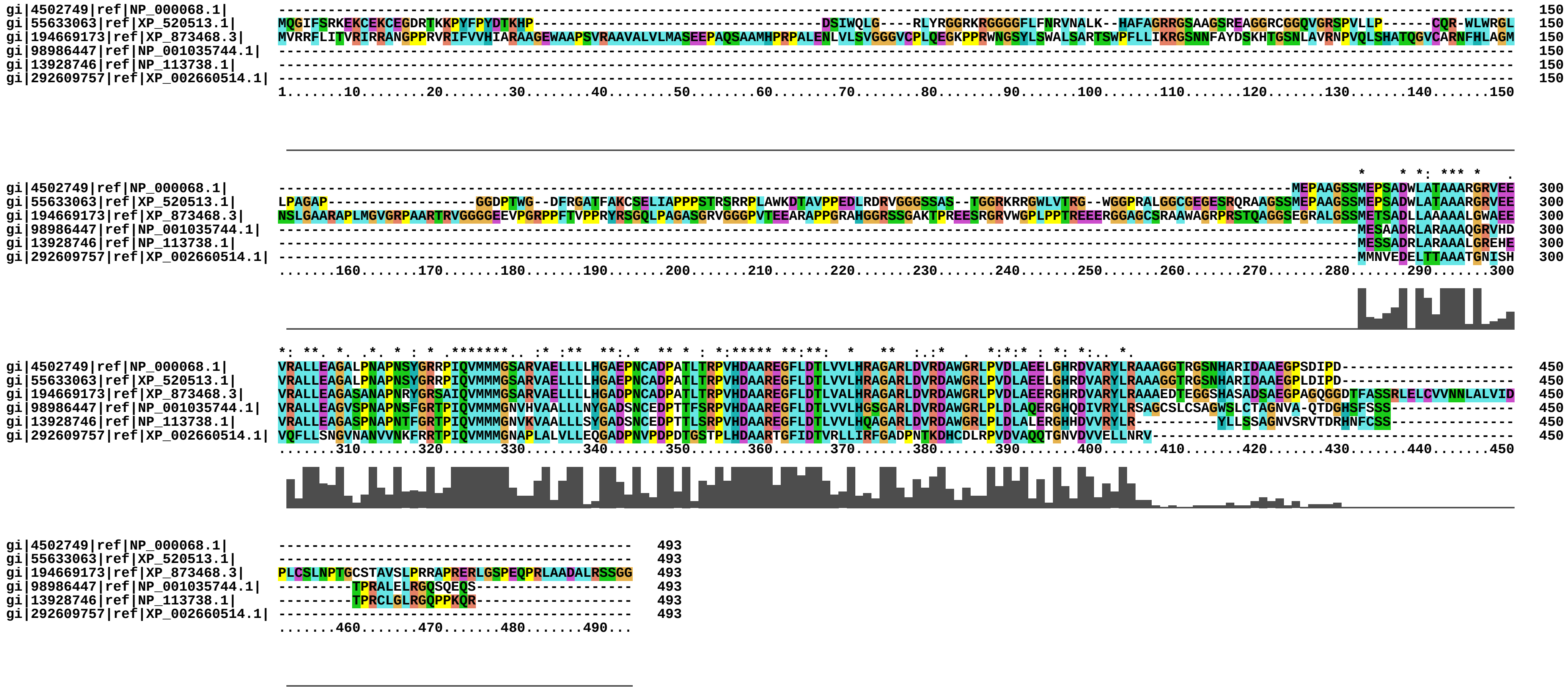

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gi|4502749|ref|NP_000068.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|55633063|ref|XP_520513.1|     MQGIFSRKEKCEKCEGDRTKKPYFPYDTKHP-----------------------------------DSIWQLG----RLYRGGRKRGGGGFLFNRVNALK--HAFAGRRGSAAGSREAGGRCGGQVGRSPVLLP------CQR-WLWRGL   150
gi|194669173|ref|XP_873468.3|    MVRRFLITVRIRRANGPPRVRIFVVHIARAAGEWAAPSVRAAVALVLMASEEPAQSAAMHPRPALENLVLSVGGGVCPLQEGKPPRWNGSYLSWALSARTSWPFLLIKRGSNNFAYDSKHTGSNLAVRNPVQLSHATQGVCARNFHLAGM   150
gi|98986447|ref|NP_001035744.1|  ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|13928746|ref|NP_113738.1|     ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|292609757|ref|XP_002660514.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                                                                                                                                                    *    * *: *** *   .
