

gi|9966885|ref|NP_065137.1|MLLRLLLAWAAAGPTLGGDPWAAEPR-----AACGFPSSCYALFPR-----RRT 150
gi|114638554|ref|XP_522073.2|MSECVYVWQGSHLQASIGRGRGRGSRRLAAAPAHSLQLSPAPGPPPARPCEAP 150
gi|57100323|ref|XP_540833.1|MLLRLLLAWAAAGPTLGGAPWAAEPR-----AVCGPSSCYALFPR-----RRT 150
gi|16923944|ref|NP_473383.1|MLLRLLLAWAAAVPALGQVPTPEPR-----AACGFPSSCYALFPR-----RRT 150
gi|109459747|ref|XP_238151.4| MSLSRRECSLLILLVPLPLLCPSPLTPPPPTPLLPAPAAPGELAGELAAAPVHSLQGVSPGPPPALPPEALIPPPVKSSGRPEPGOSGGVAMLLRLLLAWAAAVPALGQAPWTPPEPR-----AACGFPSSCYALFPR-----RRT 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|9966885|ref|NP_065137.1|FLFAWRACR----ELGGDLATPRTPPEAQRVDSLVGAGPASRLWLWIGLQARQCQLRPLRGTWITGDQDTAFNTWAQPAAGGCPAQRCALEASGEHRWLEGSCTLAVDGYLCOFGFEGACPALQDEAGQAGPAVYITPFHLVST 300
gi|114638554|ref|XP_522073.2|GPPPVKSCRRPGAGPLGGDLATPRTPPEAQRVDSLVGAGPASRLWLWIGLQARQCQLRPLRGTWITGDQDTAFNTWAQPAAGGCPAQRCALEASGEHRWLEGSCTLAVDGYLCOFGFEGACPALQDEAGQAGPAVYITPFHLVST 300
gi|57100323|ref|XP_540833.1|FLFAWRACR----ELGGDLATPRTPPEAQRVDSLVGAGPASRLWLWIGLQARQCQLRPLRGTWITGDQDTAFNTWAQPAAGGCPAQRCALEASGEHRWLEGSCTLAVDGYLCOFGFEGACPALQDEAGQAGPAVYITPFHLVST 300
gi|16923944|ref|NP_473383.1|FLFAWRACR----ELGGDLATPRTPPEAQRVDSLVGAGPASRLWLWIGLQARQCQLRPLRGTWITGDQDTAFNTWAQPAAGGCPAQRCALEASGEHRWLEGSCTLAVDGYLCOFGFEGACPALQDEAGQAGPAVYITPFHLVST 300
gi|109459747|ref|XP_238151.4|FLFAWRACR----ELGGDLATPRTPPEAQRVDSLVGAGPASRLWLWIGLQARQCQLRPLRGTWITGDQDTAFNTWAQPAAGGCPAQRCALEASGEHRWLEGSCTLAVDGYLCOFGFEGACPALQDEAGQAGPAVYITPFHLVST 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|9966885|ref|NP_065137.1|EFEWLPFGSVAAVQCQAGRGASLLCVKQPEGVGSWGRAGPLCLGTGCGSPDNGGCEHECVVEVDGHSVCRCEGFRLAADGRSCEDPCAAPCEQCEPGGPGYSGCHRLGFRPAEDDPRHRCVDTDECCQIAGVCOQMCVNYVGGFECYCS 450
gi|114638554|ref|XP_522073.2|EFEWLPFGSVAAVQCQAGRGASLLCVKQPEGVGSWGRAGPLCLGTGCGSPDNGGCEHECVVEVDGHSVCRCEGFRLAADGRSCEDPCAAPCEQCEPGGPGYSGCHRLGFRPAEDDPRHRCVDTDECCQIAGVCOQMCVNYVGGFECYCS 450
gi|57100323|ref|XP_540833.1|EFEWLPFGSVAAVQCQAGRGASLLCVKQPEGVGSWGRAGPLCLGTGCGSPDNGGCEHECVVEVDGHSVCRCEGFRLAADGRSCEDPCAAPCEQCEPGGPGYSGCHRLGFRPAEDDPRHRCVDTDECCQIAGVCOQMCVNYVGGFECYCS 450
gi|16923944|ref|NP_473383.1|EFEWLPFGSVAAVQCQAGRGASLLCVKQPEGVGSWGRAGPLCLGTGCGSPDNGGCEHECVVEVDGHSVCRCEGFRLAADGRSCEDPCAAPCEQCEPGGPGYSGCHRLGFRPAEDDPRHRCVDTDECCQIAGVCOQMCVNYVGGFECYCS 450
gi|109459747|ref|XP_238151.4|EFEWLPFGSVAAVQCQAGRGASLLCVKQPEGVGSWGRAGPLCLGTGCGSPDNGGCEHECVVEVDGHSVCRCEGFRLAADGRSCEDPCAAPCEQCEPGGPGYSGCHRLGFRPAEDDPRHRCVDTDECCQIAGVCOQMCVNYVGGFECYCS 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|9966885|ref|NP_065137.1|EGHELEADGISCSAPAGAMGASQDLGDELDDGDEDEDEDEAWKAFNGGWTMPGILWMEPTQPPDFALAYRSPFPEDREPOIPYPEPTWPPPLSAPRVVYHSSVLSVTRPVVVSATHPILPSAHPQ-----PVIPAT 600
