

gi|6680486|ref|NP_032428.1|
 gi|109468378|ref|XP_230950.4|
 gi|4504763|ref|NP_002201.1|
 gi|114582305|ref|XP_515967.2|
 gi|27805957|ref|NP_776792.1|
 gi|74004771|ref|XP_850989.1|
 gi|45382133|ref|NP_990770.1|
 gi|189523320|ref|XP_001918557.1|
 gi|24642641|ref|NP_523378.2|
 gi|158289389|ref|XP_311131.4|

 MVTQRDACIYVNPKFLKPLVARKFPAGGGNVGALATPVDDAGRLGRWTVSPRPRPHASSEGRLESPPTSSSSSTAAERAGSSSFQVSSQCRRGSCARGAALTPAVPELRRCVERREARRDRRLRCCPPRARSAPLVPGGRSEAQPSCLPRSC

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

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 MAAPGRLLLRPRPGGLLLLLPGLLLPLADAFNLDVESPAEYAGPEGSYFGFAVDFFE---PSTSSRMFLLVGAPKANT---TOPGIVEGGQVLKCECSSRRRC

 MAFPPIRRRLRIGPRGLPLLLSGLLLPLCRAFNLDVDSPAEYSGPEGSYFGFAVDFFV---PSASSRMFLLVGAPKANT---TOPGIVEGGQVLKCDWSSSTRRC

 PGLAEKRAAGKFGRAQAAGRGHWAPRWGGGRWLPAPWRPARTSAMAFPIRRRLRIGPRGLPLLLSGLLLPLCRAFNLDVDSPAEYSGPEGSYFGFAVDFFV---PSASSRMFLLVGAPKANT---TOPGIVEGGQVLKCDWSSSTRRC

 MAFPPIRRRLRIGPRGLPLLLSGLLLPLCRAFNLDVDSPAEYSGPEGSYFGFAVDFFV---PSASSRMFLLVGAPKANT---TOPGIVEGGQVLKCDWSSSTRRC

 MAALRASLLLS-CALTAARAFNLDAERPAVYSGAEGSYFGFAVDFFA---FDASSMFLLVGAPKANT---TOPGIVEGGQVLKCDWSSSTRRC

 MGKHFVRYWLVWALVALFTTKRAPAFNLDISKPIVFSGPPGSYFGFAVDFFV---PDNSQ-LNLLVGAAPRANTSDOTPSAVTERGAVFSCVPQKSGTC

 MSGDSIHRRMALHCPITSLILLIAMSAGHYNIDLPSVYRFRQSSNEMFQFSIAMEKGRSGFYGNQNNVSLTVGAPKFDTSR-YOQGVTEAGGVFKCSLNDDD-C

 FIMSPTHTHTHTTTN-RVIVGAPTANTG-OPGVIKGGAVYRCDIYDDYRC

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



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 gi|24642641|ref|NP_523378.2|
 gi|158289389|ref|XP_311131.4|

 QPIEFDSIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--TKTVEYAPCRSKNIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIIISKYDP-----
 QPIEFDSIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--TKTVEYAPCRSKNIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIIISKYDP-----
 QPIEFDAIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--TKTVEYAPCRSQIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIVSKYDP-----
 QPIEFDAIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--TKTVEYAPCRSQIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIVSKYDP-----
 QPIEFDAIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--TKTVEYAPCRSKNIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIVSKYDP-----
 QPIEFDTIGNRDYAKDDPLEFKSHQWFGASVRSKQ--DKILACAPLYHWRTMCK--EREVPGICFLQDG--AKTVEYAPCRSKNIDADGGFCQGGFSIDFTK-ADRVLGGPGSFYWGQLISDQVAEIVSKYDP-----
 QPIIFDSIGNRDFADDDPLEFKSHQWFGASVRSKN--DKILACAPLYHWRTMCK--EREVPGICFLQDG--EKSVEYAPCRSTTIDADGGFCQGGFSIDFTK-GDRVLGGPGSFYWGQLISDRVAEILAKYSY-----
 TQIQFDSIDDRKHSNGQOMEKSNQWFGATVRSQG--DQILACAPLYQWSTYGFSS--EREVPGICYLKKG--NNIVEYSPCRSKSNSPEGGFCQAGFSADFVK-RNRVVIIGPGSFYWGQLISDDVTEVINRYN-----
 KLVVFDKGNRNRNVDKVVDRKSYQWLGATVAGRDSDLVVACAPRVVPHMTPSRAFRIDPVGCFTSHN-EEFVEVSPCRINNNGVYHRGSCQAGFSAAINGSRSLFAGAPGSWYWGQYISIPDDAKFFPKPLLYOPFGTGGMAS
 YLLPFDKGNRYNDQNEQIDIKSNQWFGATVASAGIDGPLVACAPRVVPHQLOPKAERVEVPGICVYLAKNNMNFEDISPCRTAYWGVYHRGSCQAGFSAAINDGSRSLFAGAPGSYWGQYISINLVDVVFYKPPRYGHPGEGGQIY

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



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 gi|74004771|ref|XP_850989.1|
 gi|45382133|ref|NP_990770.1|
 gi|189523320|ref|XP_001918557.1|
 gi|24642641|ref|NP_523378.2|
 gi|158289389|ref|XP_311131.4|

