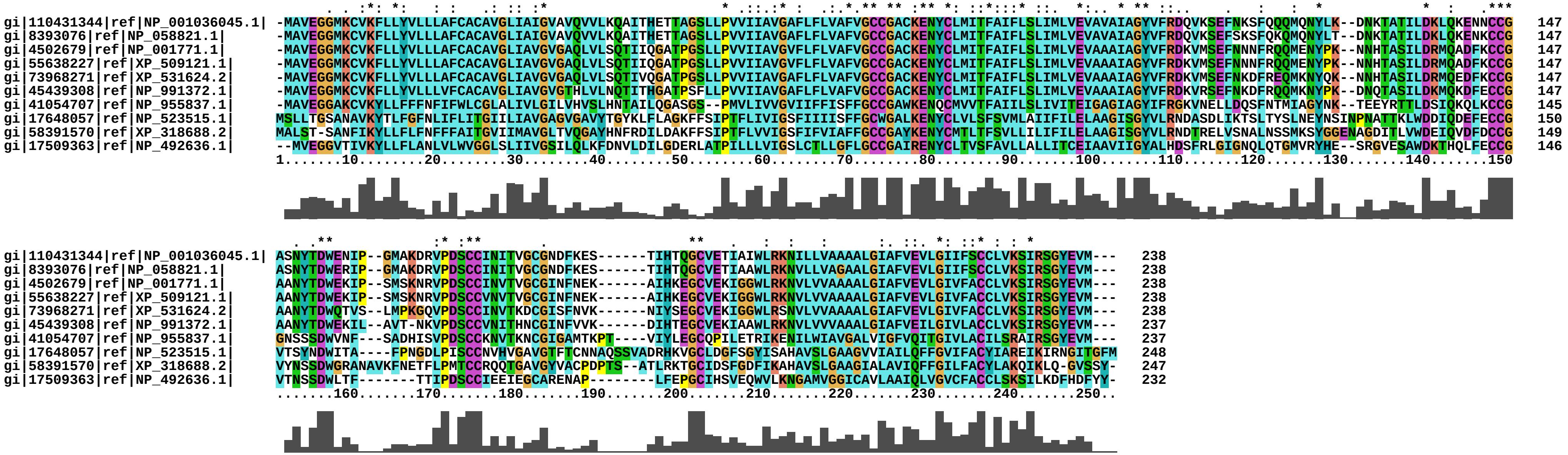

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                                       . . :*: *:   : :   .: :: :*                     * .::.:* :  .:.*.** ** :** *: ::*:::* ::.  *:.. * ** ::..    .   :   :  *            *  :   .***
gi|110431344|ref|NP_001036045.1| -MAVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAITHETTAGSLLPVVIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQVKSEFNKSFQQQMQNYLK--DNKTATILDKLQKENNCCG   147
gi|8393076|ref|NP_058821.1|      -MAVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAITHETTAGSLLPVVIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQVKSEFSKSFQKQMQNYLT--DNKTATILDKLQKENKCCG   147
gi|4502679|ref|NP_001771.1|      -MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIIQGATPGSLLPVVIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEFNNNFRQQMENYPK--NNHTASILDRMQADFKCCG   147
gi|55638227|ref|XP_509121.1|     -MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIIQGATPGSLLPVVIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEFNNNFRQQMENYPK--NNHTASILDRMQADFKCCG   147
gi|73968271|ref|XP_531624.2|     -MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIVQGATPGSLLPVVIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEFNKDFREQMKNYQK--NNHTASILDRMQEDFKCCG   147
gi|45439308|ref|NP_991372.1|     -MAVEGGMKCVKFLLYVLLLVFCACAVGLIAVGVGTHLVLNQTITHGATPSFLLPVVIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVRSEFNKDFRQQMKNYPK--DNQTASILDKMQKDFECCG   147
gi|41054707|ref|NP_955837.1|     -MAVEGGAKCVKYLLFFFNFIFWLCGLALIVLGILVHVSLHNTAILQGASGS--PMVLIVVGVIIFFISFFGCCGAWKENQCMVVTFAIILSLIVITEIGAGIAGYIFRGKVNELLDQSFNTMIAGYNK--TEEYRTTLDSIQKQLKCCG   145
gi|17648057|ref|NP_523515.1|     MSLLTGSANAVKYTLFGFNLIFLITGIILIAVGAGVGAVYTGYKLFLAGKFFSIPTFLIVIGSFIIIISFFGCWGALKENYCLVLSFSVMLAIIFILELAAGISGYVLRNDASDLIKTSLTYSLNEYNSINPNATTKLWDDIQDEFECCG   150
gi|58391570|ref|XP_318688.2|     MALST-SANFIKYLLFLFNFFFAITGVIIMAVGLTVQGAYHNFRDILDAKFFSIPTFLVVIGSFIFVIAFFGCCGAYKENYCMTLTFSVLLILIFILELAAGISGYVLRNDTRELVSNALNSSMKSYGGENAGDITLVWDEIQVDFDCCG   149
