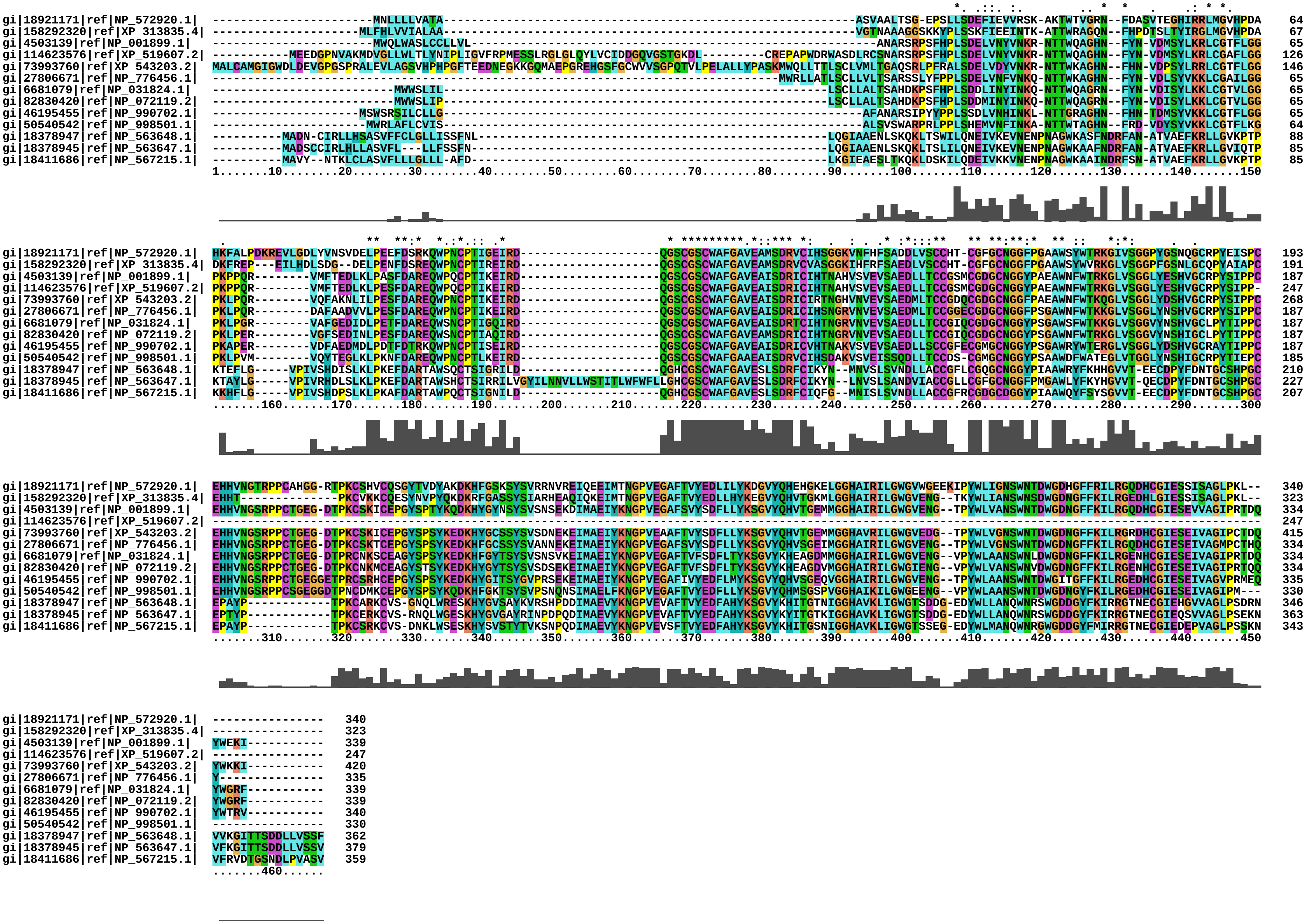

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                                                                                                                                          *. .::. :.        ..  *  *   .    .: * *.
