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gi | 73989207 | ref | XP_859496.1 | -----MALNVAPVRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPTHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTPLHP--VPTFFVGPATIGTNTAISFPAYLAPVTPGV 141
gi | 30425032 | ref | NP_780550.1 | -----MALNVAPVRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPTHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTPLHP--VPTFFVGPATIGTNTAISFPAYLAPVTPGV 141
gi | 114650365 | ref | XP_001141210.1 | -----MALNVAPVRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPTHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTPLHP--VPTFFVGPATIGTNTAISFPAYLAPVTPGV 141
gi | 118084671 | ref | XP_416979.2 | -----MALNVAPVRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPTHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTPLHP--VPTFFVGPATIGTNTAISFPAYLAPVTPGV 141
gi | 21464125 | ref | NP_659002.1 | -----MALNVAPVRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPTHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTPLHP--VPTFFVGPATIGTNTAISFPAYLAPVTPGV 141
gi | 153792357 | ref | NP_001093468.1 | -----MALNIASIRDTKWLILEVCRQFORGTCSRSDDEECKFAHPPKSCOVENGRVIACFDSLKGRCSREN--CKYLHPPAHLKTQLEINGRNNLIQOKTAAAMLAAQOMFMPGPTMOP--VPTFFVSOGLGSNPLSYAPVLTPMHGM 141
gi | 28573504 | ref | NP_788391.1 | -----MALNVNMSLLNGKDSRWLQLEVCRFQRNKCSRQDTECKFAHPPANVEVQNGKVIACVDSLKGRCSRENCKYFHPHQHLDOLLINGRHLAKN---ALMQMG-IAPQPVISGQVPAVATNFYLTGIPANYSFYIT----M 140
gi | 5174663 | ref | NP_005971.1 | -----MTELETAMGMIDVFSRYS----- 19
gi | 114593120 | ref | XP_001156309.1 | -----MTELETAMGMIDVFSRYS----- 19
gi | 73951727 | ref | XP_852856.1 | -----MDLDAALVLDLGSLLPSSPKRQFFVSLLSAFAFSLPIPSPRGWLLEHTSVPLINIEAP-----ELLEECHSICFNFSRLAFTIKLQKASGERFLRHASSQGEGGSIS--MTELETAMGMISVFARYA----- 121
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 73989207 | ref | XP_859496.1 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 291
gi | 30425032 | ref | NP_780550.1 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 291
gi | 114650365 | ref | XP_001141210.1 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 291
gi | 118084671 | ref | XP_416979.2 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 291
gi | 21464125 | ref | NP_659002.1 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 291
gi | 153792357 | ref | NP_001093468.1 | GLVPTTEILPTTPVIVPGSPPVTVPGSTATQKLLRDKLEVCREFORGNCCARGETDCRFADPADSTMIDTNDNTVTVCMDYIKGRCMRECKYFHPPAHLQAKIKAAQHOANQAAVAAQAAAAAAVMTQSTAKAMKRPLEASVDLAFPPG 273
gi | 28573504 | ref | NP_788391.1 | GHLVPALLGDPVVSQLGPFVVFQVQVQAKIPRSRDLRETSPLAAHHHQQLQHLQNLN-----INNNN-----HSTAGAATSTATTNNAAAAAAAAAAAAA-----AAA 240
gi | 5174663 | ref | NP_005971.1 | -----GSEGSIQQLTKGELKVLMEKELPGFLQSGKDKDAVDKLLKLDLDA--GDAQVDFSE-----FIVFVAATTSACHKHFKEAGLK----- 95
gi | 114593120 | ref | XP_001156309.1 | -----GSEGSIQQLTKGELKVLMEKELPGFLQSGKDKDAVDKLLKLDLDA--GDAQVDFSE-----FIVFVAATTSACHKHFKEAGLK----- 95
gi | 73951727 | ref | XP_852856.1 | -----GVEGSKQSLTKGELKVLMEKELPGFLQTKRDRDSVDKLLKLDLDA--GDAEVDVDFSE-----FIVFVATLTAACHQVFERAGLP----- 197
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 73989207 | ref | XP_859496.1 | ALHPLPKROALEKSNASTVFNPSVLYHQALTSACLQ--HAAFIPT-----VPMHSAATSAATTPATSVVFAAATATANOIILK 373
gi | 30425032 | ref | NP_780550.1 | ALHPLPKROALEKSNASTVFNPSVLYHQALTSACLQ--HTAFIPT-----VPMHSAATSAATTPATSVVFAAATATANOIILK 373
gi | 114650365 | ref | XP_001141210.1 | ALHPLPKROALEKSNASTAVFNPSVLYHQALTSACLQ--HAAFIPT-----VPMHSAATSAATTPATSVVFAAATATANOIILK 373
gi | 118084671 | ref | XP_416979.2 | VLEHPLPKROALEKSNASTAVFNPSVLYHQALANACLQ--HAAFIPT-----VPMHNAATAATSAATTPATSVVFAAATATANOIILK 373
gi | 21464125 | ref | NP_659002.1 | ALHPLPKROALEKSNASTAVFNPSVLYHQALTSACLQ--HAAFIPTGSLVLCMTPATSIIVPMHSAATSAATTPATSVVFAAATATANOIILK 367
gi | 153792357 | ref | NP_001093468.1 | VLQPLPKRPALEKSNASTLTFNPSVLYHQALASACLQPTAAFFFP-----ATTPATSVVFAATAPANOIILK 339
gi | 28573504 | ref | NP_788391.1 | VMGHHTELVGKKRAADTLDMFPLVFFCSFSPSCVFAFLN-----CSIFGFLRLWFSLFNLRH----- 297
gi | 5174663 | ref | NP_005971.1 | ----- 95
gi | 114593120 | ref | XP_001156309.1 | ----- 95
gi | 73951727 | ref | XP_852856.1 | ----- 197
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....

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