCAHTPFDVVAWHGNYVPKYDLGRFNIGSISFDHDDPSIFTVLTAKSLRPGVAIADFVIFPPRWVLAHFRPPYIYHRCMSEFMGLITGDAYDAKGGKGGFVPGGASLHSMTPHGPDAASYEG 450



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gi | 158298465 | ref | XP_318638.4 | -ASNADLKPERVADGTQAFMFESSLSMAVTRWGEETCQKLDARVYE-CWQALEKHFH-----I----- 530
gi | 7549763 | ref | NP_038575.1 | -ASKAKLEPERIADGTMAFMFESSLSLAVTKWGLKTCSCLDENYYK-CWEPLRSHFT-----PNSRSPTEPK--- 530
gi | 58865860 | ref | NP_001012145.1 | -ASKAKLEPERIADGTMAFMFESSLSLAVTKWGLKTCGLDEDYYK-CWEPLQAHFT-----PFSRSPTEPK--- 530
gi | 115527117 | ref | NP_000178.2 | -ASKVKLAPERIADGTMAFMFESSLSLAVTKWGLKASRCLDENYHK-CWEPLKSHFT-----PNSRNPAPNP--- 530
gi | 114588728 | ref | XP_516674.2 | -ASKAKLAPERIADGTMAFMFESSLSLAVTKWGLKASRCLDENYHK-CWEPLKSHFT-----PNSRNPAPNP--- 530
gi | 74002858 | ref | XP_535754.2 | -ASKAKLAPERIADGTMAFMFESSLSMAVTKWGLKSSCLDENYYK-CWEPLKSHFT-----PDSRKPAGPN--- 530
gi | 50729534 | ref | XP_416553.1 | -ASKAKLEPERVAEGTMAFMFESSLSMAVTEWGLKTSNRLLDKNYYK-CWEPLKSHFN-----PNCK----- 530
gi | 148298760 | ref | NP_694498.2 | -NSTALLKPERVAEGTMAFMFESSFSMAVTKWGLETCQRLDKNYYK-CWEALKSHFN-----PNWKPSK----- 530
gi | 17507969 | ref | NP_492433.1 | -ASNADLKPERVAEGTMSFMFESSLNMAITNWAVYQN--VDKDYK-DWQPLKHFH-----MPK----- 530
gi | 15239545 | ref | NP_200219.1 | TLRVNMAMPKSLTGTMAFMFESALIPRVCHWALESPF-LDHDYYQ-CWIGLKSHFSRISLDKTNVSTEKEPGASE--- 530
gi | 115465882 | ref | NP_001056540.1 | TLRPDANEPKSLTGTMAFMFESALIPRVCHWALESPF-LDHDYYQ-CWIGLKSHFSRISLDKTNVSTEKEPGASE--- 530
gi | 39974845 | ref | XP_368813.1 | -AREAEKPAKVGAGSCAFMFESCFMVGVLDWGLRITCQKVQEGYSQESWGGVKTLYWK-----RPEGASADVHLLK 530
gi | 85097536 | ref | XP_960461.1 | -ARNADLKPERKVGEGSCAFMFESCLMVGVLDWGLRITCQKVQEGYSQESWGGVKTLYWK-----MPEGKGGCHLL 530
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