

gi|38348448|ref|NP_941002.1|-----MDPRVGRX--ADQKGPANALWQVWETSQG---VGRGGS--GFASYFCLSSALDIAAAPGAAG---RAAPAAGGGPPAPAASSPPPPA---GPAALPPALLTALGPAADGARR----- 102
 gi|109504544|ref|XP_225072.4|-----MDPRVGRX--ADQKGPANALWQVWETSQG---VGRGGS--GFASYFCLSSALDIAAAPGAAG---RAAPAAGGGPPAPAASSPPPPA---GPAALPPALLTALGPAADGARR----- 102
 gi|5902142|ref|NP_008930.1|-----MDPRVGRX--ADQKGPANALWQVWETSQG---VGRGGS--GFASYFCLSSALDIAAAPGAAG---RAAPAAGGGPPAPAASSPPPPA---GPAALPPALLTALGPAADGARR----- 102
 gi|119913404|ref|XP_601308.3|MRFRRYSHNRNSMLPPTACVREDAGEHVGGADTGRGVTVGRPRD---PGGREG--VFVASLVCPWGGDRPAEGPVE--SLRTACSLRTAWGGRREGNVPHRRRRTTPAHARRGAAKRPPDTRACLHASAGAWWRVCPADADCTEGGA 144
 gi|74003095|ref|XP_545180.2|-----MDPRVAVIC--PEOKGPANALWQVWETSQG---VGRGGGAFPHYLCLNSPALDIAAASPPRHGHCARLGATGGGCCSSSSPPSTSPSP---ALLTGLVPAAGPAAVVNGGEGGRRLQKPSVSSSSCSSEV 43
 gi|118086607|ref|XP_001233759.1|-----MDPRVAVIC--PEOKGPANALWQVWETSQG---VGRGGGAFPHYLCLNSPALDIAAASPPRHGHCARLGATGGGCCSSSSPPSTSPSP---ALLTGLVPAAGPAAVVNGGEGGRRLQKPSVSSSSCSSEV 129
 gi|189532420|ref|XP_686065.3|-----MDPRVAVIC--PEOKGPANALWQVWETSQVNRINTGQHNNHHHHHNFCVNSPAFVYKTVANANNSINLNNTATIPGSGSAVLALNGN---AVDGEMSQKTGSSVDSASSCTRIRTTSPNVIAGNMN--- 127
 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|38348448|ref|NP_941002.1|-----LHKSPSLSSSSISLGRAGSDRT-----FFSFADG---AAHAHPGPRGPTPAGSPF--DQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 197
 gi|109504544|ref|XP_225072.4|-----LHKSPSLSSSSISLGRAGSDRT-----FFSFADG---AAHAHPGPRGPTPAGSPF--DQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 197
 gi|5902142|ref|NP_008930.1|-----LHKSPSLSSSSISLGRAGSDRT-----FFSFADG---AAHAHPGPRGPTPAGSPF--DQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 197
 gi|119913404|ref|XP_601308.3|PSGFPLCPHRCPSLGARRLHKSPSLSSSSSSSSSSSNAESGTESPGCCSSSSSSSALGRAGGGRRGAFHFADGPP--SAPNGHAGRGPAAGSPPPDQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 288
 gi|74003095|ref|XP_545180.2|-----ASSGPGSGRRSASVSG-----WHQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 107
 gi|118086607|ref|XP_001233759.1|ESG-----TESPGFSSSSCGGGGSSSSSCGPRAAVA PGLPGSGAGPGEFFNHEGKANGAHGHHPASHLSRNP PPPPASFPQDQHYHPGRRKRENKASTYGMNYLLSGSRGVVVAASPHQQRQPPQPALQSPGTF 263
 gi|189532420|ref|XP_686065.3|-----KGQFFFLNESVLNHNHHP-----PHPLRHFFHQEQQCKMRHPSYPTAIHNNHHHHHPGRRKSDNKASTYGINYLLNWTNGNNESS-----GTF 217
160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi|38348448|ref|NP_941002.1|-----MSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 127
 gi|109504544|ref|XP_225072.4|-----MSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 347
 gi|5902142|ref|NP_008930.1|-----MSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 127
 gi|119913404|ref|XP_601308.3|WKSRAYSPIGLHEEIIDFYNFMSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 438
 gi|74003095|ref|XP_545180.2|-----ASSGPGSGRRSASVSG-----WHQFHPGRRKRENKASTYGLNYLLSGSRAALTSGGGGPGAQAAR-----PGTF 257
 gi|118086607|ref|XP_001233759.1|WKSRAYSPIGLHEEIIDFYNFMSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 413
 gi|189532420|ref|XP_686065.3|WKTIRKYSPIGVDGLHEEIIDFYNFMSPCPEEAAMRREVVKRIETVVKDLWPTADVIFGFSFTGLYLPSTSDIDLVVFGKWERPPLQLLEQALRKHNVAEPCSIKVLDKATVPIIKLDOEIEVKVDISFNMETGVRAAEFIKNYMKKYSLL 367
