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gi|117647257|ref|NP_076043.2|-----
gi|109504805|ref|XP_573999.2|-----MFRGLRIS 8
gi|13569843|ref|NP_057251.2|-----
gi|114605542|ref|XP_518245.2|-----
gi|77735715|ref|NP_001029556.1|-----
gi|74004089|ref|XP_535892.2|-----
gi|50733613|ref|XP_418926.1|-----
gi|189515946|ref|XP_687281.2|-----
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|117647257|ref|NP_076043.2|-----* . : : . . . * * * * * : : * . . : : * : * * * * * : * **
gi|109504805|ref|XP_573999.2|-----IAFFPLAMVLRPRSSRIPAPAEAMVDEDAASEEEEE--AEHGLLLAQSSGAAAEPLDEE--EDADD---EAPPELTFASQAQAEAREEELRVRSARRDKTLLKEKRRREELFIEOK 105
gi|13569843|ref|NP_057251.2|-----MVOLRPRASRAPASAEAMVDEGQASAE-----AEHGLLLAQSSGAAAEPLDEE--EDGDD---EAPPELTFASQAQAEAREEELRVRSARRDKTLLKEKRRREELFIEOK 141
gi|114605542|ref|XP_518245.2|-----MVOLRPRASRAPASAEAMVDEGQASAE-----AEHGLLLAQSSGAAAEPLDEE--EAGDDEFDDEAPELTFASQAQAEAREEERRVRETVRRDKTLLKEKRRREELFIEOK 109
gi|77735715|ref|NP_001029556.1|-----MVOLRPRASRAPASAEAMVDEGQASAE-----AEHGLLLAQSSGAAAEPLDEE--EAGDDEFDDEAPELTFASQAQAEAREEERRVRETVRRDKTLLKEKRRREELFIEOK 109
gi|74004089|ref|XP_535892.2|-----MVOLRPRASRAPASAEAMVDEGQASAE-----AEHGLLLAQSSGAAAEPLDEE--EAGDDEFDDEAPELTFASQAQAEAREEERRVRETVRRDKTLLKEKRRREELFIEOK 108
gi|50733613|ref|XP_418926.1|-----MVRRRRR-----AEK-----AAPVAPAAAPSSSD-----DEAPEELTFASQAQAEAREEERRVRETVRRDKTLLKEKRRREELFIEOK 298
gi|189515946|ref|XP_687281.2|-----MALVCLSSISVQRCWYLIWRAPYVNCAKIS--LSTFKKVEMLDTQTQFESS-----DDELPEEVAFDASKQAALKSVKDALESAREKRNLLKEKRRRQQLFQEQK 75
1.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|117647257|ref|NP_076043.2|-----: * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
KRKLLPDAVLEQLTASADIKKSPENVK-VNLKKKSE--HAKGRNSK--KVKVQKVSQVGSYMAVRLKDEDLDRSRQEAAKHFIHSCLYGSDSKRTTVNKFLSLNKRSPVKKAAAFITSTWGAKQONAKRFKRWMAKMKKK 251
gi|109504805|ref|XP_573999.2|-----KRKLLPDAVLEQLTASADIKKSPGNVK-VNLKKEHEQPAKGRNSK--KVKIQKVSQVGTQSYLAVRLKDEDLDRSRQEAAKHFIHSCLYGS--KVKIQKVSQVGTQSYLAVRLKDEDLDRSRQEAAKHFIHSCLYGS 233
gi|13569843|ref|NP_057251.2|-----KRKLLPDTILEKLTASQTNIKKSPGKVEVNLQKK-NEDCEKGNDSK--KVKVQKVSQVSONKSYLAVRLKDDLDLDRSRQQAQAFIHNLSLYGPGTNRRTVNVKFLSLANKRLLPVKRAAVQFLNNAWGIQKQONAKRFKRRWVRKMKTK 256
gi|114605542|ref|XP_518245.2|-----KRKLLPDTILEKLTASQTNIKKSPGKVEVNLQKK-NEDCEKGNDSK--KVKVQKVSQVSONKSYLAVRLKDDLDLDRSRQQAQAFIHNLSLYGPGTNRRTVNVKFLSLANKRLLPVKRAAVQFLNNAWGIQKQONAKRFKRRWVRKMKTK 256
gi|77735715|ref|NP_001029556.1|-----KRKLLPDTILEKLTASQTVKKSQPKLKEVNLQKK-NEEREKGNDSK--KAKVQKVSQVSONKSYMAVRLKDDLDLDRSRQEAAKAFIQKSLYGPNTNRRTVNVKFLSLANKRLLPVKRAAVQFLNNAWGIQKQONAKRFKRRWVRKMKTK 255
gi|74004089|ref|XP_535892.2|-----KRKLLPEDVLEKLTAAAGQTDIKKASGKLEANLKKKDEDVEKGGDSKNTKEKVKIQSVGQNKSYLAVRLKDDLDLDRSRQQAQAFIQKSLYGPNTNRRTVNVKFLSLANKRLLPVKRAAVQFLNNAWGIQKQONAKRFKRRWVRKMKTK 448
gi|50733613|ref|XP_418926.1|-----KRKLLPEALLQELAAAPPARADERSPAAPADKRFQVSAKQNEGRIPG--QVKKDKAGGFRSKGNVIAVHLKDENLTLGLHQQAKDFIHSQLYGPGTNRRTSANEFFSLANKKDSVKKAAVQFVDSWGLEKKQRTKTKTVVARKVTNT 223
gi|189515946|ref|XP_687281.2|-----KRKLLPEDLLEFDPEPKQKEVNTN-----NNKDEE--EINSEALSKSLPENVTVMRLKDESASNLQSAVDFTIQRFVGPRTNRRTNTELLSLNKRKGVNKGAAVQFANKKWAVDMKAVAKTNKRFMHKVKLIIP 231
1.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|117647257|ref|NP_076043.2| TYK 254
gi|109504805|ref|XP_573999.2| --- 233
gi|13569843|ref|NP_057251.2| K-- 257
gi|114605542|ref|XP_518245.2| K-- 257
gi|77735715|ref|NP_001029556.1| K 257
gi|74004089|ref|XP_535892.2| K-- 449
gi|50733613|ref|XP_418926.1| L-- 224
gi|189515946|ref|XP_687281.2| T-- 232
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