gi|4502749|ref|NP_000068.1|      ---------------------------------------------------------------------------------------------------------------------------MEPAAGSSMEPSADWLATAAARGRVEE   300
gi|55633063|ref|XP_520513.1|     LPAGAP------------------GGDPTWG--DFRGATFAKCSELIAPPPSTRSRRPLAWKDTAVPPEDLRDRVGGGSSAS--TGGRKRRGWLVTRG--WGGPRALGGCGEGESRQRAAGSSMEPAAGSSMEPSADWLATAAARGRVEE   300
gi|194669173|ref|XP_873468.3|    NSLGAARAPLMGVGRPAARTRVGGGGEEVPGRPPFTVPPRYRSGQLPAGASGRVGGGPVTEEARAPPGRAHGGRSSGAKTPREESRGRVWGPLPPTREEERGGAGCSRAAWAGRPRSTQAGGSEGRALGSSMETSADLLAAAAALGWAEE   300
gi|98986447|ref|NP_001035744.1|  -----------------------------------------------------------------------------------------------------------------------------------MESAADRLARAAAQGRVHD   300
gi|13928746|ref|NP_113738.1|     -----------------------------------------------------------------------------------------------------------------------------------MESSADRLARAAALGREHE   300
gi|292609757|ref|XP_002660514.1| -----------------------------------------------------------------------------------------------------------------------------------MMNVEDELTTAAATGNISH   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                 *: **. *. .*. * : * .*******.. :* :**  **:.*  ** * : *:***** **:**:  *   **  :.:*  .  *:*:* : *: *:.. *.
gi|4502749|ref|NP_000068.1|      VRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD---------------------   450
gi|55633063|ref|XP_520513.1|     VRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPLDIPD---------------------   450
gi|194669173|ref|XP_873468.3|    VRALLEAGASANAPNRYGRSAIQVMMMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVALHRAGARLDVRDAWGRLPVDLAEERGHRDVARYLRAAAEDTEGGSHASADSAEGPAGQGGDTFASSRLELCVVNNLALVID   450
gi|98986447|ref|NP_001035744.1|  VRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVA-QTDGHSFSSS---------------   450
gi|13928746|ref|NP_113738.1|     VRALLEAGASPNAPNTFGRTPIQVMMMGNVKVAALLLSYGADSNCEDPTTLSRPVHDAAREGFLDTLVVLHQAGARLDVRDAWGRLPLDLALERGHHDVVRYLR----------YLLSSAGNVSRVTDRHNFCSS---------------   450
gi|292609757|ref|XP_002660514.1| VQFLLSNGVNANVVNKFRRTPIQVMMMGNAPLALVLLEQGADPNVPDPDTGSTPLHDAARTGFIDTVRLLIRFGADPNTKDHCDLRPVDVAQQTGNVDVVELLNRV--------------------------------------------   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

gi|4502749|ref|NP_000068.1|      -------------------------------------------   493
gi|55633063|ref|XP_520513.1|     -------------------------------------------   493
gi|194669173|ref|XP_873468.3|    PLCSLNPTGCSTAVSLPRRAPRERLGSPEQPRLAADALRSSGG   493
gi|98986447|ref|NP_001035744.1|  ---------TPRALELRGQSQEQS-------------------   493
gi|13928746|ref|NP_113738.1|     ---------TPRCLGLRGQPPKQR-------------------   493
gi|292609757|ref|XP_002660514.1| -------------------------------------------   493
                                 .......460.......470.......480.......490...
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