gi|18921171|ref|NP_572920.1|    -----------------------MNLLLLVATA-----------------------------------------------------------ASVAALTSG-EPSLLSDEFIEVVRSK-AKTWTVGRN--FDASVTEGHIRRLMGVHPDA    64
gi|158292320|ref|XP_313835.4|   ---------------------MLFHLVVIALAA-----------------------------------------------------------VGTNAAAGGSKKYPLSSKFIEEINTK-ATTWRAGQN--FHPDTSLTYIRGLMGVHPDA    67
gi|4503139|ref|NP_001899.1|     -----------------------MWQLWASLCCLLVL----------------------------------------------------------ANARSRPSFHPLSDELVNYVNKR-NTTWQAGHN--FYN-VDMSYLKRLCGTFLGG    65
gi|114623576|ref|XP_519607.2|   -----------MEEDGPNVAKMDVGLLWLTLYNIPLIGVFRPMESSLRGLGLQYLVCIDDGQVGSTGKDL---------CREPAPWDRWASDLRCSNARSRPSFHPLSDELVNYVNKR-NTTWQAGHN--FYN-VDMSYLKRLCGAFLGG   126
gi|73993760|ref|XP_543203.2|    MALCAMGIGWDLDEVGPGSPRALEVLAGSVHPHPGFTEEDNEGKKGQMAEPGREHGSFGCWVVSGPQTVLPELALLYPASKMWQLLTTLSCLVMLTGAQSRLPFRALSDELVDYVNKR-NTTWKAGHN--FHN-VDPSYLRRLCGTFLGG   146
gi|27806671|ref|NP_776456.1|    ---------------------------------------------------------------------------------MWRLLATLSCLLVLTSARSSLYFPPLSDELVNFVNKQ-NTTWKAGHN--FYN-VDLSYVKKLCGAILGG    65
gi|6681079|ref|NP_031824.1|     --------------------------MWWSLIL-------------------------------------------------------LSCLLALTSAHDKPSFHPLSDDLINYINKQ-NTTWQAGRN--FYN-VDISYLKKLCGTVLGG    65
gi|82830420|ref|NP_072119.2|    --------------------------MWWSLIP-------------------------------------------------------LSCLLALTSAHDKPSFHPLSDDMINYINKQ-NTTWQAGRN--FYN-VDISYLKKLCGTVLGG    65
gi|46195455|ref|NP_990702.1|    ---------------------MSWSRSILCLLG------------------------------------------------------------AFANARSIPYYPPLSSDLVNHINKL-NTTGRAGHN--FHN-TDMSYVKKLCGTFLGG    65
gi|50540542|ref|NP_998501.1|    ----------------------MWRLAFLCVIS------------------------------------------------------------ALSVSWARPRLPPLSHEMVNFINKA-NTTWTAGHN--FRD-VDYSYVKKLCGTFLKG    64
gi|18378947|ref|NP_563648.1|    ----------MADN-CIRLLHSASVFFCLGLLISSFNL--------------------------------------------------LQGIAAENLSKQKLTSWILQNEIVKEVNENPNAGWKASFNDRFAN-ATVAEFKRLLGVKPTP    88
gi|18378945|ref|NP_563647.1|    ----------MADSCCIRLHLLASVFL---LLFSSFN---------------------------------------------------LQGIAAENLSKQKLTSLILQNEIVKEVNENPNAGWKAAFNDRFAN-ATVAEFKRLLGVIQTP    85
gi|18411686|ref|NP_567215.1|    ----------MAVY--NTKLCLASVFLLLGLLL-AFD---------------------------------------------------LKGIEAESLTKQKLDSKILQDEIVKKVNENPNAGWKAAINDRFSN-ATVAEFKRLLGVKPTP    85
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                 .                    **  **:*  *.:*.:: .*                       * *********.*::*** *:  .  : . .* :*:::**   ** **:**:*  ** ::   *:*:     .  .