310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|38348448|ref|NP_941002.1|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDS 277
 gi|109504544|ref|XP_225072.4|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDS 497
 gi|5902142|ref|NP_008930.1|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDA 277
 gi|119913404|ref|XP_601308.3|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDS 588
 gi|74003095|ref|XP_545180.2|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDS 407
 gi|118086607|ref|XP_001233759.1|PVLILVLKQFLLRDLNEVFTGGISSYSLILMAISFLQLHPRIDARRADENLGMLLVEFFELYGRNFNYLKTGIRIKEGGAYTAKEEIMKAMTSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNRDS 563
 gi|189532420|ref|XP_686065.3|PVLIFVLKQFLLRDLNEVFTGGISSYSLILMVISFLQLHPRIDTRNPNMNLGILLIEFFELYGRNFNYLKTGIRIKNGGAYMAKEDIKAMNSGYRPSMLCIEDPLLPNDVGRSSYGAMVQKVFVDYAVIVLSHAVSPPLARSYPNKDS 517
460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|38348448|ref|NP_941002.1|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 419
 gi|109504544|ref|XP_225072.4|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 639
 gi|5902142|ref|NP_008930.1|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 419
 gi|119913404|ref|XP_601308.3|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 730
 gi|74003095|ref|XP_545180.2|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 549
 gi|118086607|ref|XP_001233759.1|ESTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 705
 gi|189532420|ref|XP_686065.3|DSTLGRIIKVTQEVIDYRRRIKEKWGSRILPSPDLNRIKIKERITTCNG-----EOMSRREPSPIYQRLTSLSSPOLLSSGSSASSVSSLSGSDIDSPTTCTTPSVYQFSLQAPITLMAASLPTALPMPSSKQPAAASRLTIM 658
610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



```

      . . *   : *           *   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi | 38348448 | ref | NP_941002.1 | TNNQTRVITPPPTLGVAIPVPCRQAGVDGTSLKAVHNVTSIPAIPASAPNPLSSPHLYHKQHNMGKLSMKGSHNHQTGGGYSSVSGAVRPPVGNRGHHQYNRTGWRRKKHAHTRDRLPVSLSR 542
gi | 109504544 | ref | XP_225072.4 | TNNQTRVITPPPTLGVAIPVPCRQAGVDGTSLKAVHNVTSIPAIPASAPNPLSSPHLYHK-HNGMKLSMKGSHNHQTGGGYSSVSGAVRPPVGNRGHHQYNRTGWRRKKHAHTRDRLPVSLSR 761
gi | 5902142 | ref | NP_008930.1 | TNNQTRFITPPPTLGVAIPVPCRQAGVEGTSALKAVHHMSSIPAIPASAPNPLSSPHLYHKQHNMGKLSMKGSHGHQTGGGYSSVSGGVRPPVGNRGHHQYNRTGWRRKKHTHTRDRLPVSLSR 542
gi | 119913404 | ref | XP_601308.3 | TNNQTRFITPPPTLGVAIPVPCRQAGIEAAPALKAVHHVSSIPAIPASAPNPLSSPHLYHKQHSGMKLSMKGSHSHGQGGYSSVGTGGVRPPVGNRGHHQYNRTGWRRKKHTHTRDRLPVSLSR 853
gi | 74003095 | ref | XP_545180.2 | TNNQTRFITPPPTLGVAIPVPCRQVSEGTIPALKAVHHMSSIPAIPASAPNPLSSPHLYHKQHSGMKLSMKGSHNHSHQGGTYGSSVSGGVRPPVGNRGHHQYNRTGWRRKKHTHTRDRLPVSLSR 672
gi | 118086607 | ref | XP_001233759.1 | ASNQDSDTTP-----CTAPN-VYQFSLQAPTQLMAS---LPPALPMPSSGKPSAP-----TRTLIMAAANOV-----PVLNRRGHIQYNRTWRRK---RDSLPAASVSR 763
gi | 189532420 | ref | XP_686065.3 | PVTQARVSLPG-NLSLHTLPGRQVCMADGP--PSYLHMPPPAVPPAPPSPLPSP--LHHPKAGPKFPLKGFHNPVVH-----PVLNRRGHIQYNRTWRRK---RDSLPAASVSR 762
      .....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....

```

