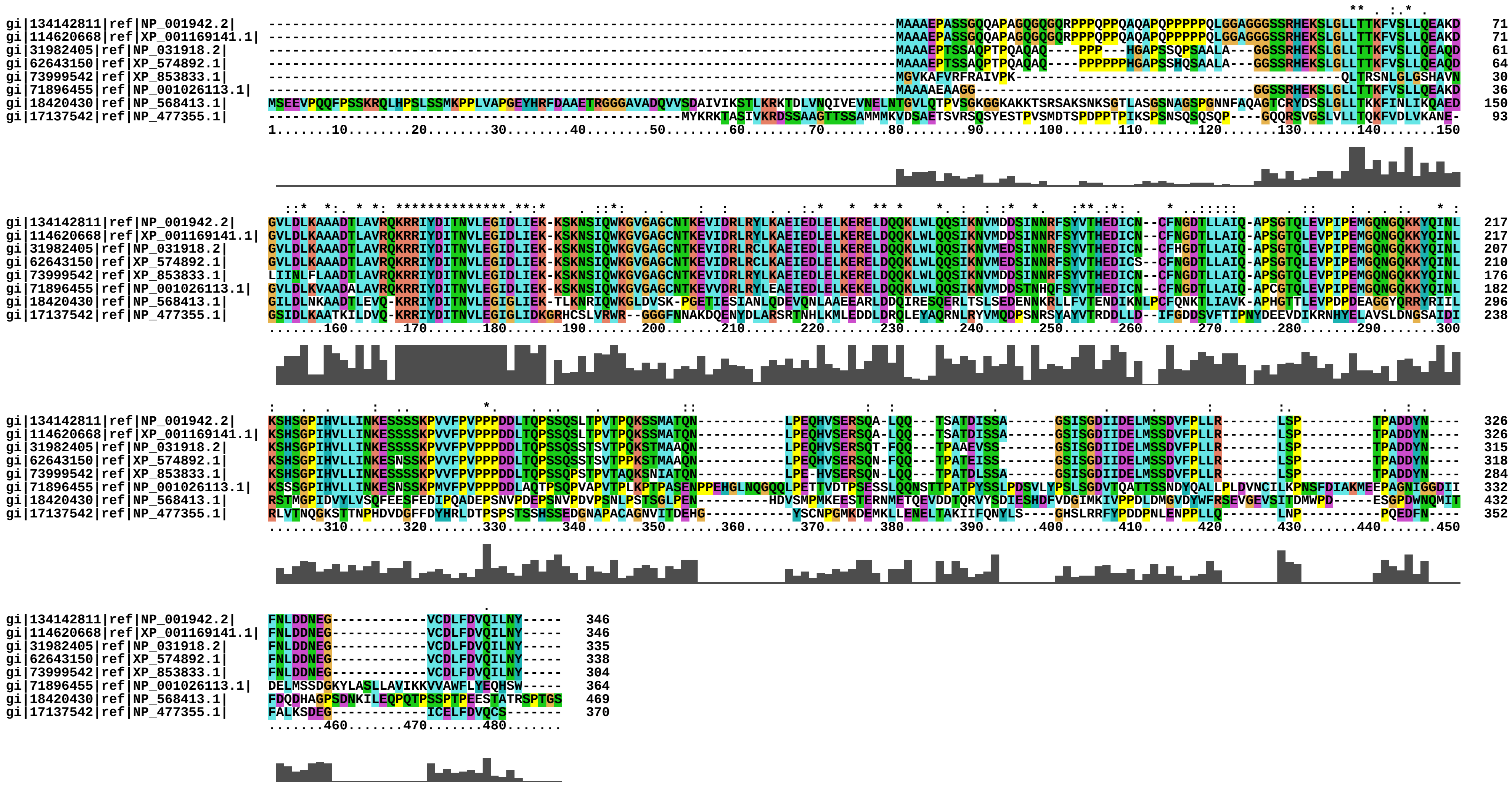

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                                                                                                                                                                          ** . :.* .
