

gi | 39841047 | ref | NP_950189.1 |MHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 62664109 | ref | XP_226125.3 | MESERDMYRQFODWCLRTYGDSGKTKTVTRKKYERIVOLLNGSESSSTDNAKFKFVVKSKGFOLGQPPDEVRRGGGGGAKOVLYVVPVKTIDGCVGDEKLSLRRVAVVEDFFDIIYSMHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 148235600 | ref | NP_003778.2 | MESERDMYRQFODWCLRTYGDSGKTKTVTRKKYERIVOLLNGSESSSTDNAKFKFVVKSKGFOLGQPPDEVRRGGGGGAKOVLYVVPVKTIDGCVGDEKLSLRRVAVVEDFFDIIYSMHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 114672728 | ref | XP_001161004.1 | MESERDMYRQFODWCLRTYGDSGKTKTVTRKKYERIVOLLNGSESSSTDNAKFKFVVKSKGFOLGQPPDEVRRGGGGGAKOVLYVVPVKTIDGCVGDEKLSLRRVAVVEDFFDIIYSMHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 194678040 | ref | XP_001788986.1 | MESERDMYRQFODWCLRTYGDSGKTKTVTRKKYERIVOLLNGSESSSTDNAKFKFVVKSKGFOLGQPPDEVRRGGGGGAKOVLYVVPVKTIDGCVGDEKLSLRRVAVVEDFFDIIYSMHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 73961290 | ref | XP_547613.2 | MESERDMYRQFODWCLRTYGDSGKTKTVTRKKYERIVOLLNGSESSSTDNAKFKFVVKSKGFOLGQPPDEVRRGGGGGAKOVLYVVPVKTIDGCVGDEKLSLRRVAVVEDFFDIIYSMHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
gi | 118086926 | ref | XP_001232142.1 |MHVETGPNGEQIRKHAGQKRTYKAISESYAFLPREA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 39841047 | ref | NP_950189.1 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 62664109 | ref | XP_226125.3 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 148235600 | ref | NP_003778.2 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 114672728 | ref | XP_001161004.1 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 194678040 | ref | XP_001788986.1 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 73961290 | ref | XP_547613.2 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
gi | 118086926 | ref | XP_001232142.1 | VTRFLMS CSECQKRMHLNPDGTDHKDNGKPPILVTSMDIDYNPITMAYMKHMKLQLLNSQQDEDESSIESDEFDMSDSTRMSAVNSDLSSNLEERMOSPQTVHGGQDDDDSAAESFNNGNETLGHSSAASGGHAGREPESSSDGKTGLEQ 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi | 39841047 | ref | NP_950189.1 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 62664109 | ref | XP_226125.3 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 148235600 | ref | NP_003778.2 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 114672728 | ref | XP_001161004.1 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 194678040 | ref | XP_001788986.1 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 73961290 | ref | XP_547613.2 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
gi | 118086926 | ref | XP_001232142.1 | EQLPLNLS DSPSAQLTSEFRIDQSGDGNKYKLLIIDLKMEREARENGSKSPAHSYSSYDSGKNEVDRGAEDLSLRGDEDEDEHDEHDESEKVNEDTGVEAERLKAFNMFVRLFVDENLDRMVPISKQPKKIQAIIDS CRRQFPE 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi | 39841047 | ref | NP_950189.1 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGG-LLSLDDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 62664109 | ref | XP_226125.3 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 148235600 | ref | NP_003778.2 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 114672728 | ref | XP_001161004.1 |SRPPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 194678040 | ref | XP_001788986.1 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 73961290 | ref | XP_547613.2 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
gi | 118086926 | ref | XP_001232142.1 | YQERARKRIRTYLKS CRRMKRS GFEMSRPIP SHLTSVAVES ILASACES ESRNAAKRMRLDRQDEAPADKCKPEAAQATYSTSTVPGSQEVLYINGNGTYSYHSYRGLGGLLNLNDTSSSGPTDLSMKRQLATSSGSSSSS SRPQ 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

gi | 39841047 | ref | NP_950189.1 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 62664109 | ref | XP_226125.3 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 148235600 | ref | NP_003778.2 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 114672728 | ref | XP_001161004.1 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 194678040 | ref | XP_001788986.1 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 73961290 | ref | XP_547613.2 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
gi | 118086926 | ref | XP_001232142.1 | LSPTEINAVRQLVAGYRESAAFLLRSADALENLILQON 638
.....610.....620.....630