 -NVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -NVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -NVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -NVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -KVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -KVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -KVYSIKYNNQLAIRTQAIFDSDYLGYSAVAGDFNGDGIEDFVSGVPRAAITLGMVYIYDGKNMSSLHNFTEGQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 -KEFLHPVSNQLSKKPAQAQYDSDYLGYSAVAGDFNEDGEDDYVTVGPRGEKALGVNIFNGRNMESMYNFTGTQMAAYFGFVAATDINGDDYADVFIGAPLFMDRGSQKLEQVGOVSVSLORA---VGDFC-TTKLNGFEVFAFSG
 HDVTRPEVQVFSISEASVNDSDYLGYSMVIGDFDGRSBDVAIGMPRGGNIVGRIVVNR-WNMANIFNITGRQIGEVFGYSLATSDVDGDLDDLLIGAPMYTDPDNEGKYDVGRVYILLGGPTTEKRKWTIEHRLDGYHSGKRFGL
 FSLNPKDKVYKLEDTKKEDSDYLGYSSITGDFNGDGIQGVAVGKPRGARLLGKVLIYS-WNMANQCNITGEQIGAYFGYSLAAVVDGDKLDDLLIGAPMYTEP-NNEGKYETGRVYIYVGGAAADG-RFRELDRDGVNKAQFGL

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




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gi|6680486|ref|NP_032428.1|----- 880
gi|109468378|ref|XP_230950.4|----- 819
gi|4504763|ref|NP_002201.1|----- 884
gi|114582305|ref|XP_515967.2|----- 1079
gi|27805957|ref|NP_776792.1|----- 883
gi|74004771|ref|XP_850989.1|----- 820
gi|45382133|ref|NP_990770.1|----- 870
gi|189523320|ref|XP_001918557.1| R----- 879
gi|24642641|ref|NP_523378.2|----- 1139
gi|158289389|ref|XP_311131.4|----- 1045
VHRRDRASQAVQEPVNVNOSTFTVYTSSSSSSGGAPSAQLRGHSTOQGHIOAGPVQHTSSSSSSNYSRWPADQQQQHQOQLLAGSGGSGLGGSPVTFNDKSFQGRNNNFHTGLDLGLLNRCGNVDNELYRSGQGYQNPPOSILGDSQGGFOA
N---RVSGGGSE-RRYQTESSDTSAGRMRGSEYQ-QMGGVYRSGYAOQG-----SHGEGYR-----DQQQHYDGGVRVDAGGYGAAG--GAGGSGFGGSSSSSSS-----ERNSTSSVYVYI-----SKNRTIY
.....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|----- 934
gi|109468378|ref|XP_230950.4|----- 873
gi|4504763|ref|NP_002201.1|----- 938
gi|114582305|ref|XP_515967.2|----- 1133
gi|27805957|ref|NP_776792.1|----- 937
gi|74004771|ref|XP_850989.1|----- 874
gi|45382133|ref|NP_990770.1|----- 924
gi|189523320|ref|XP_001918557.1|----- 935
gi|24642641|ref|NP_523378.2|----- 1288
gi|158289389|ref|XP_311131.4|----- 1192
NANQGHYGGQNOAIFQARNPGFQGGTSYGGOTQYFGQPGG-YQTHHVTYSSGSKPYYGRENEDFYDEDNLQQAIPGHWSSSSSSSSSSGTRRLRRSNDKDGAIEKPLQIDLNSPCQSARCKSIRCVVTLNLTGTEGDAAFVAIRARMVAKI
RDEDGRVHVSSESEYHRHDSDLGGQALGGTSSSAAFGSSRRRRMMSQQDGEAPPRTGLITFEMHLDGTYGSGGAAGSAAALNDLNRLENKFRTEYEGC-QQQQQQVVEEALRCHATRCATIHCKAGPIGN--SDVAFVALRTRAVAHI
.....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|----- 1044
gi|109468378|ref|XP_230950.4|----- 983
gi|4504763|ref|NP_002201.1|----- 1048
gi|114582305|ref|XP_515967.2|----- 1243
gi|27805957|ref|NP_776792.1|----- 1047
gi|74004771|ref|XP_850989.1|----- 984
gi|45382133|ref|NP_990770.1|----- 1034
gi|189523320|ref|XP_001918557.1|----- 1045
gi|24642641|ref|NP_523378.2|----- 1396
gi|158289389|ref|XP_311131.4|----- 1301
MKNKENQNHSSYSLKSSASFNIIIEFPYKNLPIEDLFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIIIEFPYKNLPIEDLFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIEFPYKNLPIEDITNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIEFPYKNLPIEDITNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGNSET
MKNKENQNHSSYSLKSSASFNIEFPYKNLPIEDIFNSTLVTNITWGIQAPMPVPPVWVILAVLAGLLLLAVLVFVVMYRMGFFKRVPPPEE-QEREQLOPHENGEGTSEA
LKAESQNKSYIVRSSASFSVIEFPPYKNLPIEDLSTQASLKVITWNE-NPQVPPGVVVALAVLAGLLLLALLIFVVMYKLGFFNRRVPPPEE-DRTEKEQLOPQENGDRNTEA
MEKLSANVPLNVSILAVANVTLPLPFIGAPKDAIVKTHEIFYKAEPEPLQVPDVVPLWVVVLAACAGALIFLLLVLLYKCGFFNRRNPTDHS--QERQPLRNG-YHGDEHL
LHQLSSSAPLHFSIMNVARVTLKLPYIGEPKDKPIKTHEIKVLAPEPTIKPEVVPVLIWVVVLAACAGALIFLLLVLLYKCGFFNRRNPTDAS--ERQPLNRNG-YHGDEHL
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610

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