

gi|31542127|ref|NP_031466.2| MGRYRVRVVTGAWLFGSSVNLVRLWLVGAEHRARLELEQLRP---ARGKEEEFDVDFVPEDLGPLQFVRLKHHQVVDVDAWFCNLIITVGGPGTSAEAVFPCYRWVQEGGILR-LPEGTARLAG---DNALDVFQKREKELKERQTYRWA 150
gi|109488313|ref|XP_213369.4| MGRYRVRVVTGAWLFGSSVNLVRLWLVGAEHRARLELEQLRP---ARGKEEEFDVDFVPEDLGPLQFVRLKHHQVVDVDAWFCNLIITVGGPGMSAEAVFPCYRWVQEGGILR-LPEGTARLAG---DNALDVFQKREKELKERQTYRWA 150
gi|154426292|ref|NP_000688.2| MGRYRVRVATGAWLFGSSVNRVQLWLVTGRGAELELEQLRP---ARGEEEFDDHVAEDLGLLQFVRLRKHHLVDDAWFCDRITVGGPGCAEAVFPCYRWVQEGDILR-LPEGTARLPG---DNALDMFQKREKELKDRQIYICWA 150
gi|114666061|ref|XP_511984.2| MGRYRVRVATGAWLFGSSVNRVQLWLVTGRGAELELEQLRP---ARGEEEFDDHVAEDLGLLQFVRLRKHHLVDDAWFCDRITVGGPGCAEAVFPCYRWVQEGDILR-LPEGTARLPG---DNALDVFQKREKELKDRQIYICWA 150
gi|73955349|ref|XP_856538.1| MGRYCVRVVTGAWLFGSSHNVRVQLWLVTGARGAELELEQLRP---ARGKEEEFDLIDKDLGPLQFVRLKHHSLVDDAWFCDDITVIRGPGASEEAAVPCYRWVQEGVLR-LPEGTGEGRGDS---DNALDVFQKREKELKERQKLYCWD 150
gi|76643361|ref|XP_590488.2| MGRYRILVATGASLFGSRNRVQLWLVTGARGAELELEQLRP---ARGKEEFHEVPEVPEDLGPLQFVRLRKHHLVDDAWFCDRITVIRGPGASEEAAVPCYRWVQEGVLR-LPEGTARLAG---DNALDVFQKREKELKERQKLYRWA 150
gi|41054537|ref|NP_955912.1| -MEYKVTVAIGTSEYSGNNRVYVTLGEGKSEKERTLLDNPGLDFCRGAVDDYIVKSDTDLGPLILVLEKHKYFIEDNWFQRYVVKVSGERCCYTFPCYRWVQEGVLRVDFVLEKGTAKKLS---EQLDLEMAHRSLELQERKTYRWA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|31542127|ref|NP_031466.2| TWKQGLPQITAAADCKDDLPPNMRPFHEEKRLDFEWTLKAGVLEMGLKRVYTLRL-SWNHLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|109488313|ref|XP_213369.4| TWKQGLPQITAAADCKDDLPPNMRPFHEEKRLDFEWTLKAGVLEMGLKRVYTLRL-SWNHLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|154426292|ref|NP_000688.2| TWKQGLPLITAAADCKDDLPPNMRPFHEEKRLDFEWTLKAGALEMALKRVYTLRL-SWNCLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|114666061|ref|XP_511984.2| TWKQGLPLITAAADCKDDLPPNMRPFHEEKRLDFEWTLKAGALEMALKRVYTLRL-SWNCLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|73955349|ref|XP_856538.1| TWKQGLPLITAAAGCDDLPPNMRPFHEEKRLDFEWTLKAGALEMALKRVYTLRL-SWNCLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|76643361|ref|XP_590488.2| TWKQGLPLITAAAGCDDLPPNMRPFHEEKRLDFEWTLKAGALEMALKRVYTLRL-SWNCLEDFDQIFWGQKSALEAKVHCWQDELEFGYQFLNGANPMLLRRSTSLPSRLVLPVSGMEEL---QAOLEKELKNGSLFEADFILLDGI 300
gi|41054537|ref|NP_955912.1| AWAPGIPKCIDAKSEADLPQDARFDNEKRSDFEGLSHYALLESLKLAIRFGKSWSDLEDFRIFWKLRSPIIARYTMEHWKEDWFFAYQFLNGSNRNITRLKRVPSNFLVTDGMSLIPITTTNLELKKGNIFLDHAILDGI 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|31542127|ref|NP_031466.2| VIRGEQYLAAPLVM-LRMDPGKLLPMAIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLQELQFHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAVAQL 450
gi|109488313|ref|XP_213369.4| VIRGEQYLAAPLVM-LRMDPSGKLLPMAIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLQELQFHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAVAQL 450
gi|154426292|ref|NP_000688.2| VIRGEQYLAAPLVM-LKMEPENGKLPQMVIIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLHEIQYHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAAAQL 450
