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gi | 22779928 | ref | NP_036150.1 | MMASYPPEPDTAGILLAPESGRAVKEAEASPP-SPGKGGG---TPEKPDPAQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 145
gi | 109483849 | ref | XP_345976.3 | MMASYPPEPDTAGILLAPESGRAVKEAEASPP-SPGKGGG---TPEKPDPAQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 145
gi | 12751477 | ref | NP_075555.1 | MMASYPPEDAAGALLAPEIGRIVKEPEGPPP-SPGKGGGGGGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 149
gi | 114589450 | ref | XP_526323.2 | MMASYPPEDAAGALLAPEIGRIVKEPEGPPP-SPGKGGGGGGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 149
gi | 72534786 | ref | NP_001026920.1 | MMASYPPEENASGALLAPEIGRAAKEPEAPPSPGKGGGGGTGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 150
gi | 60302862 | ref | NP_001012630.1 | MMSGYADGEEADAVAMLAHDGGGKKEPERKKELSAEKGG---PEKPDPSQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 142
gi | 113675294 | ref | NP_001038717.1 | MMATYIP-GHEDNGMILMDTSSSAEKDRTKDEAPPEKGG---PDKSDPQKPPYSYVALIAMAIRESAEKRLTSLGIYQYIIAKFPFYEKNNKKGWONSIRHNLSLNECFIKVPREGGGERKGNWTLDPACEDMFEKGNVRRRRM 141
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 22779928 | ref | NP_036150.1 | KRPFPPPAHFOPGKGLFGSGGAAGCCGVPAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCOMAAAAAAAAAAAAAAAAAGPSPGAAAVVKGLAGPAASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPPFFFFFFPHPHPHA 295
gi | 109483849 | ref | XP_345976.3 | KRPFPPPAHFOPGKGLFGSGGAAGCCGVPAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCOMAAAAAAAAAAAAAAAAAGPSPGAAAVVKGLAGPAASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPPFFFFFFPHPHPHA 294
gi | 12751477 | ref | NP_075555.1 | KRPFPPPAHFOPGKGLFGAGGAAGCCGVPAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCOMAAAAAAAAAAAAAAAAAGPSPGAAAVVKGLAGPAASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPP---PPPHPHPHPHA 296
gi | 114589450 | ref | XP_526323.2 | KRPFPPPAHFOPGKGLFGAGGAAGCCGVPAGAAADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCOMAAAAAAAAAAAAAAAAAGPSPGAAAVVKGLAGPAASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPP---PPP---PHPHPHA 294
gi | 72534786 | ref | NP_001026920.1 | KRPFPPPAHFOPGKGLFGAGGAAGCCGVPAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCOMAAAAAAAAAAAAAAAAAGPSPGAAAVVKGLAGPAASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPP---PPPHPHSHPHA 297
gi | 60302862 | ref | NP_001012630.1 | KRPFPPPTHFOPGKSLFG-----PDGYGYLSPPKYLQSTFMNNSWPLPQPPAPVPYASCOMSSGGSVSPVNV-----VKGLSGP-ASYGPIYTRVQSMALPPGVVNSYGLGGPPAAPP---HH 242
gi | 113675294 | ref | NP_001038717.1 | KRPFPPPTHFOPGKSLFG-----GEGYGYLSPPKYLQSGFINNSWS---PAPMSYTCQVSSGGSVSPVNV-----MKGLSAP-SSYNPIYTRVQSIGLP-SMVNSYNGIS-----HH 237
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 22779928 | ref | NP_036150.1 | HHLHAAAAPPAPPHGAAAPPGLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL 375
gi | 109483849 | ref | XP_345976.3 | HHLHAAAAPPAPPHGAAAPPGLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL 374
gi | 12751477 | ref | NP_075555.1 | HHLHAAAAPPAPPHGAAAPPGLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL 376
gi | 114589450 | ref | XP_526323.2 | HHLHAAAAPPAPPHGAAAPPGLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL 374
gi | 72534786 | ref | NP_001026920.1 | HHLHAAAAPPAPPHGAAAPPGLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL 377
gi | 60302862 | ref | NP_001012630.1 | HHPHA-----HHP-----QLGPAS---PAPPAAPAANGAGLOFACARQPAELSMHCSYWEHDSKHGALHSRIDI 305
gi | 113675294 | ref | NP_001038717.1 | HHHHR-----THPHALPHAQQLSPAT---AAAPPVITGNGTGLQFACRSQPAELSMHCSYWEHDSKHSAHARIDI 306
.....310.....320.....330.....340.....350.....360.....370.....380

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