

gi | 24639204 | ref | NP_476665.2 | MSYMPAQNRTMSHNNQINPPDLPPMVSAREQILMWOONSYLGDSGIHSQAVTQVPSLSGKE---DEEMEGDPLMFDLDTGFPNFQDQVDDMNOQLQTRSORVRAAMPFETLEEGIEIPSTQFDPOQPFAVORLAEPSQMLKHAVVNL 147
gi | 158287189 | ref | XP_309245.4 | -----MPMPSAKEQILMWOONSYLGDSGIHSQAVTQVPSLSGK---DDMEDDPLMFDMDQGFSPNFQDQVDDMNOQLQTRSORVRAAMPFETLEEGIEIPSTQFDPOQPFAVORLAEPSQMLKHAVVNL 124
gi | 148233338 | ref | NP_001091679.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 114586319 | ref | XP_001138191.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 6671684 | ref | NP_031640.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 46048609 | ref | NP_445809.2 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 115497488 | ref | NP_001069609.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 46048792 | ref | NP_990412.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 73989826 | ref | XP_861136.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 139
gi | 40254712 | ref | NP_571134.2 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 138
gi | 17507973 | ref | NP_493566.1 | -----MATQADLMELDMAMEPDRKAAVSHWQQOOSYL-DSGIHSQAVTQVPSLSGKNGPEEDVDTSQVLYEWEQGFSSQSFQEQVADIDGOYAMTRAOVRRAAMPFETLEEGIEIPSTQFDAAHPTNVORLAEPSQMLKHAVVNL 138
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 24639204 | ref | NP_476665.2 | INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 296
gi | 158287189 | ref | XP_309245.4 | -----INYQDADLATAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 273
gi | 148233338 | ref | NP_001091679.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 114586319 | ref | XP_001138191.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 6671684 | ref | NP_031640.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 46048609 | ref | NP_445809.2 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 115497488 | ref | NP_001069609.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 46048792 | ref | NP_990412.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 73989826 | ref | XP_861136.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 288
gi | 40254712 | ref | NP_571134.2 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 287
gi | 17507973 | ref | NP_493566.1 | -----INYQDAELATRAIPELTKLLNDEDQVVVSAAMVHQLSKKEASRHAIMNSPO-MVAALVRAISNSDLESTKAAVGLTLLHNSSHREGLLAIFKSGGIPALVKLLSSPVESVLFYAITLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 216
LTYEGSNDMSGLSLPDLVILMCPDHSRVARAVHRAVMSLSEPNFNAKPGFDHRSFVVALMAASKSNVNVNRNATGALSHMSRQGGPGLLIFRSGLLAIIRMLYDSLESVVHYAVTTLHNLHLLHODGSKMAVRLAGGLQKVMVLLQR 216
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 24639204 | ref | NP_476665.2 | NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 444
gi | 158287189 | ref | XP_309245.4 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 421
gi | 148233338 | ref | NP_001091679.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 114586319 | ref | XP_001138191.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 6671684 | ref | NP_031640.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 46048609 | ref | NP_445809.2 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 115497488 | ref | NP_001069609.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 46048792 | ref | NP_990412.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 73989826 | ref | XP_861136.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 436
gi | 40254712 | ref | NP_571134.2 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 435
gi | 17507973 | ref | NP_493566.1 | -----NNVKFLAIVTDCQLIILAYGNQESKLIILASGGPQALVNIIMRTY-TYEKLLWTTSRVLKVLVSCSSNKPAIVEAGGMOALGLHLTDP-SQRLVONCLWTLRNLSDAAIKQEGMEGLLGTIVOLLGSDDDINVVVCAAGILSNLTCNNYKMK 366
TNPKLLAQVADGLYFLLIDBAPSKITFLSILGPOILLVSIILREYDHRKLIYTVRCSRSLVCPENKPAISLGLCLPALVVELCTAKDERSQATILVAMRNLSDAINEENLQLIKLEITRVANDGMTACACGTLNLTCTNTRKQ 366
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 24639204 | ref | NP_476665.2 | MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 594
gi | 158287189 | ref | XP_309245.4 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 571
gi | 148233338 | ref | NP_001091679.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 114586319 | ref | XP_001138191.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 6671684 | ref | NP_031640.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 46048609 | ref | NP_445809.2 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 115497488 | ref | NP_001069609.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 46048792 | ref | NP_990412.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 581
gi | 73989826 | ref | XP_861136.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 585
gi | 40254712 | ref | NP_571134.2 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 580
gi | 17507973 | ref | NP_493566.1 | -----MVCCVGGTEALVRIINAGDREDITEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 510
VCSHGGIDALVTAIRRLPVEVEVTEPAICALRHLSRHOEAEMAONAVRLHYGLPVVVKLLHPPSHWPLIKAVGLIRNLALCPANHAPLREOGAIPRLVQLVRAHODTOR-RTSMGGTQQO----FVEGVRMBEIVEGCTGALHILA 510
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



