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gi|6753568|ref|NP_034124.1|      -MATSLSADSPQQLSSLSTQQTTLLLLFSVLAAVHLGQWLLRQWQRKPWSSPPGPFPWPLIGNAAAVGQASHLYFARLARRYGDVFQIRLGSCPVVVLNGESAIHQALVQQGSIFADRPPFASFRVVSGGRSLAFGHYSEHWKTQRRSAY   150
gi|6978737|ref|NP_037072.1|      -MATSLSADSPQQLSSLSTQQTTLLLLLVSVLAIVHLGQWLLRQWRRKPWSSPPGPFPWPLIGNAASVGRASHLYFARLARRYGDVFQIRLGSCPVVVLNGESAIHQALVQQGGVFADRPPFASFRVVSGGRSLAFGHYSERWKERRRAAY   150
gi|189491763|ref|NP_000095.2|    -MGTSLSPNDPWPLNPLSIQQTTLLLLLLSVLATVHVGQRLLRQRRRQLRSAPPGPFAWPLIGNAAAVGQAAHLSFARLARRYGDVFQIRLGSCPIVVLNGERAIHQALVQQGSAFADRPAFASFRVVSGGRSMAFGHYSEHWKVQRRAAH   150
gi|114576990|ref|XP_001167556.1| -MGTSLSPNDPWPLNPLSIQQTTLLLLLLSVLATVHVGQRLLRQRRRQLGSAPPGPFAWPLIGNAAAVGQAAHLSFARLARRYGDVFQIRLGSCPIVVLNGERAIHQALVQQGSAFADRPSFASFRVVSGGRSMAFGHYSEHWKVQRRAAH   150
gi|73980746|ref|XP_540153.2|     -MATSLGPDAPLQPSALSAQQTTLLLLLLSVLAAVHAGQWLLRQRRRQPGSAPPGPFAWPLIGNAAAMGPAPHLSFARLARRYGDVFQIRLGSCRVVVLNGERAIRQALVQQGAAFADRPRFASFRVVSGGRSLAFGQYSPRWKVQRRAAH   150
gi|61887409|ref|XP_588813.1|     -MATGLSPDDHLSPTLLSVQQTMLLLLLSVLAAVHVGQWLLRQRRRQPGSAPPGPFAWPLIGNAASMGSAPHLLFARLARRYGDVFQIHLGSCRVVVLNGERAIRQALVHQSAAFADRPPFASFRLVSGGRSLAFGQYSESWKAQRRAAH   150
gi|113675230|ref|NP_001038721.1| MMDVLLALRDLLQLSTRSVLLSLMVCLM------------LMFRRRQ---LVPGPFSWPVIGNAAQLGNTPHFYFSRMAQKYGDVFQIKLGSRNVVVLNGD-AIKEALVKKATDFAGRPDFASFRFVSNGKSMAFGNYTPWWKLLRKVAQ   150
gi|118091033|ref|XP_001233595.1| -MGTPNGAAMAPVLSPHSALLLIAVVLTAILLLAR------TRHKATRGQSPPGPFASPLVGNVLQMGRLPHLTFMRMACRYGAIFQLRLGRHRVVVLNGEAAIRRALVGLGTRFAGRPDFPSFGLVSGGRSIAFGGCTPQWRARRRLAH   150
                          1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|6753568|ref|NP_034124.1|      STMRAFSTRHPRSRGLLEGHALAEARELVAVLVRRCAGGAFLDPTQPVIVAVANVMSAVCFGCRYNHDDAEFLELLSHNEEFGRTVGAGSLVDVLPWLQLFPNPVRTTFRKFEQLNRNFSNFVLDKFLRHRESLVPGAAPRDMTDAFILS   300
gi|6978737|ref|NP_037072.1|      GTMRAFSTRHPRSRGLLEGHALGEARELVAVLVRRCAGGACLDPTQPIIVAVANVMSAVCFGCRYNHDDAEFLELLSHNEEFGRTVGAGSLVDVMPWLQLFPNPVRTIFREFEQINRNFSNFVLDKFLRHRESLVPGAAPRDMMDAFILS   300