gi|114666061|ref|XP_511984.2| LVVCRNSDIAWPCQEGLOCSRAGRKVRKCHIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLHEIQYHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAAAQL 450
gi|73955349|ref|XP_856538.1| VIRGEQYLAAPLVM-LKMEPENGKLLPMLIIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLHQLQYHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAMAQL 450
gi|76643361|ref|XP_590488.2| VIRGEQYLAAPLVM-LKMDPESKLLPMLIIQIOPPNSSPAPLFLFSPDPLAWLLAKIIVRNSDFOLHQLQYHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAAAQL 450
gi|41054537|ref|NP_955912.1| VIRNSQYLAAPLCL-LYEHPEKGLPIVAIQLEQ-KPKDDLP-VFLFSPDPLAWLLAKIIVRNSDFOLHQLQYHLLNTHLVAEVIAVATMRCPLPGLHPIFKLLVPHIRYTMENIRSRTOQLISDGGIFDQVSTGGGHHVOLLTRAAAQL 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|31542127|ref|NP_031466.2| TVHSLCPPDDLADRGLLRVPSALYARDALQWVEVTARYVNGMVHLFYQSDDIVRGGPELQAWCREITEVGLCHAQDRGFVPSFQSRACLCHFLTMCVFTCTAQHAAINQGLDWDYGWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|109488313|ref|XP_213369.4| TVCSLCPDLDLADRGLLRVPSALYARDALQWVEVTARYVNGMVHLFYQSDDIVRGGPELQAWCREITEVGLCHAQDRGFVPSFQSRACLCHFLTMCVFTCTAQHAAINQGLDWDYGWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|154426292|ref|NP_000688.2| TVCSLCPDLDLADRGLLRVPSALYARDALRLEWIIARYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLCQAQDRGFVPSFQSQSOLCHFLTMCVFTCTAQHAAINQGLDWDYAWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|114666061|ref|XP_511984.2| TVCSLCPDLDLADRGLLRVPSALYARDALRLEWIIARYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLCQAQDRGFVPSFQSQSOLCHFLTMCVFTCTAQHAAINQGLDWDYAWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|73955349|ref|XP_856538.1| TVRSLCPDLDLADRGLLRVPSALYARDALRWGIIAQYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLCHAQDRGFVPSFQSRKOLCHFLTMCVFTCTAQHAAINQGLDWDYAWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|76643361|ref|XP_590488.2| TVRSLCPDLDLADRGLLRVPSALYARDALRWGIIAQYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLCHAQDRGFVPSFQSQNQLCHFLTMCVFTCTAQHAAINQGLDWDYAWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
gi|41054537|ref|NP_955912.1| TVRSLQPKDFDLDRGVTKGAYVACDALRLWEITARYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLCHAQDRGFVPSFQSQNQLCHFLTMCVFTCTAQHAAINQGLDWDYAWVNPAPCMRMPPTTKEDVMAIVMGSGLPDVQK 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|31542127|ref|NP_031466.2| ACLQMTITWHLGRLQPDMPVPLGHHKTKYFSDPRITKAVLSQFQADLDNLEKEITARNQQLDLPYEYKPSRIENSITTI 677
gi|109488313|ref|XP_213369.4| ACLQMTITWHLGRLQPDMPVPLGHHKTKYFSDPRITKAVLSQFQADLDNLEKEITARNQQLDLPYEYKPSRIENSITTI 677
gi|154426292|ref|NP_000688.2| ACLQMAISWHLGRLQPDMPVPLGHHKTKYFSDPKKAVLNQFRIDLEKLEKEITARNQQLDWPYEYKPSRIENSITTI 677
gi|114666061|ref|XP_511984.2| ACLQMAISWHLGRLQPDMPVPLGHHKTKYFSDPKKAVLNQFRIDLEKLEKEITARNQQLDWPYEYKPSRIENSITTI 677
gi|73955349|ref|XP_856538.1| ACLQMTITWHLGRLQPDMPVPLGHHKTKYFSDPKKAVLNQFONDLENEREITARNQQLDLPYDYLKPSRIENSITTI 677
gi|76643361|ref|XP_590488.2| ACLQMAITWHLGRLQPDMPVPLGHHKTKYFSDPKKAVLNQFONDLENEREITARNQQLDLPYEYKPSRIENSITTI 677
gi|41054537|ref|NP_955912.1| SCVQMAITWHLGRLQPDMPVPLGHHKTKYFSDPKKAVLNQFONDLENEREITARNQQLDLPYEYKPSRIENSITTI 677
.....610.....620.....630.....640.....650.....660.....670.....

