

gi | 110347431 | ref | NP_001036009.1 | MPRPCTSGRRPLLLVLLPLFAAATAAASPSPP--SQVVEVGVVPRPASAIVAVCCCPGQSRSRRCIRAFRCVRSQPKKAGPQRCINLVPV-APVSPSPS-VRKROVSLNWOPLTLEARALLKRRRPRGPGGRLLRRRPPORAPA 150
gi | 73948320 | ref | XP_533664.2 | MRRPGPSGRRPLLLVLLPLFAAATAAASPSPPGSAEAVVAGIPGRRAGLAVCCCPGRPRRRCFRASCRVECPPEKAGPQCLTSVPLVVPSPS-VRKROVSLNWOPLTLEARALLRRLRRRPGGRALLRRRPPORAPA 150
gi | 32189330 | ref | NP_783572.1 | MRRPGLGGPCPLLLLLLP---AATSASGSSPSPPS-PIEKAVVPHQAGVAACHCCLDQPKSSRCTRASCRVRNCPAKCTGLEGCLTPTP-SVPSPSRSVPEKSOVSLNWOPLTLEARALLRRLRRRPGPWARALLKRRRPPHRAPA 150
gi | 109458418 | ref | XP_238093.4 | MRRPGLGCHCPLLLLLLP---AATSASGSSPSPPS-PIEKAVVPHQAGVAACHCCLDQPKSSRCTRASCRVRNCPAKCTGLEGCLTPTP-SVPSPSRSVPEKSOVSLNWOPLTLEARALLRRLRRRPGPWARALLKRRRPPHRAPA 150
gi | 292629992 | ref | XP_002667678.1 | -----MLCKNGGVCVQKDCCHCPNFITKFKCHIVSITTTNDIEKPEGAADSANQAMTVEVILPLQTPQINTDVSFPMVVR--VQHPPEASVKIHOVILKVGYGPTVHEHSEIVTWS--AGLSG-ARHGLPGERSEA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 110347431 | ref | NP_001036009.1 | GKAPVLCPLICHNGGVCVKPDRCLCPDFAGKFCQLHSSGARPPAPAVPGLTRSVYIMPLANHRDDEHGVAISMVSVHEHPQEAASVVVHVQVERVGPWEADAEAVARAEEAAAAPYTVLAQSAAPREDGYSDAAGFGYCFRELRG 300
gi | 73948320 | ref | XP_533664.2 | GQTRVLCPLICHNGGVCVKPDRCLCPDFAGKFCQLHSSGARPPAPAMPGLTRSVYIMPLANHRDDEHGIE-----GQTRVLCPLICHNGGVCVKPDRCLCPDFAGKFCQLHSSGARPPAPAMPGLTRSVYIMPLANHRDDEHGIE----- 300
gi | 32189330 | ref | NP_783572.1 | GQARVLCPLICHNGGVCVKPDRCLCPDFAGKFCQLHSSGARPPAPAMPGLTRSVYIMPLANHRDDEHGVAISMVSVHEHPQEAASVVVHVQVERVGPWEANPEALARAEAAAAPYTVLAQSAAPREDGYSDAAGFGYCFRELRG 300
gi | 109458418 | ref | XP_238093.4 | GQARVLCPLICHNGGVCVKPDRCLCPDFAGKFCQLHSSGARPPAPAMPGLTRSVYIMPLANHRDDEHGVAISMVSVHEHPQEAASVVVHVQVERVGPWEANPEALARAEAAAAPYTVLAQSAAPREDGYSDAAGFGYCFRELRG 300
gi | 292629992 | ref | XP_002667678.1 | PPPRIIQATIRGDSVYTE-----SSGFKYCFREVRNGQCSSPLPLGLRSQEMCCRGVQKAWGIN-ECTLCPAIS----- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 110347431 | ref | NP_001036009.1 | ECASPLPGLRTOEVCCRGAGLAWGVHDCQLCSERLGNSEKRVSAIDPQCPPTGFERNVNG-FCEDVDECAQGGRCQHGECANTRGGYTCVCPDGFLLDSSRSSCISOHVISEAKGPCFRVLRDGGCSLPILRNITKQICCCSRVKGAWGRCC 450
gi | 73948320 | ref | XP_533664.2 | -----DRVGTDPGCPPTGFERNVNG-FCEDVDECAQGGRCQHGECANTRGGYTCVCPDGFLLDSSRSSCISOHVISEAKGPCFRVLRDGGCSLPILRNITKQICCCSRVKGAWGRCC 450
gi | 32189330 | ref | NP_783572.1 | ECASPLPGLRTOEVCCRGAGLAWGVHDCQPCAEHLRNSNRVSGNGLCPPTGFERNVNG-SCVDVDECAQGGRCQHGECANTRGGYTCVCPDGFLLDSSRSSCISOHVISEAKGPCFRVLRDGGCSLPILRNITKQICCCSRVKGAWGRCC 450
gi | 109458418 | ref | XP_238093.4 | ECASPLPGLRTOEVCCRGAGLAWGVHDCQPCAEHLRNSNRVSGNGLCPPTGFERNVNG-SCVDVDECAQGGRCQHGECANTRGGYTCVCPDGFLLDSSRSSCISOHVISEAKGPCFRVLRDGGCSLPILRNITKQICCCSRVKGAWGRCC 450
