

gi|6680486|ref|NP\_032428.1| ..... 150  
 gi|109468378|ref|XP\_230950.4| ..... 150  
 gi|4504763|ref|NP\_002201.1| ..... 150  
 gi|114582305|ref|XP\_515967.2| **MVTQRD**ACIY**NPKFLKPLVARKFPAGCGGNV**GALAT**IPVD**AGRLGR**WTVSPRPRPHASSEGR**LS**PTSSSSSS**TAAS**RAGSSSFQVSSQ**CRRG**SQ**ARGAAL**TPAVPELRRCV**ERRR**REAR**DRLR**CCPP**ARS**APLVP**GGRS**EAQPS**CL**PR**SC 150  
 gi|27805957|ref|NP\_776792.1| ..... 150  
 gi|74004771|ref|XP\_850989.1| ..... 150  
 gi|45382133|ref|NP\_990770.1| ..... 150  
 gi|76253792|ref|NP\_001028893.1| ..... 150  
 gi|281360999|ref|NP\_001162777.1| ..... 150  
 gi|158289389|ref|XP\_311131.4| ..... 150

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|6680486|ref|NP\_032428.1| ..... 300  
 gi|109468378|ref|XP\_230950.4| ..... 300  
 gi|4504763|ref|NP\_002201.1| ..... 300  
 gi|114582305|ref|XP\_515967.2| **PGLAEKRAAGK**FGRA**QAAGRGHWAPRWGGGRWLP**PAWR**PARTSAMAF**PPRRRL**LCPRGL**PLLL**SGLLL**PLCRAF**NLDV**SPA**EYS**GP**EGSY**FG**FAVD**FFV---**PSASS**RM**FLLV**GAPK**ANT**---**TOPGI**VEGG**QVLK**CD**WSS**TR**RC** 300  
 gi|27805957|ref|NP\_776792.1| ..... 300  
 gi|74004771|ref|XP\_850989.1| ..... 300  
 gi|45382133|ref|NP\_990770.1| ..... 300  
 gi|76253792|ref|NP\_001028893.1| ..... 300  
 gi|281360999|ref|NP\_001162777.1| ..... 300  
 gi|158289389|ref|XP\_311131.4| ..... 300

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|6680486|ref|NP\_032428.1| ..... 450  
 gi|109468378|ref|XP\_230950.4| ..... 450  
 gi|4504763|ref|NP\_002201.1| ..... 450  
 gi|114582305|ref|XP\_515967.2| **QPIEF**DTGN**RDYAK**DD**PLEFK**SH**QWFG**AS**VR**SK**Q**---**DKIL**ACAP**L**YHW**RT**EM**KQ**---**ERE**PV**GC**FL**QD**G---**IKT**VEY**AP**CR**SK**NI**DAD**GG**FC**GG**FS**ID**FT**K---**ADR**VLLGG**PG**S**F**W**OG**LI**S**DD**VAE**II**SK**Y**DP**--- 450  
 gi|27805957|ref|NP\_776792.1| ..... 450  
 gi|74004771|ref|XP\_850989.1| ..... 450  
 gi|45382133|ref|NP\_990770.1| ..... 450  
 gi|76253792|ref|NP\_001028893.1| ..... 450  
 gi|281360999|ref|NP\_001162777.1| ..... 450  
 gi|158289389|ref|XP\_311131.4| ..... 450

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|6680486|ref|NP\_032428.1| ..... 600  
 gi|109468378|ref|XP\_230950.4| ..... 600  
 gi|4504763|ref|NP\_002201.1| ..... 600  
 gi|114582305|ref|XP\_515967.2| **NVYS**IK**YNN**QL**AR**TA**QAI**F**DD**S**YL**G**Y**SV**AV**GD**FN**GD**GI**ED**FV**SG**V**PR**AAR**TL**GM**V**Y**Y**D**G**KN**M**SS**L**H**N**F**T**GE**Q**MA**Y**FG**F**V**A**AT**D**ING**DD**Y**AD**VF**I**G**AP**L**F**M**DR**G**S**D**G**KL**Q**EV**G**Q**V**S**L**Q**R**A**---**VG**D**F**C---**TK**L**NG**F**EV**F**AR**F**G**S 600  
 gi|27805957|ref|NP\_776792.1| ..... 600  
 gi|74004771|ref|XP\_850989.1| ..... 600  
 gi|45382133|ref|NP\_990770.1| ..... 600  
 gi|76253792|ref|NP\_001028893.1| ..... 600  
 gi|281360999|ref|NP\_001162777.1| ..... 600  
 gi|158289389|ref|XP\_311131.4| ..... 600

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



Multiple sequence alignment of protein segments (gi | accession | ref | accession). Amino acid sequences are shown with color-coding for conservation. Asterisks indicate conserved positions. A phylogenetic tree is visible at the bottom.

