

gi | 189533098 | ref | XP_001920213.1 | -----MDKVERLKKI GEGSFGKAILVKSRTDGRQYVIK-----EIGISRMSNKERQESRKEVAVLANM-SHPNIVQYKESFEBSGCLYIVMDYCEGGDLFKKINNORG--SLFPPEEILDWFVQICLALKHVHDKRILHRDIK 130
gi | 189533094 | ref | XP_683784.3 | -----MDS-----ELGIK-----SGCLYIVMDYCEGGDLFKKINNORG--SLFPPEEILDWFVQICLALKHVHDKRILHRDIK 66
gi | 124107627 | ref | NP_780298.2 | -----MEKVVRLQKIGEGSFGKAVLVKSTEDGRHYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAOKG--ALFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 109503303 | ref | XP_214340.4 | -----MEKVVRLQKIGEGSFGKAVLVKSTEDGRHYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAOKG--TLFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 41872673 | ref | NP_036356.1 | -----MEKVVRLQKIGEGSFGKAILVKSRTEDGRQYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAOKG--VLFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 114596800 | ref | XP_526727.2 | -----MEKVVRLQKIGEGSFGKAILVKSRTEDGRQYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAOKG--VLFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 73993594 | ref | XP_543184.2 | -----MEKVVRLQKIGEGSFGKAILVKSRTEDGRQYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAOKG--ILFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 118089809 | ref | XP_420401.2 | -----MDKYLVKVIKIGEGSFGKAVLVKDKENSQYVIK-----EINISRMSDKEREESRREVAVLANM-KHPNIVQYKESFEENGSLYIVMDYCEGGDLFKKINAOKG--VLFQEDQILDWFVQICLALKHVHDKRILHRDIK 130
gi | 124506435 | ref | XP_001351815.1 | -----MSKPKMIGPVYEVVKSIRGSGFGIVTAVKDENEKMYDKINNMDIKCVYELDISCMNKEKMNVVNEIRALIKMSVHPFIVRYKEAFVDCVLYVMDYCEGGDLGKVIKHKHELETPIPEKKIKRWLLQITMAIKFIHDKKILHRDLK 147
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 189533098 | ref | XP_001920213.1 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYEMCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLAQLFKRNPRRPSVSTILDKPFLLARRIHKFLSPOLIAEBSFS 278
gi | 189533094 | ref | XP_683784.3 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYEMCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLAQLFKRNPRRPSVSTILDKPFLLARRIHKFLSPOLIAEBSFS 214
gi | 124107627 | ref | NP_780298.2 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYELCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFCKL 278
gi | 109503303 | ref | XP_214340.4 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYELCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFCKL 278
