

gi | 120587003 | ref | NP_062610.2 | MEAIFFTAR-----KHFFPN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLCSKK-----EPRFKQVRLWVSPGLRCEPDLE-KSQPWPDLICSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 109499693 | ref | XP_341216.3 | MEAIFFTAR-----KHFFPN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLCSKK-----EPMKQVRLWVSPGLRCEPDLE-KSQPWPDLICSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 50658061 | ref | NP_055988.2 | MEPIITFTAR-----KHLLSN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLSTRK-----EPVTKQVRLCVSPSGLRCEPEPG-RSQQWDPDLIYSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 114593540 | ref | XP_001137272.1 | MEPIITFTAR-----KHPLPN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLSTRK-----EPVTKQVRLCVSPSGLRCEPEPG-RSQQWDPDLIYSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 73951584 | ref | XP_536262.2 | MEPIITFTAR-----KHFFPN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLASRK-----EPGTRQVRLCVSPSGLRCEPEPG-KSQQWDPDLICSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 119893781 | ref | XP_611974.3 | MEPIITFTAR-----KHFFPN-----EVSVDLGLQVLSLPVHSLTTPMPLPWWVAEVRRLSGLCSKK-----EPGKQVRLCVSPSGLRCEPEPG-KSQQWDPDLICSSIFECKPQRVHKLHNSHDPSSYFA 115
gi | 118090617 | ref | XP_423827.2 | -----MSPLFSWVAVKVG---GGGHPAR-----GGGIRPVGIRGGSGALLLRLGA-SSE--GKLVFRFGLGGLLAVRCGGEGGESCRKV 75
gi | 189514560 | ref | XP_689617.3 | MEGICFEVKPRDSDITAHPLCDLITQTFPQSEKRRKEDGEEVIQVYRPTLVGSLAIHPQITMAILPWWVAEIRRPVGRREKRNLEFNGNYSPEIRDQPVVLOIQAASVCCILDTAGPQKPNWNLQHMVLEDRPHVHVKLIHNSQEPSSYFA 150



gi | 120587003 | ref | NP_062610.2 | CLIKEDAHRQSLCYVFKADDQTKVPEIISIRQAGKIARQEEELR-CPSEFDDTFAKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHVS-CGR-----RTDWEAFTGGPF---APGPRPMRKSFSQPGI 235
gi | 109499693 | ref | XP_341216.3 | CLIKEDAHRQSLCYVFKADDQTKVPEIISIRQAGKIARQEEELR-CPSEFDDTFAKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHVS-CGR-----RIDWDAFTGGPF---APGARPMRKSFSQPGI 235
gi | 50658061 | ref | NP_055988.2 | CLIKEDAVHRQSI CYVFKADDQTKVPEIISIRQAGKIARQEEELH-CPSEFDDTFSKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHVS-GSR-----GSESPRPNPPHAAPGSGQEPVRRRMRKSFSQPGI 241
gi | 114593540 | ref | XP_001137272.1 | CLIKEDAVHRQSI CYVFKADDQTKVPEIISIRQAGKIARQEEELH-CPSEFDDTFSKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHVS-GSR-----GSESPRPNPPHAAPGSGQEPVRRRMRKSFSQPGI 241
gi | 73951584 | ref | XP_536262.2 | CLIKDNAASQOSI CYVFKADDQTKVPEIISIRQAGKIARQEEELH-CPSEFDDTFAKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHVS-CERKAEFALVAQNPPAPPEAPPGPAGGRSLAAKVRGVLQPVNGGQARRRMRKSFSQPGI 264
gi | 119893781 | ref | XP_611974.3 | CLIKNDAAANQOSI CYVFKADDQTKVPEIISIRQAGKIARQEEELR-CPSEFDDTFAKKEVFLVFCGRVIVAHKKAPPALIDECIEGSHVS-----GGFSDQSRSLAPPDGERGPRRMRKSFSQPGI 238
gi | 118090617 | ref | XP_423827.2 | WYVPSPP-----ACSGIRVPEIISIRQAGKIARQEEFNLLSDIEDPFAKKEVFLVFCGRVIVAHKKAPPALIDECIEKFNHASCILK-----KSDSSSSSQOETHADNQGEEKRPIRKSFSQPGI 192
gi | 189514560 | ref | XP_689617.3 | CLLREKK---AACYVFCQDQLKVPPEIISIRQAGKSSARQEDT---PSLPSIAFAKKEVFLVFCGRVIVAHKKAPPALIDECIEKFRVSVVIG-----SLAAGIRRAFSLNIVVNG--TNEGDDGGK 265



gi | 120587003 | ref | NP_062610.2 | RSLAFRKEFDASLRSS-TFSSFDN-----DIENHLIGHNVVQPTDMEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGGGGFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 379
gi | 109499693 | ref | XP_341216.3 | RSLAFRKEFDASLRSS-TFSSFDN-----DIENHLIGHNVVQPTDMEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGGGGFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 379
gi | 50658061 | ref | NP_055988.2 | RSLAFRKELDGGLRSGGFFSFEES-----DIENHLIGHNVVQPTDIEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGG--GFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 385
gi | 114593540 | ref | XP_001137272.1 | RSLAFRKELDGGLRSGGFFSFEES-----DIENHLIGHNVVQPTDIEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGG--GFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 385
gi | 73951584 | ref | XP_536262.2 | RSLAFRKELDGGLRSGGFFSFEES-----DIENHLIGHNVVQPTDIEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGG--GFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 408
gi | 119893781 | ref | XP_611974.3 | RSLAFRKEFDAGLRSSGFFSFEES-----DIENHLIGHNVVQPTDIEENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSGGGG--GFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 382
gi | 118090617 | ref | XP_423827.2 | RSLAFRKEFDGEGSHRSNSFVRSFEEDAIENLNLKSLIYGHVSVVQPTDIAENRIMLFTIGQSEVYLLISPDTKKIALEKNFKIEISFCQGIHVVDHDFGFCIRCSSENG--GFHFVFCYVFCCTNEALVDEIMMLKQAFVVAAVOQTAKAPAG 340
gi | 189514560 | ref | XP_689617.3 | RPLFFKRQD-----SFPFLQALDENGLSPELORRAADGATGVQPTSLQENRIMLFTIGRSQIFLVSPDTKKVALEKSFREISFCQGIHVVDHDFGFCIRCSVECC--GCQFVFCYVFCCTNEALVDEIMMLKQAFVVAALQNSRTQSG 407