gi|17509363|ref|NP_492636.1|     --MVEGGVTIVKYLLFLANLVLWVGGLSLIIVGSILQLKFDNVLDILGDERLATPILLLVIGSLCTLLGFLGCCGAIRENYCLTVSFAVLLALLITCEIAAVIIGYALHDSFRLGIGNQLQTGMVRYHE--SRGVESAWDKTHQLFECCG   146
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                   . .**            :* :**       .                 **   .   :  :   :      :. ::. *: ::* : : *
gi|110431344|ref|NP_001036045.1| ASNYTDWENIP--GMAKDRVPDSCCINITVGCGNDFKES------TIHTQGCVETIAIWLRKNILLVAAAALGIAFVEVLGIIFSCCLVKSIRSGYEVM---   238
gi|8393076|ref|NP_058821.1|      ASNYTDWERIP--GMAKDRVPDSCCINITVGCGNDFKES------TIHTQGCVETIAAWLRKNVLLVAGAALGIAFVEVLGIIFSCCLVKSIRSGYEVM---   238
gi|4502679|ref|NP_001771.1|      AANYTDWEKIP--SMSKNRVPDSCCINVTVGCGINFNEK------AIHKEGCVEKIGGWLRKNVLVVAAAALGIAFVEVLGIVFACCLVKSIRSGYEVM---   238
gi|55638227|ref|XP_509121.1|     AANYTDWEKIP--SMSKNRVPDSCCVNVTVGCGINFNEK------AIHKEGCVEKIGGWLRKNVLVVAAAALGIAFVEVLGIVFACCLVKSIRSGYEVM---   238
gi|73968271|ref|XP_531624.2|     AANYTDWQTVS--LMPKGQVPDSCCINVTKDCGISFNVK------NIYSEGCVEKIGGWLRSNVLVVAAAALGIAFVEVLGIVFACCLVKSIRSGYEVM---   238
gi|45439308|ref|NP_991372.1|     AANYTDWEKIL--AVT-NKVPDSCCVNITHNCGINFVVK------DIHTEGCVEKIAAWLRKNVLVVVAAALGIAFVEILGIVLACCLVKSIRSGYEVM---   237
gi|41054707|ref|NP_955837.1|     GNSSSDWVNF---SADHISVPDSCCKNVTKNCGIGAMTKPT----VIYLEGCQPILETRIKENILWIAVGALVIGFVQITGIVLACILSRAIRSGYEVM---   237
gi|17648057|ref|NP_523515.1|     VTSYNDWITA----FPNGDLPISCCNVHVGAVGTFTCNNAQSSVADRHKVGCLDGFSGYISAHAVSLGAAGVVIAILQFFGVIFACYIAREIKIRNGITGFM   248
gi|58391570|ref|XP_318688.2|     VYNSSDWGRANAVKFNETFLPMTCCRQQTGAVGYVACPDPTS--ATLRKTGCIDSFGDFIKAHAVSLGAAGIALAVIQFFGILFACYLAKQIKLQ-GVSSY-   247
gi|17509363|ref|NP_492636.1|     VTNSSDWLTF-------TTIPDSCCIEEIEGCARENAP--------LFEPGCIHSVEQWVLKNGAMVGGICAVLAAIQLVGVCFACCLSKSILKDFHDFYY-   232
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250..
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