gi | 41872673 | ref | NP_036356.1 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYELCLKHAFAEAG--SMKNLVLKIIRGSPVPSIHYSPDLRSLVLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFCKL 278
gi | 114596800 | ref | XP_526727.2 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYELCLKHAFAEAG--SMKNLVLKIIRGSPVPSIHYSPDLRSLVLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFCKL 278
gi | 73993594 | ref | XP_543184.2 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYEMCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFCKL 278
gi | 118089809 | ref | XP_420401.2 |SONIFLTKDGIQVGLGDFGIARVLNSIVELARICIGTPYLLSPEICENKPNYNNKSDIWAIGCVLYEMCLKHAFAEAG--NMKNLVLKIIRGSPVPSIHYSPDLRSLLSOLFKNRPRDRPSVNSILEKGFIAKRIEKFLSPOLIAEBSFSHK 278
gi | 124506435 | ref | XP_001351815.1 |CNIIFLDEKERAKIGDFGLAKFIEQIEGTN-LLCGTIGYMAPEICKINISFPADIWSLGIILYELIILKPPFKSNNSNMLSAQKICEDEPDLPSDFSQDLINLCYWLKDKDRPPIYDIISTDIQDELQFKREMLQERNISQI- 295
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 189533098 | ref | XP_001920213.1 |IHLQPKMSVAHAAPAKRPAPG--PIPIITSAQKITKPAAKYGVPLTVRRPSEVARKVPDAAKPKVLLKQAPPPAAVORRVSRYVEERRKHBEQVRRKRMEMMERERKQREOML-LLKAAQMKRFEREKLNRIINRAREQWRHVLSSSGGSS 425
gi | 189533094 | ref | XP_683784.3 |IHLQPKMSVAHAAPAKRPAPG--PIPIITSAQKITKPAAKYGVPLTVRRPSEVARKVPDAAKPKVLLKQAPPPAAVORRVSRYVEERRKHBEQVRRKRMEMMERERKQREOML-LLKAAQMKRFEREKLNRIINRAREQWRHVLSSSGGSS 361
gi | 124107627 | ref | NP_780298.2 |ILSK---FGPQIPGKRPASGGVSVFVPAQKITKPAAKYGVPLTVRKYGD--KKLLER-KPPPKHQAQIIP--VKKMNSGEERKMSBEAAKRRLEFIEKKEKQDQIIR-FLKAEQMKRQEKQRLERINRAREQWRNVLRAGSGSGE 419
gi | 109503303 | ref | XP_214340.4 |ILVSK---FGPQIPGKRPASGGVSVFVPAQKITKPAAKYGVPLTVRKYGD--KKLLER-KPPPKHQAQIIP--VKKMNSGEERKMSBEAAKRRLEFIEKKEKQDQIIR-FLKAEQMKRQEKQRLERINRAREQWRNVLRAGSGSGE 419
gi | 41872673 | ref | NP_036356.1 |IFSK---FGSQIPAKRPASGNSISVMPAQKITKPAAKYGIPLAVKYGQD--KKLHEK-KPLQKHQAQIIP--EKRVNTGEERKMSBEAAKRRLEFIEKKEKQDQIISLMKAEQMKRQEKERLERINRAREQWRNVLRAGSGSGE 420
gi | 114596800 | ref | XP_526727.2 |IFSK---FGSQIPAKRPASGNSISVMPAQKITKPAAKYGIPLAVKYGQD--KKLHEK-KPLQKHQAQIIP--EKRVNTGEERKMSBEAAKRRLEFIEKKEKQDQIISLMKAEQMKRQEKERLERINRAREQWRNVLRAGSGSGE 420
gi | 73993594 | ref | XP_543184.2 |IFSK---CGAQIPAKRPASGSLASVVSQAQKITKPAAKYGVPLTVRKYGD--KKLHEK-KPLQKHQAQIIP--VKKVNPGEERKMFBEAAKRRLEFIEKKEKQDQIVISLMKAEQMKRQEKERLERINRAREQWRNVLRAGSGSGE 420
gi | 118089809 | ref | XP_420401.2 |IFSK---VPHK---FGPHAGPAKRPAGHISASIAFVQKITKPAAKYGVPLAMKKCYDAPKLLHEK--KSLIKLRQAFPP--KKKIIPGEERKMFBEAPSKKRLLEPEKEKQDQIS-LLKAEEMRRLKERMERINRAREQWRNVLRAGSGSGD 421
