

gi | 47419907 | ref | NP_057653.3 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 114647148 | ref | XP_001154426.1 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 73995264 | ref | XP_534692.2 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 194674676 | ref | XP_001787873.1 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 37622347 | ref | NP_035665.2 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 31745146 | ref | NP_853669.1 | MSLSMRDPVPIPTGSMAYHFLPHRAPDFAMSAVLGHQPPFPALTLPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLG -- PQAHLRPLKLTMEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 118098874 | ref | XP_001234535.1 | -----MAYHFLPHRAPDFAMSAVLGHQPPFPALALPPNGAAALS LPGAALAKPIMDQLVGAAGTGFIPSSSLGQAHLRPLKLTLEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
gi | 156104899 | ref | NP_001095140.1 | ----MRDPVIOGSSMAYHFLPHRGPEFAMSAVLGHQPPFPALALPPNGS--LSLPGAALAKPIMEQLVGAAGTGLHFS--SLG--HQAHLRPLKLTLEPEEVEDDPKVHLEAKELWDQFHKRGTEMVIKSGRRMFPFPKVRCSGLDKKAK 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 47419907 | ref | NP_057653.3 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 114647148 | ref | XP_001154426.1 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 73995264 | ref | XP_534692.2 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 194674676 | ref | XP_001787873.1 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 37622347 | ref | NP_035665.2 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 31745146 | ref | NP_853669.1 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 118098874 | ref | XP_001234535.1 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
gi | 156104899 | ref | NP_001095140.1 | YILLMDIIAADDCKRYKFNHRMVAAGKADPEMPKRMVYIHPDSPAATGEQWMSKVVTFHKLKLTNNISDKHGFILAFPSDHATWQGNYSFGTQILNSMHKYQPRFHIVRANDILKLPYSTFRITVLPFETEFIAVAYONDKITQLKIDNNP 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 47419907 | ref | NP_057653.3 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKENGTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPAVKAHLFAAE---RPRDSGRLDKKASP 450
gi | 114647148 | ref | XP_001154426.1 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKENGTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPAVKAHLFAAE---RPRDSGRLDKKASP 450
gi | 73995264 | ref | XP_534692.2 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKENGTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPAVKAHLFAAE---RPRDSGRLDKKASP 450
gi | 194674676 | ref | XP_001787873.1 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKENGTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPAVKAHLFAAE---RPRDSGRLDKKASP 450
gi | 37622347 | ref | NP_035665.2 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKET--SDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPATRAQLFPAPFP--RARDTARLDKASP 450
gi | 31745146 | ref | NP_853669.1 | FAKGFRDTGNRRREKRKQLIQLSMRVFDERHKKETGTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGSDAEAEKKEEHPGACDAAKISTTTSEEPF-----RDKGSPATRAQLFPAPFP--RARDTARLDKASP 450
gi | 118098874 | ref | XP_001234535.1 | FAKGFRDTGNRRREKRKQLIQLSMRVYDERQKKNPTSDSSSEQAAFNCFQAASSPAVSTVGTSNLKDLCPSSEGS--DSADSKDDPLLEAESGKISTTTATTPAPASGAAASDDPRDKGSPSKSHFFPSDSA--TSRRETEKAPF 450
