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                                 *    ***.:***:  .* *  **.**: *:*.::* *** * *  :  * *: *    :*******:.*.*:*******:.******** . *** **********:* **** *. .:.****:  ***:** *:******:***. *
gi|117422433|ref|NP_001070968.1| MRAPHLHLSAASGAR-ALAK--LLPLLMAQLWAAEAALLPQNDTRLDPEAYGSPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGN-KPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARP   146
gi|114678731|ref|XP_001174085.1| MRAPHLHLSAASGAR-ALAK--LLTLLMAQLWAAEAALLPKNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGN-KPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARP   146
gi|115497120|ref|NP_001069358.1| MTPRHLHLSAASGAQGGLGKLLLLPLLVAQFWVSEALLLPANDTSSNFVASGAPCAHGSQPWQVSLFNGLSFHCAGVLVDRSWVLTAAHCGNNKPLWARVGDDHLLLLQGEQLRRTSRPIVHPKYQQGSGPILPRRTDEHDLMLLKLGRP   150
gi|19526892|ref|NP_598473.1|    MRVPLLHLSTASGSW-SLVK-LLLPLLMVQLWAAQALLLPGNATRVDLEASGAQCERDYHPWQVSLFHNLQFQCAGVLVDQNWVLTAAHCWRNKPLRARVGDDHLLLFQKEQLRSTSSPVFHPKYQACSGPILPHRSDEHDLMMLKLSSP   148
gi|51870931|ref|NP_001004100.1| MRVPLLHLPTASGSL-SLVK-LLLPLLMMQLWAAQALLLPGNTTREDLEAFGTLCPSVSQPWQVSLFHNLQFQCAGVLVDQNWVLTAAHCWRNKPLRARVGDDHLLLFQSEQLRSTNSPVFHPKYQPCSGPVLPLRSDEHDLMMLKLSSP   148
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 *:  ...:.::**::*:** ::**::**.*:: ******:.*:** :*:** *:**.*****:*..*:**  * .**.************:**:*:***.:****:* *:*:**::**:*  **.:.** :
gi|117422433|ref|NP_001070968.1| VVLGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSA-QHPAVYTQICKYMSWINKVIRSN   276
gi|114678731|ref|XP_001174085.1| VVLGPRARALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSVTILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSA-QHPAVYTQICKYMSWINKVIRSN   276
gi|115497120|ref|NP_001069358.1| VVPGPRVRPLRLPFRCTQPGDQCQIAGWATTSSRRVKYNKGLSCSRVTILSPKECEVFYPGVITSNMMCAGLDQGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSA-QHPAVYTQICKYRSWIEKTIRSN   280
gi|19526892|ref|NP_598473.1|    VMLTSNVHPVQLPFRCSQPGQECQVSGWGTSASRRVKYNRSLSCSKVTLLSQKQCETFYPGVITNSMICAEADGNQDSCQSDSGGPLVCDDTLHGVLSWGIYPCGAA-QHPSVYSEICKYTPWIRRVIRFK   278
gi|51870931|ref|NP_001004100.1| VVLTSKVHPVQLPFQCAQPRQECQVSGWGTTANRRVKYNRSLSCSRVTLLSQKQCETFYPGVITNNMICAGMDRDQDSCQSDSGGPLVCDNTLHGILSWSIYPCGAATQYPAVYAKICNYTNWIRRVIRSK   279
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.
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