gi | 124506435 | ref | XP_001351815.1 |IFSK---VPHK---FGPHAGPAKRPAGHISASIAFVQKITKPAAKYGVPLAMKKCYDAPKLLHEK--KSLIKLRQAFPP--KKKIIPGEERKMFBEAPSKKRLLEPEKEKQDQIS-LLKAEEMRRLKERMERINRAREQWRNVLRAGSGSGD 295
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



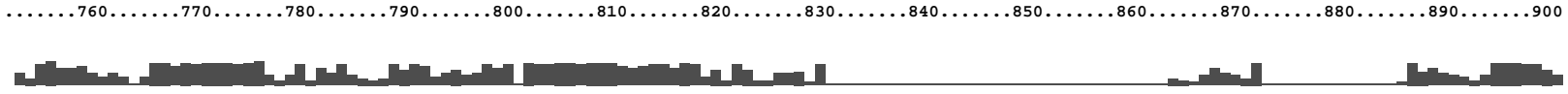
gi | 189533098 | ref | XP_001920213.1 |PERKFYGGGGNGAPHSPIGSPFPVPGPSVVPASALAPSRAPYDRIHPSAEKLTPTTP-KDGAGEGAVHAGDNGRTSDDSGTLNGHACTIPVKNVIRREQ-----RKTSLQNEQISKIDYANRRFGQLAVEKSKOVEEFLORKREAMLN 567
gi | 189533094 | ref | XP_683784.3 |PERKFYGGGGNGAPHSPIGSPFPVPGPSVVPASALAPSRAPYDRIHPSAEKLTPTTP-KDGAGEGAVHAGDNGRTSDDSGTLNGHACTIPVKNVIRREQ-----RKTSLQNEQISKIDYANRRFGQLAVEKSKOVEEFLORKREAMLN 503
gi | 124107627 | ref | NP_780298.2 |VKASFFGIGGA-----VSPSPCS-----PRGOYEHYHAIFDQMOQL--RAEDNEARWKGRIYGRWLPER-----DKGHLAVERANOVEEFLORKREAMON 502
gi | 109503303 | ref | XP_214340.4 |VKASFFGIGGA-----VSPSPCS-----PRGOYEHYHAIFDQMOQL--RAEDNEARWKGRIYGRWLPER-----DKGHLAVERANOVEEFLORKREAMON 502
gi | 41872673 | ref | NP_036356.1 |VKAPFLGSGGT-----IAPSFSS-----SRGOYEHYHAIFDQMOQL--RAEDNEAKWKREIYGRGLPERGILPGVRRPGFFYGAAGHHHFPDADDIRKTLKRLKAVSKQANARQKGLAVERAKOVEEFLORKREAMON 547
gi | 114596800 | ref | XP_526727.2 |VKAPFLGSGGT-----IAPSFSS-----SRGOYEHYHAIFDQMOQL--RAEDNEAKWKREIYGRGLPERGILPGVRRPGFFYGAAGHHHFPDADDIRKTLKRLKAVSKQANARQKGLAVERAKOVEEFLORKREAMON 547
gi | 73993594 | ref | XP_543184.2 |VKAPFLGSGGA-----VAPSFSS-----SRGOYEHYHAIFDQMOQL--RVENNEAKWKGRIYGRRLPERGISEIHSFGRNGARGHYFPNADAFKSLNRLKIMSKQASISRQKGLAVERAKOVEEFLORKREAMON 547
gi | 118089809 | ref | XP_420401.2 |VKAPFYGGGG-----VGPFPAS-----FRGOYEHYHAIFDQMQETFAVTKERQAKWRAEVQCGEAVERGIPPGVRRPGVPGKQAGHHHLPDADAIRKVKRLKEVSKQASANRQKGLPAERAKOVEEFLORKREAMON 551
gi | 124506435 | ref | XP_001351815.1 |VKAPFYGGGG-----VGPFPAS-----FRGOYEHYHAIFDQMQETFAVTKERQAKWRAEVQCGEAVERGIPPGVRRPGVPGKQAGHHHLPDADAIRKVKRLKEVSKQASANRQKGLPAERAKOVEEFLORKREAMON 295
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



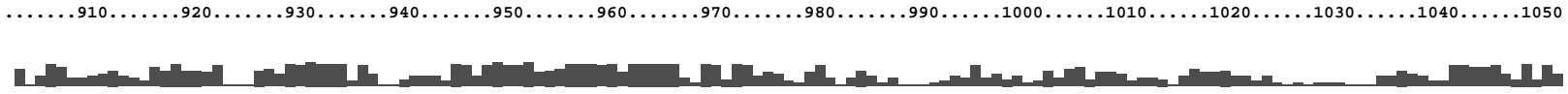
gi | 189533098 | ref | XP_001920213.1 |KVRABGQI-----EVLTRLQIRLONFNERQOIKARLRGEKYSDSGSDSESCBEAVLRMKKIEALKASKARAAVLKEOLEKKREAYEREKKAWEHDHVSPPTPPSPDPTP-----GEAP 677
gi | 189533094 | ref | XP_683784.3 |KVRABGQI-----EVLTRLQIRLONFNERQOIKARLRGEKYSDSGSDSESCBEAVLRMKKIEALKASKARAAVLKEOLEKKREAYEREKKAWEHDHVSPPTPPSPDPTP-----GEAP 613
gi | 124107627 | ref | NP_780298.2 |KARABGHV-----VYLARLQIRLONFNERQOIKAKLRGENKEADGTGQDAAETDMRLKMMESLKAQANARAAVLKEOLEKKREAYEREKKEVVEEHLVLR-VKSSDVP-----LPLLELL 614