gi|189491763|ref|NP_000095.2|    SMMRNFFTRQPRSRQVLEGHVLSEARELVALLVRGSADGAFLDPRPLTVVAVANVMSAVCFGCRYSHDDPEFRELLSHNEEFGRTVGAGSLVDVMPWLQYFPNPVRTVFREFEQLNRNFSNFILDKFLRHCESLRPGAAPRDMMDAFILS   300
gi|114576990|ref|XP_001167556.1| SMMRNFFTRQPRSRQVLEGHVLSEARELVALLVRGSADGAFLDPRPLTVVAVANVMSAVCFGCRYSHDDPEFRELLSHNEEFGRTVGAGSLVDVMPWLQYFPNPVRTVFREFEQLNRNFSNFILDKFLRHCESLRPGAAPRDMMDAFILS   300
gi|73980746|ref|XP_540153.2|     STMRAFSTRQPRSRRVLEGHVLAETRELVALLARGSAGGAFLDPRPLTVVAVANVMSAVCFGCRYSHDDAEFRELLSHNEEFGRTVGAGSLVDVLPWLQRFPNPVRTAFREFEQLNRNFSNFVLRKFLRHRESLQPGAAPRDMMDAFILS   300
gi|61887409|ref|XP_588813.1|     STMRAFSTRQPRGRRVLEGHVVGEVRELVELLVRRSAGGAFLDPRPLTLVAVANVMSALCFGCRYSHDDAEFLELLSHNEEFGRTVGAGSLVDVLPWLQRFPNPVRTAFREFEQLNRNFSNFVLDKFLRHRESLRPGAAPRDMMDAFIHS   300
gi|113675230|ref|NP_001038721.1| STVRNFSTANIQTKQTFEKHIVSEIGELIRLFLNKSREQQFFQPHRYLVVSVANTMSAVCFGNRYAYDDAEFQQVVGRNDQFTKTVGAGSMVDVMPWMQYFPNPIRTLFDQFKELNKEFCAFIELKVSEHRKTISP-SHVRDMTDAFIVA   300
gi|118091033|ref|XP_001233595.1| AALRAHST-----VAEVERHVVAEAGDLVRLFLRHSQGGAYFQPCPLLVVANANVLCALCFGRRYDHADGEFTALLGRNDRFGQTVGAGSLVDVLPWLLRFPNPVRHVYRDFQALNRELHGFVQAKVAQHRQTFDW-RAVRDISDVMIAS   300
                          .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6753568|ref|NP_034124.1|      AEKKASGAPGDDSSGLDLEDVPATITDIFGASQDTLSTALLWLLILFTRYPDVQARVQAELDQVVGRDRLPCMSDQPNLPYVMAFLYESMRFSSFLPVTIPHATTANTFVLGYYIPKNTVVFVNQWSVNHDPAKWPNPEDFDPARFLDKD   450
gi|6978737|ref|NP_037072.1|      AEKKATGDPGDSPSGLDLEDVPATITDIFGASQDTLSTALLWLLILFTRYPDVQARVQAELDQVVGRDRLPCMSDQPNLPYVMAFLYESMRFTSFLPVTLPHATTANTFVLGYYIPKNTVVFVNQWSVNHDPAKWSNPEDFDPARFLDKD   450
gi|189491763|ref|NP_000095.2|    AEKKAAGDSHGGGARLDLENVPATITDIFGASQDTLSTALQWLLLLFTRYPDVQTRVQAELDQVVGRDRLPCMGDQPNLPYVLAFLYEAMRFSSFVPVTIPHATTANTSVLGYHIPKDTVVFVNQWSVNHDPLKWPNPENFDPARFLDKD   450
gi|114576990|ref|XP_001167556.1| AEKKAAGDSDDGGARLDLENVPATVTDIFGASQDTLSTALQWLLLLFTRYPDVQTRVQAELDQVVGRDRLPCMGDQPNLPYVLAFLYEAMRFSSFVPVTIPHATTANTSVLGYHIPKDTVVFVNQWSVNHDPVKWPNPENFDPARFLDKD   450