gi | 156104899 | ref | NP_001095140.1 | FAKGFRDTGNRRREKRKQLALQSMRVEEQKKNPTSDSSSEQAASFQFRQASSPAVSTAGHNLKDFCSDSE--DSDEKDNANAKGPDSSKISTTTEDSKD--DAG--LKGSVFGESDS-----SGRRSEKTRA 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 47419907 | ref | NP_057653.3 | DSRHSPATISSSTR--GLGAERRSPVREGTAPAK--VEEARALPGKEAFAPLTVQDAAAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 114647148 | ref | XP_001154426.1 | DSRHSPATISSSTR--GLGAERRSPVREGTAPAK--VEEARALPGKEAFAPLTVQDAAAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 73995264 | ref | XP_534692.2 | DSRHSPATISSSTR--GLGADERRSPREGAAPS--VEEARALPGKEAFAPLTVQDAAAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 194674676 | ref | XP_001787873.1 | DSRHSPATISSSTR--GLGAERRSPGRDSAATSKAAEARVLPKGEAFAPLTVQDAAAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 37622347 | ref | NP_035665.2 | DSRHSPATISSSTR--VPGADERRSPREGVATR--VDEARAIKADAFAPLTVQD--ATAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 31745146 | ref | NP_853669.1 | DSRHSPATISSSTR--VPGADERRSPREGVATR--VDEARAIKADAFAPLTVQD--ATAHLAAGPLPLGLGFAPGLAGQOFF---NGHPLFLHPSQFAMGGAFSSMAAAGMGPLLATVSGASTVSGSLDSTAMASAAAQGLSGASAA 600
gi | 118098874 | ref | XP_001234535.1 | DSRHSPATISSSTRSGGLSGLLEKSLDRDG--PK--VDENRLLAG-----IALLHPSQFAMGGALSGKAAG--MGLLLATVSGASAGGLDSTAMP--TEAAQGLSGASAS 600
gi | 156104899 | ref | NP_001095140.1 | DSRSPITLISSTR---SHEELKSPVREP---AKTIDDCRTVSK--ENYMLTVQD--GAHLNHLNHPGPTGLAGQOFFNHLGGAHFPFLHPSQFAMGGAFSSMAAAGMGPLLAAYS--SGVSLDGLSGLP--SRSPSLTAP-- 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 47419907 | ref | NP_057653.3 | LPPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAASAAAASSVHRHPFLNLTMRPRLRYSYSPYIPVVPVDSGLLTLALPMAAAAGPLDGKVAALAAAPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 114647148 | ref | XP_001154426.1 | LPPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAASAAAASSVHRHPFLNLTMRPRLRYSYSPYIPVVPVDSGLLTLALPMAAAAGPLDGKVAALAAAPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 73995264 | ref | XP_534692.2 | LPPFHLQOHVLASQGLGRRRKLRRH--LAPFNALLSVREPLLETSSVHG-----SRGYSIFMVPVDSGLLTLALPMAAAAGPLDGAALAAAPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 194674676 | ref | XP_001787873.1 | LPPFHLQOHVLASQGL-----VEEGWMMR--APPH-----RAG-----PAXXXXXXXXXXXXXXXXXXSPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 37622347 | ref | NP_035665.2 | LPPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAASTAAASSVHRHPFLNLTMRPRLRYSYSPYIPVVPVDSGLLTLALPMAAAAGPLDGKVAALAAAPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 31745146 | ref | NP_853669.1 | LPPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAASAAAASSVHRHPFLNLTMRPRLRYSYSPYIPVVPVDSGLLTLALPMAAAAGPLDGKVAALAAAPASVAVDSSGSELNSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 118098874 | ref | XP_001234535.1 | ALPPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAAS--SAAASSVHRHPFLN--AVRPRRLRYSYSPYIPVVPVDSGLLTLAMPALAAAS--GETKGSALAS--PGAVPLDASDLTSSRSSLSSSSVSLPKLCAEKAATSELOSIQR 750
gi | 156104899 | ref | NP_001095140.1 | --MPFHLQOHVLASQGLAMSPFGSLFPYPTMMAAAAAAS--SAAASSVHRHPFLS--AVRPRRLRYSYSPYIPVVPVDSGLLTLAMPALAAAS--LGVKGDGNTTSPASALDS--EVTSS--EGVSLSPKCTEKDSS--SELOSIQR 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi |47419907|ref|NP_057653.3| LVSGLEAKPDRSRASG----- 822
gi |114647148|ref|XP_001154426.1| LVSGLEAKPDRSRASG----- 822
gi |73995264|ref|XP_534692.2| LVSGLEAKPDRSRASG----- 822
gi |194674676|ref|XP_001787873.1| LVSGLEAKPDRSRASG----- 822
gi |37622347|ref|NP_035665.2| LVSGLEAKPDRSRASG----- 822
gi |31745146|ref|NP_853669.1| LVSGLEAKPDRSRASG----- 822
gi |118098874|ref|XP_001234535.1| LVSGLEAKPDRSRASG----- 822
gi |156104899|ref|NP_001095140.1| LVSGLEPKDRARVSP----- 822
.....760.....770.....780.....790.....800.....810.....820..

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