gi | 109503303 | ref | XP_214340.4 |KARABGHV-----VYLARLQIRLONFNERQOIKAKLRGENKEADGTGQDAAETDMRLKMMESLKAQANARAAVLKEOLEKKREAYEREKKEVVEEHLVLR-VKSSDVP-----LPLLELL 614
gi | 41872673 | ref | NP_036356.1 |KARABGHM-----VYLARLQIRLONFNERQOIKAKLRGEKKEANHSSEGGSEADAMRRKKIIESLKAHANARAAVLKEOLEKKREAYEREKKEVVEEHLVAKGVKSSDVS-----PPLGQHE 660
gi | 114596800 | ref | XP_526727.2 |KARABGHMGIILONLAAMYGRPSSSSGGGKPRNKEEVLARLRQIRLONFNERQOIKAKLRGEKKEANHSSEGGSEADAMRRKKIIESLKAHANARAAVLKEOLEKKREAYEREKKEVVEEHLVAKGVKSSDVS-----PPLGQHE 688
gi | 73993594 | ref | XP_543184.2 |KARABGHMGIILONLAAMYGRSSSSSGGGKPRNKEEVLARLRQIRLONFNERQOIKAKLRGEKKEADYSSEGGSEADAMRRKKIIESLKAHANARAAVLKEOLEKKREAYEREKKEVVEEHLVAKGVKSSDVS-----PPLGQHE 688
gi | 118089809 | ref | XP_420401.2 |KARABGHM-----EVLARLRQIRLONFNERQOIKAKLRGEKKEANHSSEGGSEADAMRRKKIIESLKAHANARAAVLKEOLEKKREAYEREKKEVVEEHLVAKGVKSSDVS-----PPLGQHE 673
gi | 124506435 | ref | XP_001351815.1 |KARABGHM-----EVLARLRQIRLONFNERQOIKAKLRGEKKEANHSSEGGSEADAMRRKKIIESLKAHANARAAVLKEOLEKKREAYEREKKEVVEEHLVAKGVKSSDVS-----PPLGQHE 295
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



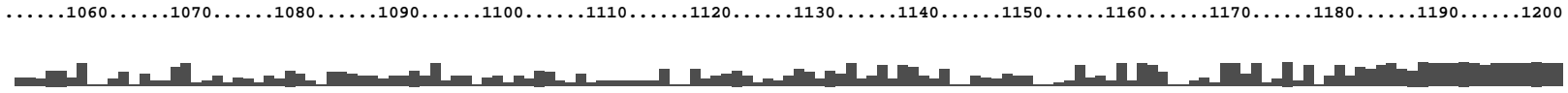
gi | 189533098 | ref | XP_001920213.1 | SKATPSSRPSTP-AISMIAALKDVGAISSGQSSPMKEDSLKVESDQVSDKKEILRRLNOKVQITEEVSVKETPPSNPCPPDPPVQPSITEERPSTAAADRRKWEAVAPPILSVARQTLLETTCATLAVSQVAFPEPTNTPCGDRKKWOT 826
gi | 189533094 | ref | XP_683784.3 | SKATPSSRPSTP-AISMIAALKDVGAISSGQSSPMKEDSLKVESDQVSDKKEILRRLNOKVQITEEVSVKETPPSNPCPPDPPVQPSITEERPSTAAADRRKWEAVAPPILSVARQTLLETTCATLAVSQVAFPEPTNTPCGDRKKWOT 762
gi | 124107627 | ref | NP_780298.2 | TGGSPSKQOVKP-VISVTSALKVEGLDGLSDTQET--EEMKSNNAISS--KREILRRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 714
gi | 109503303 | ref | XP_214340.4 | AGGSPSQOQMKP-VISVTSALKVEGLDGLSDTQETSEEMKSNNAISS--KREILRRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 716
gi | 41872673 | ref | NP_036356.1 | TGGSPSKQOQMRV-VISVTSALKVEGLDGLSDTQETSEEMKSNNAISS--KREILRRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 762
gi | 114596800 | ref | XP_526727.2 | TGGSPSKQOQMRV-VISVTSALKVEGLDGLSDTQETSEEMKSNNAISS--KREILRRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 790
gi | 73993594 | ref | XP_543184.2 | AGGSPSQOQMRV-VISVTSALKVEGLDGLSDTQETSEEMKSNNAISS--KREILRRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 790
gi | 118089809 | ref | XP_420401.2 | PGVSPKQQLPVKPISTMSALKEVGVGDNVTAQVFKVEIKKPDLMQN--KRIILKRLNENLKAQDEDEKQHHSSGCE-----TVGHRDERE-----YETENAISSDRKKWEM 777
gi | 124506435 | ref | XP_001351815.1 | -----SDGSEDGKEE-----QDNHPLLGDGRRKWA 295



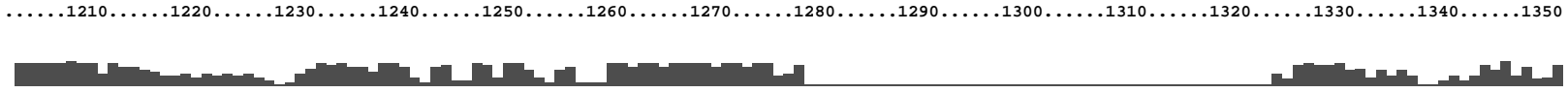