gi|73980746|ref|XP_540153.2|     AGTEAAEGSGDGGARLDMEYVPATVTDIFGASQDTLSIALQWLLILFTRYPQVQARVQEELDQVVGRNRLPCLDDQPNLPYTMAFLYEGMRFSSFVPVTIPHATTTSACVLGYHIPKDTVVFVNQWSVNHDPVKWPNPEDFDPVRFLDKD   450
gi|61887409|ref|XP_588813.1|     AGAD----SGDGGPRLDVDYVPATVTDIFGASQDTLSTALQWLLVLFTRYSEVQARVQAELDQVVGRHRLPTLEDQPRLPYVMAFLYEAMRFSSFVPVTIPHATTANASVLGYHIPKDTVVFVNQWSVNHDPVKWSNPEDFDPTRFLDKD   450
gi|113675230|ref|NP_001038721.1| LDKG---LSGGSGVSLDKEFVPPTISDIFGASQDTLSTALQWIILLLVRYPEIQNRLQEDVGRVVDRSRLPTIADQPHLPYLMAFIYEVMRFTSFTPLTIPHSTTKDTSINGYPIPKDTVIFVNQWSLNHAPAKWDQPEVFNPQRFLDED   450
gi|118091033|ref|XP_001233595.1| VERG-----GGSPDGLGPEDVEGAMTDIFGAGQDTTSTALSWIILLLLKHPQVQQDLQAELDRVVGRSRLPTAEDRPHLPLLEAFIYETLRYSSFVPITIPHATTADVELEGFRIPKGTVVFVNQWSVNHDCSKWPEPQRFDPTRFLDKQ   450
                          .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|6753568|ref|NP_034124.1|      GFINKALASSVMIFSVGKRRCIGEELSKMLLFLFISILAHQCNFKANQNESSNMSFSYGLTIKPKSFRIHVSLRESMELLDNAVKKLQTEEGCK----   548
gi|6978737|ref|NP_037072.1|      GFINKALASSVMIFSVGKRRCIGEELSKTLLFLFISILAHQCNFKANQNEPSNMSFSYGLSIKPKSFKIHVSLRESMKLLDSAVEKLQAEEACQ----   548
gi|189491763|ref|NP_000095.2|    GLINKDLTSRVMIFSVGKRRCIGEELSKMQLFLFISILAHQCDFRANPNEPAKMNFSYGLTIKPKSFKVNVTLRESMELLDSAVQNLQAKETCQ----   548
gi|114576990|ref|XP_001167556.1| GFINKDLTSRVMIFSVGKRRCIGEELSKMQLFLFISILAHQCNFRANPNEPAKMNFSYGLTIKPKSFKVNVTLRESMELLDSAVQKLQAKETCQ----   548
gi|73980746|ref|XP_540153.2|     GFIDKDLASSVMIFSVGKRRCIGEELSKMQLFLFISILAHQCNFKANPDEPSKMDFNYGLTIKPKAFSINVTLRESMELLDSAVQKLQAEEDCQ----   548
gi|61887409|ref|XP_588813.1|     GLINKDLTGSVMVFSVGKRRCIGEEISKMQLFLFISILAHQCNFKANPDEPSKMDFNYGLTIKPKSFKINVTLRESMELLDSAVQKLQVEKECQ----   548
gi|113675230|ref|NP_001038721.1| GSLNKDLTTNVLIFSLGKRRCIGEDVSKIQLFLFTSVLVHQCSFKAES--TPNMDYEYGLTLKPKPFKVSVTARDSSDLLDSLVGTSQTPTEKRLKCN   548
gi|118091033|ref|XP_001233595.1| QRLDRERAGSVMIFSAGQRRCIGDQLSKLQIFLFTAILLHQCSFHANPAEHLTMDCIHGLALKPLPFTVNVRPR--IPLLIQP--------------   548
                          .......460.......470.......480.......490.......500.......510.......520.......530.......540.......
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