gi | 120587003 | ref | NP_062610.2 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKEHSHTGEPKOTLQVAENIGSDLPSSASFRFLDSLKNRAKRSLETESLESILSRGNKARG-LQDHSASVLDLSS 528
gi | 109499693 | ref | XP_341216.3 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKEHSHTGEPKOTLQVAENIGSELPPSASFRFLDSLKNRAKRSLETESLESILSRGNKARG-LQDHSASVLDLSS 528
gi | 50658061 | ref | NP_055988.2 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKEHIIHIGEMKQTSQMAAENIGSELPPSATFRFLDMLKNAKRSLETESLESILSRGNKARG-LQEHISVLDLSS 534
gi | 114593540 | ref | XP_001137272.1 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKEHIIHIGEMKQTSQMAAENIGSELPPSATFRFLDMLKNAKRSLETESLESILSRGNKARG-LQEHSTVLDLSS 534
gi | 73951584 | ref | XP_536262.2 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKVHIIHIGEIKQTSQIAAENIGSELPPSATFRFLDMLKNAKRSLETESLESILSRGNKARG-LQEHASVLDLSS 557
gi | 119893781 | ref | XP_611974.3 | LCEGCPLQGLHKLKERIEGMNSKTKLELQKHLTLTINQEQATIFEEVQKLRPRNEQRENELIISFLRCLYEEKQKVHIIHIGEIKQTSQIAAENIGSELPPSATFRFLDMLKNAKRSLETESLESILSRGNKARG-LQEHASVLDLSS 531
gi | 118090617 | ref | XP_423827.2 | LCETCPLQGLHKLKERIEGLHPSKTKLELQKHLTLTINQEQASVFEVVKLRPRNEQRENELIISFLRCLYEEKQKQVHIIHIGEIKQTSQIAAENAVNEVPSSAPFRFLDMLKNAKRSLETESLESILSRGNKARG-LQDSSGVLDLSS 490
gi | 189514560 | ref | XP_689617.3 | QCDGCPLQGLHKLCDRIEGLHPSKTKLELQKHLADLNQEQAAVFEVVKLRPRNEQRENELIISFLRCLYEEKQKQVHIIHIGEIKQTSQIAAENAVNEVPSSAPFRFLDMLKNAKRSLETESLESILSRGNKARG-LQDSSGVLDLSS 550



gi | 120587003 | ref | NP_062610.2 | SSTLSNTSKELSMGDKAEAFVPS---ETSFKLLGSSDDLSSDSESHIAEESALLSPQAFRRRANTLSHPVVECP-APPEPAQSPGVSQRKLMRYHSVSTETPHER-----VDHLPGGESSRCCPGQSPDPPPLPPLNPSASSPNFFKVLKHSNS 630
gi | 109499693 | ref | XP_341216.3 | SSTLSNTSKELSMGDKAEALPIS---ESSFKLLGSSDDLSSDSESHIAEESALLSPQAFRRRANTLSHPVVECP-APPEPAQSPGVSQRKLMRYHSVSTETPHER-----VDHLPGGESSRCCPGQSPDPPPLPPLNPSASSPNFFKVLKHSNS 675
gi | 50658061 | ref | NP_055988.2 | SSTLSNTSKEPSVCEKALPIS---ESSFKLLGSSDDLSSDSESHLPEEPAPLSPQAFRRRANTLSHPVVECC-EPPQARGSPGVSQRKLMRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 636
gi | 114593540 | ref | XP_001137272.1 | SSTLSNTSKEPSVCEKALPIS---ESSFKLLGSSDDLSSDSESHLPEEPAPLSPQAFRRRANTLSHPVVECC-EPPQARGSPGVSQRKLMRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 660
gi | 73951584 | ref | XP_536262.2 | SSTLSNTSKEPSVCEKALPAS---ESSFKLLGSSDDLSSDSESHLPEEPAPLSPQAFRRRANTLSHPVVECC-EPPQARGSPGVSQRKLMRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 659
gi | 119893781 | ref | XP_611974.3 | SSMFNTSKEPSGYEKEALPIS---EFCFRLLGSSDDLSSDSESLTEEPALLSPQAFRRRANTLSHPVVECC-EPPQVLRGSPGVSQRKLMRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 633
gi | 118090617 | ref | XP_423827.2 | SSNLSSTNKVSKACDAHRVPTLPPENAVKSSGSDDLSSDPSYADHSVTL-POQAFRRRANTLSHLPSESR-ESLVPVETSPVSPQRKLMRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 593
gi | 189514560 | ref | XP_689617.3 | SSTLSSTHGETSLQELCSLLL---SPLRSHNSTGNLKHLEGSDRGQE-DPEEPPQGFRRRASLISHSPMLSSSEPSLPLQPTAANKPKLVRYHSVSTETPHER-----VDPSPMGESKHPGQSSAPAPPF 652