gi | 189533098 | ref | XP_001920213.1 | DGVPLLSVAQQTLEETSFRAGQLTEKTVGEVICMDAQQEGLRKAQWQSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 963
gi | 189533094 | ref | XP_683784.3 | DGVPLLSVAQQTLEETSFRAGQLTEKTVGEVICMDAQQEGLRKAQWQSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 899
gi | 124107627 | ref | NP_780298.2 | GG-QLVPLDDELTDTSFSAI---EKHTVGEVIKLD---SNGSPRKVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 854
gi | 109503303 | ref | XP_214340.4 | GG-QLVPLDDELTDTSFSAI---EKHTVGEVIKLD---SNGSPRKVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 855
gi | 41872673 | ref | NP_036356.1 | GG-QLVPLDDELTDTSFSAI---EKHTVGEVIKLD---SNGSPRKVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 906
gi | 114596800 | ref | XP_526727.2 | GG-QLVPLDDELTDTSFSAI---EKHTVGEVIKLD---SNGSPRKVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 934
gi | 73993594 | ref | XP_543184.2 | GG-QLVPLDDELTDTSFSAI---EKHTVGEVIKLD---SNGSPRKVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 934
gi | 118089809 | ref | XP_420401.2 | RASDLVVPALQLSMEDLSG---DRQTMGEVIRLD---IGEPKRVWGKSPDSEVLKVLVEAEALSFQRDLDPASTCDQTLTESLN---PIESDATNEAKVPPPEPCQPADHDHQEVT-----CQETVPIIEVKSQELIIT 922
gi | 124506435 | ref | XP_001351815.1 | -----SDGSEDGKEE-----QDNHPLLGDGRRKWA 295



gi | 189533098 | ref | XP_001920213.1 | LAEGTEK--HSAE--DIEVVDMEVSVLDDVDPQKTAEPPEAVIQAQWIKDIPESLPAEGRVIAQECTVPPREKHPPEPPADESLFVKLSSPAHRRTVALAMLAAQSLDSSAAASRSRVSPLRSHRHDALLIGLSTGLFDANNPKM 1112
gi | 189533094 | ref | XP_683784.3 | LAEGTEK--HSAE--DIEVVDMEVSVLDDVDPQKTAEPPEAVIQAQWIKDIPESLPAEGRVIAQECTVPPREKHPPEPPADESLFVKLSSPAHRRTVALAMLAAQSLDSSAAASRSRVSPLRSHRHDALLIGLSTGLFDANNPKM 1048
gi | 124107627 | ref | NP_780298.2 | STHFDGS--LPPVNDVWTRKEEAAKETELEDKAVAVQSEVCEDRIPGVNDQSCDRDPAVD--DSPOSGCDVEKSVQPELFFQKVVHS--KDLNLV---QAVHCSPEEP--IPRSHSDSPPK--TKSKNSLLIGLSTGLFDANNPKM 992
gi | 109503303 | ref | XP_214340.4 | SAIPSDGS--LPPVNDVWTRKEEAAKETELEDKAVAVQSEVCEDRIPGVNDQSCDRDPAVD--DSPOSGCDVEKSVQPELFFQKVVHS--KDLNLV---QAVHCSPEEP--IPRSHSDSPPK--TKSKNSLLIGLSTGLFDANNPKM 989
gi | 41872673 | ref | NP_036356.1 | SGTNKDES--LPCITIDVWISSEKETEKEKQSDADRTITIDENVEVSDGSSVVDQLSDIHIPEPTN--DQHQKCDVDRKSVQPELFFQKVVHS--KDLNLV---QAVHCSPEEP--IPRSHSDSPPK--TKSKNSLLIGLSTGLFDANNPKM 1047
gi | 114596800 | ref | XP_526727.2 | SGTNKDES--LPCITIDVWISSEKETEKEKQSDADRTITIDENVEVSDGSSVVDQLSDIHIPEPTN--DQHQKCDVDRKSVQPELFFQKVVHS--KDLNLV---QAVHCSPEEP--IPRSHSDSPPK--TKSKNSLLIGLSTGLFDANNPKM 1075