gi|134142811|ref|NP_001942.2|     -------------------------------------------------------------------------------MAAAEPASSGQQAPAGQGQGQRPPPQPPQAQAPQPPPPPQLGGAGGGSSRHEKSLGLLTTKFVSLLQEAKD 71
gi|114620668|ref|XP_001169141.1|  -------------------------------------------------------------------------------MAAAEPASSGQQAPAGQGQGQRPPPQPPQAQAPQPPPPPQLGGAGGGSSRHEKSLGLLTTKFVSLLQEAKD 71
gi|31982405|ref|NP_031918.2|      -------------------------------------------------------------------------------MAAAEPTSSAQPTPQAQAQ----PPP---HGAPSSQPSAALA---GGSSRHEKSLGLLTTKFVSLLQEAQD 61
gi|62643150|ref|XP_574892.1|      -------------------------------------------------------------------------------MAAAEPTSSAQPTPQAQAQ----PPPPPPHGAPSSHQSAALA---GGSSRHEKSLGLLTTKFVSLLQEAQD 64
gi|73999542|ref|XP_853833.1|      -------------------------------------------------------------------------------MGVKAFVRFRAIVPK-----------------------------------------QLTRSNLGLGSHAVN 30
gi|71896455|ref|NP_001026113.1|   -------------------------------------------------------------------------------MAAAAEAAGG-----------------------------------GGSSRHEKSLGLLTTKFVSLLQEAKD 36
gi|18420430|ref|NP_568413.1|      MSEEVPQQFPSSKRQLHPSLSSMKPPLVAPGEYHRFDAAETRGGGAVADQVVSDAIVIKSTLKRKTDLVNQIVEVNELNTGVLQTPVSGKGGKAKKTSRSAKSNKSGTLASGSNAGSPGNNFAQAGTCRYDSSLGLLTKKFINLIKQAED 150
gi|17137542|ref|NP_477355.1|      ----------------------------------------------------MYKRKTASIVKRDSSAAGTTSSAMMMKVDSAETSVRSQSYESTPVSMDTSPDPPTPIKSPSNSQSQSQP----GQQRSVGSLVLLTQKFVDLVKANE- 93
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                    ::*  *:. * *: **************.**:*    . ::*:  . .    :  :     . . :.*   *  ** *    *. :  : :*  *.   :**.:*: .   * ..:::::      . ::    : . . :.   * :
gi|134142811|ref|NP_001942.2|     GVLDLKAAADTLAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVIDRLRYLKAEIEDLELKERELDQQKLWLQQSIKNVMDDSINNRFSYVTHEDICN--CFNGDTLLAIQ-APSGTQLEVPIPEMGQNGQKKYQINL 217
gi|114620668|ref|XP_001169141.1|  GVLDLKAAADTLAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVIDRLRYLKAEIEDLELKERELDQQKLWLQQSIKNVMDDSINNRFSYVTHEDICN--CFNGDTLLAIQ-APSGTQLEVPIPEMGQNGQKKYQINL 217
gi|31982405|ref|NP_031918.2|      GVLDLKAAADTLAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVIDRLRCLKAEIEDLELKERELDQQKLWLQQSIKNVMEDSINNRFSYVTHEDICN--CFHGDTLLAIQ-APSGTQLEVPIPEMGQNGQKKYQINL 207
gi|62643150|ref|XP_574892.1|      GVLDLKAAADTLAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVIDRLRCLKAEIEDLELKERELDQQKLWLQQSIKNVMEDSINNRFSYVTHEDICS--CFNGDTLLAIQ-APSGTQLEVPIPEMGQNGQKKYQINL 210
gi|73999542|ref|XP_853833.1|      LIINLFLAADTLAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVIDRLRYLKAEIEDLELKERELDQQKLWLQQSIKNVMDDSINNRFSYVTHEDICN--CFNGDTLLAIQ-APSGTQLEVPIPEMGQNGQKKYQINL 176
gi|71896455|ref|NP_001026113.1|   GVLDLKVAADALAVRQKRRIYDITNVLEGIDLIEK-KSKNSIQWKGVGAGCNTKEVVDRLRYLEAEIEDLELKEKELDQQKLWLQQSIKNVMDDSTNHQFSYVTHEDICN--CFNGDTLLAIQ-APCGTQLEVPIPEMGQNGQKKYQINL 182
gi|18420430|ref|NP_568413.1|      GILDLNKAADTLEVQ-KRRIYDITNVLEGIGLIEK-TLKNRIQWKGLDVSK-PGETIESIANLQDEVQNLAAEEARLDDQIRESQERLTSLSEDENNKRLLFVTENDIKNLPCFQNKTLIAVK-APHGTTLEVPDPDEAGGYQRRYRIIL 296
gi|17137542|ref|NP_477355.1|      GSIDLKAATKILDVQ-KRRIYDITNVLEGIGLIDKGRHCSLVRWR--GGGFNNAKDQENYDLARSRTNHLKMLEDDLDRQLEYAQRNLRYVMQDPSNRSYAYVTRDDLLD--IFGDDSVFTIPNYDEEVDIKRNHYELAVSLDNGSAIDI 238
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                  :   .  .     :  ..         *.    . ..    .          ::                     :  :            .             .     .      :        :.           .  : .