gi|18921171|ref|NP_572920.1|    HKFALPDKREVLGDLYVNSVDELPEEFDSRKQWPNCPTIGEIRD--------------------QGSCGSCWAFGAVEAMSDRVCIHSGGKVNFHFSADDLVSCCHT-CGFGCNGGFPGAAWSYWTRKGIVSGGPYGSNQGCRPYEISPC   193
gi|158292320|ref|XP_313835.4|   DKFREP---EILHDLSDG--DELPENFDSREQWPNCPTIREIRD--------------------QGSCGSCWAFGAVEAMSDRVCVASGGKIHFRFSAEDLVSCCHT-CGFGCNGGFPGAAWSYWVRKGLVSGGPFGSNLGCQPYAIAPC   191
gi|4503139|ref|NP_001899.1|     PKPPQR--------VMFTEDLKLPASFDAREQWPQCPTIKEIRD--------------------QGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPC   187
gi|114623576|ref|XP_519607.2|   PKPPQR--------VMFTEDLKLPESFDAREQWPQCPTIKEIRD--------------------QGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPP-   247
gi|73993760|ref|XP_543203.2|    PKLPQR--------VQFAKNLILPESFDAREQWPNCPTIKEIRD--------------------QGSCGSCWAFGAVEAISDRICIRTNGHVNVEVSAEDMLTCCGDQCGDGCNGGFPAEAWNFWTKQGLVSGGLYDSHVGCRPYSIPPC   268
gi|27806671|ref|NP_776456.1|    PKLPQR--------DAFAADVVLPESFDAREQWPNCPTIKEIRD--------------------QGSCGSCWAFGAVEAISDRICIHSNGRVNVEVSAEDMLTCCGGECGDGCNGGFPSGAWNFWTKKGLVSGGLYNSHVGCRPYSIPPC   187
gi|6681079|ref|NP_031824.1|     PKLPGR--------VAFGEDIDLPETFDAREQWSNCPTIGQIRD--------------------QGSCGSCWAFGAVEAISDRTCIHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTKKGLVSGGVYNSHVGCLPYTIPPC   187
gi|82830420|ref|NP_072119.2|    PKLPER--------VGFSEDINLPESFDAREQWSNCPTIAQIRD--------------------QGSCGSCWAFGAVEAMSDRICIHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWNFWTRKGLVSGGVYNSHIGCLPYTIPPC   187
gi|46195455|ref|NP_990702.1|    PKAPER--------VDFAEDMDLPDTFDTRKQWPNCPTISEIRD--------------------QGSCGSCWAFGAVEAISDRICVHTNAKVSVEVSAEDLLSCCGFECGMGCNGGYPSGAWRYWTERGLVSGGLYDSHVGCRAYTIPPC   187
gi|50540542|ref|NP_998501.1|    PKLPVM--------VQYTEGLKLPKNFDAREQWPNCPTLKEIRD--------------------QGSCGSCWAFGAAEAISDRVCIHSDAKVSVEISSQDLLTCCDS-CGMGCNGGYPSAAWDFWATEGLVTGGLYNSHIGCRPYTIEPC   185
gi|18378947|ref|NP_563648.1|    KTEFLG-----VPIVSHDISLKLPKEFDARTAWSQCTSIGRILD--------------------QGHCGSCWAFGAVESLSDRFCIKYN--MNVSLSVNDLLACCGFLCGQGCNGGYPIAAWRYFKHHGVVT-EECDPYFDNTGCSHPGC   210
gi|18378945|ref|NP_563647.1|    KTAYLG-----VPIVRHDLSLKLPKEFDARTAWSHCTSIRRILVGYILNNVLLWSTITLWFWFLLGHCGSCWAFGAVESLSDRFCIKYN--LNVSLSANDVIACCGLLCGFGCNGGFPMGAWLYFKYHGVVT-QECDPYFDNTGCSHPGC   227
gi|18411686|ref|NP_567215.1|    KKHFLG-----VPIVSHDPSLKLPKAFDARTAWPQCTSIGNILD--------------------QGHCGSCWAFGAVESLSDRFCIQFG--MNISLSVNDLLACCGFRCGDGCDGGYPIAAWQYFSYSGVVT-EECDPYFDNTGCSHPGC   207
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

gi|18921171|ref|NP_572920.1|    EHHVNGTRPPCAHGG-RTPKCSHVCQSGYTVDYAKDKHFGSKSYSVRRNVREIQEEIMTNGPVEGAFTVYEDLILYKDGVYQHEHGKELGGHAIRILGWGVWGEEKIPYWLIGNSWNTDWGDHGFFRILRGQDHCGIESSISAGLPKL--   340
gi|158292320|ref|XP_313835.4|   EHHT--------------PKCVKKCQESYNVPYQKDKRFGASSYSIARHEAQIQKEIMTNGPVEGAFTVYEDLLHYKEGVYQHVTGKMLGGHAIRILGWGVENG--TKYWLIANSWNSDWGDNGFFKILRGEDHLGIESSISAGLPKL--   323