gi | 73993594 | ref | XP_543184.2 | GGANKDGS--LPCITIDVWISSEKETEKEKQSDADRTITIDENVEVSDGSSVVDQLSDIHIPEPTN--DQHQKCDVDRKSVQPELFFQKVVHS--KDLNLV---QAVHCSPEEP--IPRSHSDSPPK--TKSKNSLLIGLSTGLFDANNPKM 1075
gi | 118089809 | ref | XP_420401.2 | EEDKKHQSEKFPPIAVNVEVWVKEKQDENEAPEKEVVDENLVSAHFSYLLHSLLELYVISICNGLSYTAECSDDLOPELRFORVQP--PAVPLASVPLSSCSQEEP--FVPRRSISPAK--NKGKSLFFGLSTGLFDANNPKM 1067
gi | 124506435 | ref | XP_001351815.1 | -----SDGSEDGKEE-----QDNHPLLGDGRRKWA 295



gi | 189533098 | ref | XP_001920213.1 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1255
gi | 189533094 | ref | XP_683784.3 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1190
gi | 124107627 | ref | NP_780298.2 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1094
gi | 109503303 | ref | XP_214340.4 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1091
gi | 41872673 | ref | NP_036356.1 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1149
gi | 114596800 | ref | XP_526727.2 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1177
gi | 73993594 | ref | XP_543184.2 | LRTCSLPDLSKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1177
gi | 118089809 | ref | XP_420401.2 | LRTCSLPDLYKLVFSDAIPGEGAAAPD--SNLEIEDLEDKADEC--SEPEDVYEDD---DLRELASMERLLOEHSBDDDD--EEDEEGGSSNGSPADEEPAGLNLASAGDKRSPEEETFNMGMAHDDDEVSHGEEPPGGPVITNGMEFED 1170
gi | 124506435 | ref | XP_001351815.1 | -----SDGSEDGKEE-----QDNHPLLGDGRRKWA 295



gi | 189533098 | ref | XP_001920213.1 | DDEQ--NSSEAQLNEEWQSDGSEEDDEELEDQDSIFSRLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1375
gi | 189533094 | ref | XP_683784.3 | DDEQ--NSSEAQLNEEWQSDGSEEDDEELEDQDSIFSRLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1310
gi | 124107627 | ref | NP_780298.2 | EEDN--PSESALNEEWSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1203
gi | 109503303 | ref | XP_214340.4 | EEDN--PSESALNEEWSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1200
gi | 41872673 | ref | NP_036356.1 | EEDN--PSESALNEEWSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1258
gi | 114596800 | ref | XP_526727.2 | EEDN--PSESALNEEWSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1286
gi | 73993594 | ref | XP_543184.2 | EEDN--PSESALNEEWSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1286
gi | 118089809 | ref | XP_420401.2 | ADENNPSESALNEEWQSDNSDAETTSEC--EYDSVFNHLEELRLHLEQAMGFENFIOAYNKIKAIHEDEDENIAMGSSMVONILGTEHOHLVYKILHLVMDGAYQEDCNFSFRSRSVSSGGI 1281
gi | 124506435 | ref | XP_001351815.1 | -----SDGSEDGKEE-----QDNHPLLGDGRRKWA 295