gi|114638554|ref|XP_522073.2|EGHELEADGISCSAPAGAMGASQDLGDELDDGDEDEDEDEAWKAFNGGWTMPGILWMEPTQPPDFALAYRSPFPEDREPOIPYPEPTWPPPLSAPRVVYHSSVLSVTRPVVVSATHPILPSAHPQ-----PVIPAT 600
gi|57100323|ref|XP_540833.1|EGHELEADGISCSAPAGAMGASQDLGDELDDGDEDEDEDEAWKAFNGGWTMPGILWMEPTQPPDFALAYRSPFPEDREPOIPYPEPTWPPPLSAPRVVYHSSVLSVTRPVVVSATHPILPSAHPQ-----PVIPAT 600
gi|16923944|ref|NP_473383.1|EGHELEADGISCSAPAGAMGASQDLRDLRDLDDGEEGEEDEEPEWDFDGTWTEQGIILWLAPTHPPDFGLPYRNFPPDGEPRHLHLEPTWPPPLSAPRGVYHSSVLSVTRPMVISAIRPILPSAHTSVISAIRPILPSVHPMAPAPAT 600
gi|109459747|ref|XP_238151.4|EGHELEADGISCSAPAGAMGASQDLRDLRDLDDGEEGEEDEEPEWDFDGTWTEQGIILWLAPTHPPDFGLPYRNFPPDGEPRHLHLEPTWPPPLSAPRGVYHSSVLSVTRPMVISAIRPILPSAHTSVISAIRPILPSVHPMAPAPAT 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|9966885|ref|NP_065137.1|HPALSRDHQIPVIAANYPDLPSSAYQPGILSVSHSAQPPAHQPPMISTKYPELFAHOSPMFPTDRVAGTQTTTLHPGIPPNHAPLVITLGAQLPQPAPDALVLRTOATQLPIPTAQPSTLTTSSRSPVSAHQISVPAATQPAALP-TLL 750
gi|114638554|ref|XP_522073.2|HPALSRDHQIPVIAANYPDLPSSAYQPGILSVSHSAQPPAHQPPMISTKYPELFAHOSPMFPTDRVAGTQTTTLHPGIPPNHAPLVITLGAQLPQPAPDALVLRTOATQLPIPTAQPSTLTTSSRSPVSAHQISVPAATQPAALP-TLL 750
gi|57100323|ref|XP_540833.1|HPALPPDHQIPMISANHPDLSSAYQPPILSATHPAWPPAHQPPVISTAKHPQLSPGHOSPVFPDTCVTDICANHLPLQIPANETPPVATPNTHQSLVTPDVLKQATHLPLTSTVQPPPLTTPRPPVLAHQVFPVPAATQAPGLH-TTL 750
gi|16923944|ref|NP_473383.1|PPAVFSEHQIPKIKANYPDLFPGHKPGIISATHPAQPPHPPHIIITKYPQVFPVPPQAPMSPDT-----HIIITLPPVPHLDPGDITSAHQHPLLPDAPGIRTOAPQLSVS-ALQPLPTNRS---SVHETPVPANQPPAFSSPL 750
gi|109459747|ref|XP_238151.4|PPAVLPEHQIPKIKASYPDLFPGHKPGIISATHPAQPPHPPHIIITKYPQVFPVPPQAPMSPDT-----HIIITLPLPSHLDPGDITSAQHEHLLPDPVPGIRTOAPQLSVS-ALQPLPTNRS---SVHETPVPANQPPAFSSPL 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|9966885|ref|NP_065137.1|PSQ---SPINQTSIPSPHPSKAPQIPREDGSPKLLALWLPSPAPTAAPTALGEAGLAHESQRDRRLLVALLVPTCVFLVLLALGIVYCTRCSGHAPNKRITDCYRWVTHAGSKSPTEPMPPRGLSGVQTCRTSV 889
gi|114638554|ref|XP_522073.2|PSQ---SPINQTSIPSPHPSKAPQIPREDGSPKLLALWLPSPAPTAAPTALGEAGLAHESQRDRRLLVALLVPTCVFLVLLALGIVYCTRCSGHAPNKRITDCYRWVTHAGSKSPTEPMPPRGLSGVQTCRTSV 889
gi|57100323|ref|XP_540833.1|TSPPGSPTNHPSLSTPTYPHSPKSPVPREGADSKVAPWLPS----AAPTALGEASMAHESQRDRRLLVALLVPTCVFLVLLALGIVYCTRCSGHAPNKRITDCYRWVTHAGSKSPTEPMPPRGLSGVQTCRTSV 889
gi|16923944|ref|NP_473383.1|PPQ---RPTNQTSSISPTHSYSRAPLVPREGVPPKSVVQLPVPVSTAAPTALAEGLAGQSORDRRLLVALLVPTCVFLVLLALGIVYCTRCSGHAPNKRITDCYRWVTHAGSKSPTEPMPPRGLSGVQTCRTSV 889
gi|109459747|ref|XP_238151.4|PPQ---SPINQTSISPTHSYSRAPLVPREGVPPKSVVQLPVPVSTAAPTALAEGLAGQSORDRRLLVALLVPTCVFLVLLALGIVYCTRCSGHAPNKRITDCYRWVTHAGSKSPTEPMPPRGLSGVQTCRTSV 889
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....