Second multiple sequence alignment block showing protein sequences and a phylogenetic tree. Includes reference identifiers and sequence conservation markers.

Third multiple sequence alignment block with protein sequences, conservation markers, and a phylogenetic tree. Reference identifiers are present on the left.

Fourth multiple sequence alignment block, showing protein sequences and a phylogenetic tree. Includes sequence conservation indicators and reference identifiers.

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gi|6680486|ref|NP_032428.1|-----1350
gi|109468378|ref|XP_230950.4|-----1350
gi|4504763|ref|NP_002201.1|-----1350
gi|114582305|ref|XP_515967.2|-----1350
gi|27805957|ref|NP_776792.1|-----1350
gi|74004771|ref|XP_850989.1|-----1350
gi|45382133|ref|NP_990770.1|-----1350
gi|76253792|ref|NP_001028893.1| R-----1350
gi|281360999|ref|NP_001162777.1| VHRDRASQAVQEPVNVNLSFTITVSTSSSSSGGAPASALRGHSTQGHIO MAGPVQHTSSSSSSNYSRWPADQQQOHOOLL LAGSGGSGLGGSPVTFNDKSFQGRNNNFHGTLLDLGTLNRCNVNDNELVRSQGYQNPSSLSGDSGGFQA 1350
gi|158289389|ref|XP_311131.4| N---RVSGGGSE-RRYQTESSDTSAGRMRGEGYQMGGRVYRQGYAQQG-----SHGEGYR-----DQQQHYDGGVRVDAGGYGAAG---GAGGSGGGSSSSSS---ERNSTSSVVVYI-----SKNRTIY 1350
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi|6680486|ref|NP_032428.1|-----1500
gi|109468378|ref|XP_230950.4|-----1500
gi|4504763|ref|NP_002201.1|-----1500
gi|114582305|ref|XP_515967.2|-----1500
gi|27805957|ref|NP_776792.1|-----1500
gi|74004771|ref|XP_850989.1|-----1500
gi|45382133|ref|NP_990770.1|-----1500
gi|76253792|ref|NP_001028893.1|-----1500
gi|281360999|ref|NP_001162777.1|-----1500
gi|158289389|ref|XP_311131.4|-----1500
NANQGHYGGQNOA QFQARNPGFVGGTSYGGOTQYFGQPGG-YQTHHVTYSSGSKPYYGRENEDFYDEDNLQQAIPGHWSSSSSSSSSSGTRRLRRSNDKDGAIEKPLQIDLNSPCQSARCKSIRCVVNLGTEDGDAAFVAIRARMVAKI 1500
RDEDGRVHVSSESEYHRHDSDLGGGQALGGGTSSAAATGSSRRRRMMSQQDGEAPPRTGLITTFMHLGDYTGSGGAAGSAAALNDLNRLENKFRTEYEQCQQQQQVVEEARLCHATRCAIHCCKAGPIGN--SDVAFVALRTRAVAHY 1500
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500

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gi|6680486|ref|NP_032428.1|-----1611
gi|109468378|ref|XP_230950.4|-----1611
gi|4504763|ref|NP_002201.1|-----1611
gi|114582305|ref|XP_515967.2|-----1611
gi|27805957|ref|NP_776792.1|-----1611
gi|74004771|ref|XP_850989.1|-----1611
gi|45382133|ref|NP_990770.1|-----1611
gi|76253792|ref|NP_001028893.1|-----1611
gi|281360999|ref|NP_001162777.1|-----1611
gi|158289389|ref|XP_311131.4|-----1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDLFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDLFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDITNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDITNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGNSET 1611
MKNKENQHSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLLAVLVFVVMYRMGFFKRVPRPPEE-QEREQLOPHENGEGTSEA 1611
LKAESQNKSYIVRSSASFSVIEMPYKNLNPBLPTSTQSASLKVWNSSE-NPQVPPGWWVALAVLAGLLLLLALLIFVMYKLGFFNRRVPRPPEE-EDRTEKEQLPQENGDRNTEA 1611
MEKLSANVPLNVSILAVANVTLPLPFIGAPKDAIVKTHEIFYKAEPEPLQVPDVVPLWVVVLAACAGALIFLLLVLLYKCGFFNRRNRPDHS--QERQPLRNG-YHGDEHL 1611
LHQLSSAPLHFSIMNVARVLLKLPYIGEPKDKPIKTHEIKVLAPEPTIKPEVVPVLIWVVVLAACAGALIFLLLVLLYKCGFFERKRPDAS--ERQPLNRNG-YHGDEHL 1611
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610

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