gi|4503139|ref|NP_001899.1|     EHHVNGSRPPCTGEG-DTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGGHAIRILGWGVENG--TPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTDQ   334
gi|114623576|ref|XP_519607.2|   ------------------------------------------------------------------------------------------------------------------------------------------------------   247
gi|73993760|ref|XP_543203.2|    EHHVNGSRPPCTGEG-DTPKCSKICEPGYSPSYKEDKHYGCSSYSVSDNEKEIMAEIYKNGPVEAAFTVYSDFLLYKSGVYQHVTGEMMGGHAVRILGWGVEDG--TPYWLVGNSWNTDWGDNGFFKILRGRDHCGIESEIVAGIPCTDQ   415
gi|27806671|ref|NP_776456.1|    EHHVNGSRPPCTGEG-DTPKCSKTCEPGYSPSYKEDKHFGCSSYSVANNEKEIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVSGEIMGGHAIRILGWGVENG--TPYWLVGNSWNTDWGDNGFFKILRGQDHCGIESEIVAGMPCTHQ   334
gi|6681079|ref|NP_031824.1|     EHHVNGSRPPCTGEG-DTPRCNKSCEAGYSPSYKEDKHFGYTSYSVSNSVKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDMMGGHAIRILGWGVENG--VPYWLAANSWNLDWGDNGFFKILRGENHCGIESEIVAGIPRTDQ   334
gi|82830420|ref|NP_072119.2|    EHHVNGSRPPCTGEG-DTPKCNKMCEAGYSTSYKEDKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENG--VPYWLVANSWNVDWGDNGFFKILRGENHCGIESEIVAGIPRTQQ   334
gi|46195455|ref|NP_990702.1|    EHHVNGSRPPCTGEGGETPRCSRHCEPGYSPSYKEDKHYGITSYGVPRSEKEIMAEIYKNGPVEGAFIVYEDFLMYKSGVYQHVSGEQVGGHAIRILGWGVENG--TPYWLAANSWNTDWGITGFFKILRGEDHCGIESEIVAGVPRMEQ   335
gi|50540542|ref|NP_998501.1|    EHHVNGSRPPCSGEGGDTPNCDMKCEPGYSPSYKQDKHFGKTSYSVPSNQNSIMAELFKNGPVEGAFTVYEDFLLYKSGVYQHMSGSPVGGHAIKILGWGEENG--VPYWLAANSWNTDWGDNGYFKILRGEDHCGIESEIVAGIPM---   330
gi|18378947|ref|NP_563648.1|    EPAYP------------TPKCARKCVS-GNQLWRESKHYGVSAYKVRSHPDDIMAEVYKNGPVEVAFTVYEDFAHYKSGVYKHITGTNIGGHAVKLIGWGTSDDG-EDYWLLANQWNRSWGDDGYFKIRRGTNECGIEHGVVAGLPSDRN   346
gi|18378945|ref|NP_563647.1|    EPTYP------------TPKCERKCVS-RNQLWGESKHYGVGAYRINPDPQDIMAEVYKNGPVEVAFTVYEDFAHYKSGVYKYITGTKIGGHAVKLIGWGTSDDG-EDYWLLANQWNRSWGDDGYFKIRRGTNECGIEQSVVAGLPSEKN   363
gi|18411686|ref|NP_567215.1|    EPAYP------------TPKCSRKCVS-DNKLWSESKHYSVSTYTVKSNPQDIMAEVYKNGPVEVSFTVYEDFAHYKSGVYKHITGSNIGGHAVKLIGWGTSSEG-EDYWLMANQWNRGWGDDGYFMIRRGTNECGIEDEPVAGLPSSKN   343
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

gi|18921171|ref|NP_572920.1|    ----------------   340
gi|158292320|ref|XP_313835.4|   ----------------   323
gi|4503139|ref|NP_001899.1|     YWEKI-----------   339
gi|114623576|ref|XP_519607.2|   ----------------   247
gi|73993760|ref|XP_543203.2|    YWKKI-----------   420
gi|27806671|ref|NP_776456.1|    Y---------------   335
gi|6681079|ref|NP_031824.1|     YWGRF-----------   339
gi|82830420|ref|NP_072119.2|    YWGRF-----------   339
gi|46195455|ref|NP_990702.1|    YWTRV-----------   340
gi|50540542|ref|NP_998501.1|    ----------------   330
gi|18378947|ref|NP_563648.1|    VVKGITTSDDLLVSSF   362
gi|18378945|ref|NP_563647.1|    VFKGITTSDDLLVSSV   379
gi|18411686|ref|NP_567215.1|    VFRVDTGSNDLPVASV   359
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