gi|134142811|ref|NP_001942.2|     KSHSGPIHVLLINKESSSSKPVVFPVPPPDDLTQPSSQSLTPVTPQKSSMATQN-----------LPEQHVSERSQA-LQQ---TSATDISSA------GSISGDIIDELMSSDVFPLLR-------LSP---------TPADDYN---- 326
gi|114620668|ref|XP_001169141.1|  KSHSGPIHVLLINKESSSSKPVVFPVPPPDDLTQPSSQSLTPVTPQKSSMATQN-----------LPEQHVSERSQA-LQQ---TSATDISSA------GSISGDIIDELMSSDVFPLLR-------LSP---------TPADDYN---- 326
gi|31982405|ref|NP_031918.2|      KSHSGPIHVLLINKESSSSKPVVFPVPPPDDLTQPSSQSSTSVTPQKSTMAAQN-----------LPEQHVSERSQT-FQQ---TPAAEVSS-------GSISGDIIDELMSSDVFPLLR-------LSP---------TPADDYN---- 315
gi|62643150|ref|XP_574892.1|      KSHSGPIHVLLINKESNSSKPVVFPVPPPDDLTQPSSQSSTSVTPPKSTMAAQN-----------LPEQHVSERSQN-FQQ---TPATEISS-------GSISGDIIDELMSSDVFPLLR-------LSP---------TPADDYN---- 318
gi|73999542|ref|XP_853833.1|      KSHSGPIHVLLINKESSSSKPVVFPVPPPDDLTQPSSQPSTPVTAQKSNIATQN-----------LPE-HVSERSQN-LQQ---TPATDLSSA------GSISGDIIDELMSSDVFPLLR-------LSP---------TPADDYN---- 284
gi|71896455|ref|NP_001026113.1|   KSSSGPIHVLLINKESNSSKPMVFPVPPPDDLAQTPSQPVAPVTPLKPTPASENPPEHGLNQGQQLPETTVDTPSESSLQQNSTTPATPYSSLPDSVLYPSLSGDVTQATTSSNDYQALLPLDVNCILKPNSFDIAKMEEPAGNIGGDII 332
gi|18420430|ref|NP_568413.1|      RSTMGPIDVYLVSQFEESFEDIPQADEPSNVPDEPSNVPDVPSNLPSTSGLPEN---------HDVSMPMKEESTERNMETQEVDDTQRVYSDIESHDFVDGIMKIVPPDLDMGVDYWFRSEVGEVSITDMWPD-----ESGPDWNQMIT 432
gi|17137542|ref|NP_477355.1|      RLVTNQGKSTTNPHDVDGFFDYHRLDTPSPSTSSHSSEDGNAPACAGNVITDEHG-----------YSCNPGMKDEMKLLENELTAKIIFQNYLS----GHSLRRFYPDDPNLENPPLLQ-------LNP----------PQEDFN---- 352
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                                             .
gi|134142811|ref|NP_001942.2|     FNLDDNEG------------VCDLFDVQILNY----- 346
gi|114620668|ref|XP_001169141.1|  FNLDDNEG------------VCDLFDVQILNY----- 346
gi|31982405|ref|NP_031918.2|      FNLDDNEG------------VCDLFDVQILNY----- 335
gi|62643150|ref|XP_574892.1|      FNLDDNEG------------VCDLFDVQILNY----- 338
gi|73999542|ref|XP_853833.1|      FNLDDNEG------------VCDLFDVQILNY----- 304
gi|71896455|ref|NP_001026113.1|   DELMSSDGKYLASLLAVIKKVVAWFLYEQHSW----- 364
gi|18420430|ref|NP_568413.1|      FDQDHAGPSDNKILEQPQTPSSPTPEESTATRSPTGS 469
gi|17137542|ref|NP_477355.1|      FALKSDEG------------ICELFDVQCS------- 370
                                  .......460.......470.......480.......
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