gi | 292629992 | ref | XP_002667678.1 | -----GNSVNG-QASCPKGFDRVNGQCVDIINECLQGGRCENGNVNRGYSYSCVNCGFLLDASHGICISOHVISEAKGPCFRVLRDGGCSLPILRNITKQICCCSRVKGAWGRCC 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 110347431 | ref | NP_001036009.1 | LCPFFGSEGFREI CPAGPGYHYASDLRNTPLQEPVPRVLSQPRTLPAISRPAGFLPTHRLEPRPEPRP-----DPRPGPE-----LPLPPIPAWTGPEIPESGPGSSMCQR 600
gi | 73948320 | ref | XP_533664.2 | LCPFFGSEGFREI CPAGPGYHYASDLRNTPLQEPVPRVLSQPRTLPAISRPAGFLPTHRLEPRPEPRP-----EPRPGPE-----LPLPPIPAWTGPEIPESGPGAGVCR 600
gi | 32189330 | ref | NP_783572.1 | LCPFFGSEGFREI CPAGPGYHYASDLRNTPLQEPVPRVLSQPRTLPAISRPAGFLPTHRLEPRPEPRP-----DPRPGPE-----LPLPPIPAWTGPEIPESGPGSSMCQR 600
gi | 109458418 | ref | XP_238093.4 | LCPFFGSEGFREI CPAGPGYHYASDLRNTPLQEPVPRVLSQPRTLPAISRPAGFLPTHRLEPRPEPRP-----DPRPGPE-----LPLPPIPAWTGPEIPESGPGSSMCQR 600
gi | 292629992 | ref | XP_002667678.1 | LCPFFGSAAFKEI CPAGPGYHYASAVKINQRVADIVDSSGNTVNRVTSIQDKQIQEPESSRINQSTRITQTSNT-----HTIRVG-----QPIISQSRPQPDIGSVIITIP 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 110347431 | ref | NP_001036009.1 | NPQVCGPGRCSIRPSGYTCACDSGFRLSPGGTRCIDVDECRVPPPAPGRCEVNSPGSFRVCVCGPFRAGPRAAECLDVDECHRVPPPDLGRCENTPG-SFLCVCPAGYQAAPHGASCQDVDECTQSPGLCGRGACNKLPFSFRVCVPA 750
gi | 73948320 | ref | XP_533664.2 | SPOVCGSGRCTIPRPSGYTCACDSGFRLSPGGTRCIDVDECRVPPPAPGRCENTPGSFRVCVCGPFRAGPRAAECLDVDECHRVPPPDLGRCENTPG-SFLCVCPAGYQAAPHGAGCQDVDECTQSPGLCGRGVNENLSSGFRVCVPA 750
gi | 32189330 | ref | NP_783572.1 | NPQVCGPGRCSIRPSGYTCACDSGFRLSPGGTRCIDVDECRVPPPAPGRCENTPGSFRVCVCGPFRAGPRAAECLDVDECRVPPPDLGRCENTPG-SFLCVCPAGYQAAPHGASCQDVDECTQSPGLCGRGACNKLPFSFRVCVPA 750
gi | 109458418 | ref | XP_238093.4 | NPQVCGPGRCSIRPSGYTCACDSGFRLSPGGTRCIDVDECRVPPPAPGRCENTPGSFRVCVCGPFRAGPRAAECLDVDECRVPPPDLGRCENTPG-SFLCVCPAGYQAAPHGASCQDVDECTQSPGLCGRGACNKLPFSFRVCVPA 750
gi | 292629992 | ref | XP_002667678.1 | KLNQPTAGRTINIHAGNSPSSIT--QPARNVTPVIRQTSRPSVNRQVPSVPRPPVTPR-----PPPTRODVRVCSERPQVCGPGRCDLPGGRHTVCVNGFILLNQQGHQDKNCEVLP----- 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 110347431 | ref | NP_001036009.1 | GFRGSACEEDVDECAQPPPCGPRCDNTAGSFHCACPAGFRSRGPGAPQDVDECARSPPPCTVGRCENTEGSFQCVCPMGFPNITAGSECEBDVDECENHLACPGQECVNSPGSFQCRCTCPGSHHLHRGRCTDVDECSGAPP CGPHGH 900
gi | 73948320 | ref | XP_533664.2 | GFRGSACEEDVDECAQPPPCGPRCDNTAGSFHCACPAGFRSRGPGAPQDVDECARSPPPCAYGRCENTEGSFQCVCPMGFPNITAGSECEBDVDECENHLACPGQECVNSPGSFQCRCTCPGSHHLHRGRCTDVDECSGAS-CGPHGH 900
gi | 32189330 | ref | NP_783572.1 | GFRGSACEEDVDECAQPPPCGPRCDNTAGSFHCACPAGFRSRGPGAPQDVDECARSPPCAYGRCENTEGSFQCVCPMGFPNITAGSECEBDVDECENHLACPGQECVNSPGSFQCRCTCPGSHHLHRGRCTDVDECSGTP-CGLHG 900
gi | 109458418 | ref | XP_238093.4 | GFLGSAACEEDVDECAQPPPCGPRCDNTAGSFHCACPAGFRSRGPGAPQDVDECARSPPCAYGRCENTEGSFQCVCPMGFPNITAGSECEBDVDECENHLACPGQECVNSPGSFQCRCTCPGSHHLHRGRCTDVDECSGTP-CGLHG 900
gi | 292629992 | ref | XP_002667678.1 | -----RPSVGEVNTIPGFRVCPAGYQAINSQQLVDLDECRVPPNCPINGRCEVNSLGRFCVCRIGKLDQDN--SGIDIDEVDP LRCPGKECVNSQGSFRVCSQRPGLDLNGCPSDVNCEDEFSQ--CPGQ 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



