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                                 **: *.  .:   :*    . : :  .      .. **       *:*.**:******************:**************:*****************************************************************
gi|22779928|ref|NP_036150.1|     MMASYPEPEDTAGTLLAPESGRAVKEAEASPP-SPGKGGG----TTPEKPDPAQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIIAKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   145
gi|109483849|ref|XP_345976.3|    MMASYPEPEDTAGTLLSPESGRAVKEAEASPP-SPGKGGG----TAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIIAKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   145
gi|12751477|ref|NP_075555.1|     MMASYPEPEDAAGALLAPETGRTVKEPEGPPP-SPGKGGGGGGGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIIAKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   149
gi|114589450|ref|XP_526323.2|    MMASYPEPEDAAGALLAPETGRTVKEPEGPPP-SPGKGGGGGGGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIIAKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   149
gi|72534786|ref|NP_001026920.1|  MMASYPEPENASGALLAPETGRAAKEPEAPPPPSPGKGGGGGTGTAPEKPDPAQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIIAKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   150
gi|60302862|ref|NP_001012630.1|  MMSGYADGEEDAVAMLAHDGGGSKEPERGKEELSAEKG--------PEKPDPSQKPPYSYVALIAMAIRESAEKRLTLSGIYQYIISKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   142
gi|113675294|ref|NP_001038717.1| MMATYP-GHEDNGMILMDTTSSSAEKDRTKDEAPPEKG--------PDKSDPTQKPPYSYVALIAMAIRESSEKRLTLSGIYQYIISKFPFYEKNKKGWQNSIRHNLSLNECFIKVPREGGGERKGNYWTLDPACEDMFEKGNYRRRRRM   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|     KRPFRPPPAHFQPGKGLFGSGGAAGGCGVPGAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCQMAAAAAAAAAAAAAAGPGSPGAAAVVKGLAGPAASYGPYSRVQSMALPPGVVNSYNGLGGPPAAPPPPPPPHPHPHPHA   295
gi|109483849|ref|XP_345976.3|    KRPFRPPPAHFQPGKGLFGSGGGAGGCGVPGAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCQMAAAAAAAAAAAAAAGPGSPGAAAVVKGLAGPAASYGPYSRVQSMALPPGVVNSYNGLGGPPAAPPPPPPP-HPHPHPHA   294
gi|12751477|ref|NP_075555.1|     KRPFRPPPAHFQPGKGLFGAGGAAGGCGVAGAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCQMAAAAAAAAAAAAAAGPGSPGAAAVVKGLAGPAASYGPYTRVQSMALPPGVVNSYNGLGGPPAAP---PPPPHPHPHPHA   296
gi|114589450|ref|XP_526323.2|    KRPFRPPPAHFQPGKGLFGAGGAAGGCGVAGAAADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCQMAAAAAAAAAAAAAAGPGSPGAAAVVKGLAGPAASYGPYTRVQSMALPPGVVNSYNGLGGPPAAP---PPP--PHPHPHA   294
gi|72534786|ref|NP_001026920.1|  KRPFRPPPAHFQPGKGLFGAGGAAGGCGVAGAGADGYGYLAPPKYLQSGFLNNSWPLPQPPSPMPYASCQMAAAAAAAAAAAAAAGPGSPGAAAVVKGLAGPAASYGPYSRVQSMALPPGVVNSYNGLGGPPAAP---PPPPHPHSHPHA   297
gi|60302862|ref|NP_001012630.1|  KRPFRPPPTHFQPGKSLFG--------------PDGYGYLSPPKYLQSTFMNNSWPLPQPPAPVPYASCQMSGGSVSPVN---------------VKGLSGP-ASYGPYSRVQSVALP-GMVNSYNGVA-------------------HP   242
gi|113675294|ref|NP_001038717.1| KRPFRPPPTHFQPGKSLFG--------------GEGYGYLSPPKYLQSGFINNSWS----PAPMSYTSCQVSSGSVSPVN---------------MKGLSAP-SSYNPYSRVQSIGLP-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|     HHLHAAAAPPPAPPHHGAAAPPPGQLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL   375
gi|109483849|ref|XP_345976.3|    HHLHAAAAPPPAPPHHGAAAPPPGQLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL   374
gi|12751477|ref|NP_075555.1|     HHLHAAAAPPPAPPHHGAAAPPPGQLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL   376
gi|114589450|ref|XP_526323.2|    HHLHAAAAPPPAPPHHGAAAPPPGQLSPASPATAAPPAPAPTSAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL   374
gi|72534786|ref|NP_001026920.1|  HHLHAAAAPPPAPPHHGAAAPPPGQLSPASPATAAPPAPAPTNAPGLQFACARQP-ELAMMHCSYWDHDSKTGALHSRLDL   377
gi|60302862|ref|NP_001012630.1|  HHPHA---------HHP------QQLGPAS---PAPPAAPAANGAGLQFACARQPAELSVMHCSYWEHDSKHGALHSRIDI   305
gi|113675294|ref|NP_001038717.1| HHHHH---------THPHALPHAQQLSPAT---AAAPPVTTGNGTGLQFACSRQPAELSMMHCSYWDHESKHSALHARIDI   306
                                 .......310.......320.......330.......340.......350.......360.......370.......380.
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