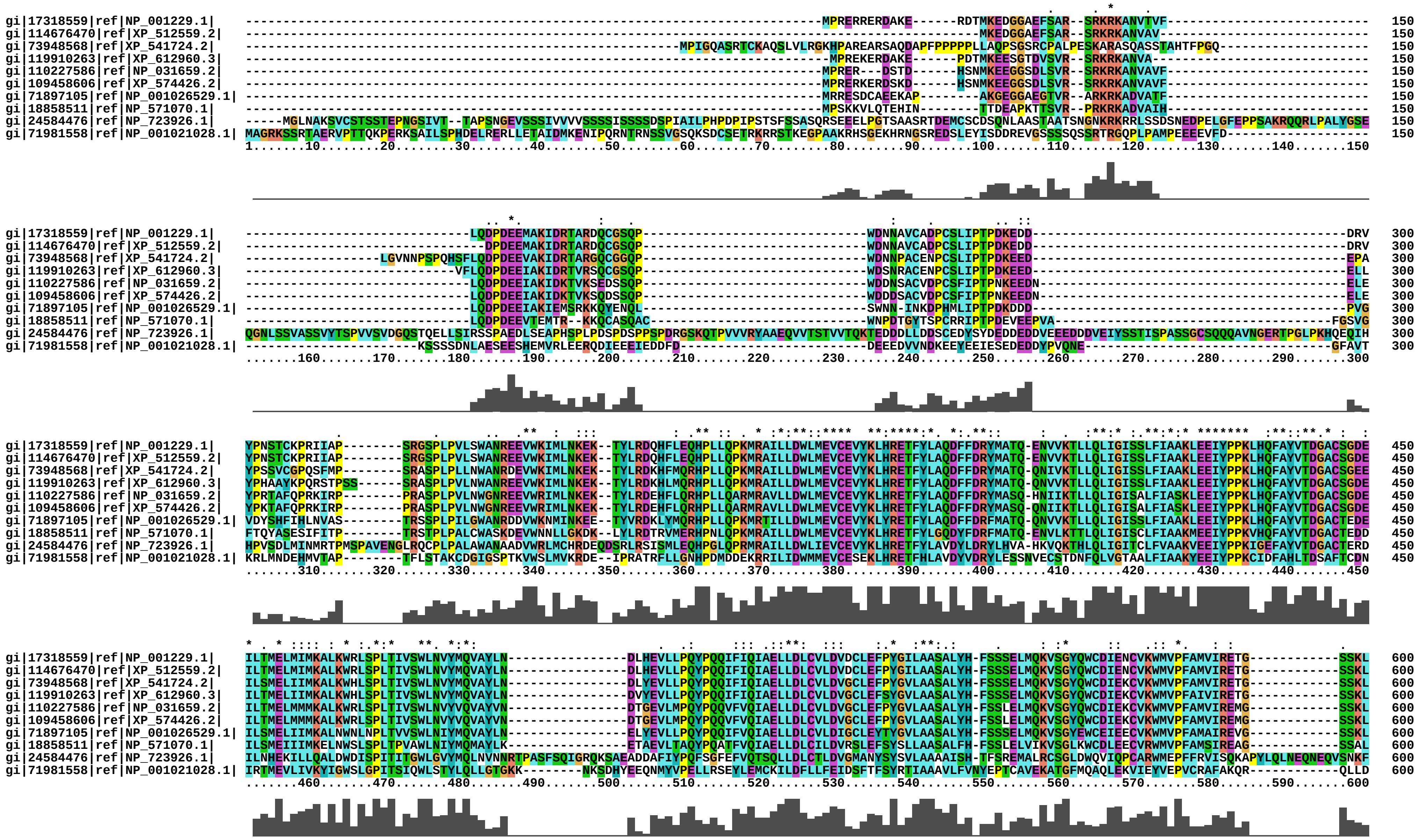

```
                                                                                                                                                                           .     . *    .
gi|17318559|ref|NP_001229.1|    -----------------------------------------------------------------------------MPRERRERDAKE------RDTMKEDGGAEFSAR--SRKRKANVTVF---------------------------   150
gi|114676470|ref|XP_512559.2|   --------------------------------------------------------------------------------------------------MKEDGGAEFSAR--SRKRKANVAV----------------------------   150
gi|73948568|ref|XP_541724.2|    ----------------------------------------------------------MPIGQASRTCKAQSLVLRGKHPAREARSAQDAPFPPPPPLLAQPSGSRCPALPESKARASQASSTAHTFPGQ--------------------   150
gi|119910263|ref|XP_612960.3|   ------------------------------------------------------------------------------MPREKERDAKE------PDTMKEESGTDVSVR--SRKRKANVA-----------------------------   150
gi|110227586|ref|NP_031659.2|   -----------------------------------------------------------------------------MPRER---DSTD------HSNMKEEGGSDLSVR--SRKRKANVAVF---------------------------   150
gi|109458606|ref|XP_574426.2|   -----------------------------------------------------------------------------MPRERKERDSKD------HSNMKEEGGSDLSVR--SRKRKANVAVF---------------------------   150
gi|71897105|ref|NP_001026529.1| -----------------------------------------------------------------------------MRRESDCAEEKAP--------AKGEGGAEGTVR--ARKRKADVATF---------------------------   150
gi|18858511|ref|NP_571070.1|    -----------------------------------------------------------------------------MPSKKVLQTEHIN--------TTDEAPKTTSVR--PRKRKADVAIH---------------------------   150
gi|24584476|ref|NP_723926.1|    -----MGLNAKSVCSTSSTEPNGSIVT--TAPSNGEVSSSIVVVVSSSSISSSSDSPIAILPHPDPIPSTSFSSASQRSEEELPGTSAASRTDEMCSCDSQNLAASTAATSNGNKRKRRLSSDSNEDPELGFEPPSAKRQQRLPALYGSE   150
gi|71981558|ref|NP_001021028.1| MAGRKSSRTAERVPTTQKPERKSAILSPHDELRERLLETAIDMKENIPQRNTRNSSVGSQKSDCSETRKRRSTKEGPAAKRHSGEKHRNGSREDSLEYISDDREVGSSSSQSSRTRGQPLPAMPEEEEVFD-------------------   150
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                                                 .. *.          :   .                                  :    .        .. ::
gi|17318559|ref|NP_001229.1|    ------------------------------LQDPDEEMAKIDRTARDQCGSQP------------------------------WDNNAVCADPCSLIPTPDKEDD------------------------------------------DRV   300
gi|114676470|ref|XP_512559.2|   --------------------------------DPDEEMAKIDRTARDQCGSQP------------------------------WDNNAVCADPCSLIPTPDKEDD------------------------------------------DRV   300
gi|73948568|ref|XP_541724.2|    ------------------LGVNNPSPQHSFLQDPDEEVAKIDRTARGQCGGQP------------------------------WDNNPACENPCSLIPTPDKEED------------------------------------------EPA   300
gi|119910263|ref|XP_612960.3|   ----------------------------VFLQDPDEEIAKIDRTVRSQCGSQP------------------------------WDSNRACENPCSLIPTPDKEED------------------------------------------ELL   300
gi|110227586|ref|NP_031659.2|   ------------------------------LQDPDEEIAKIDKTVKSEDSSQP------------------------------WDDNSACVDPCSFIPTPNKEEDN-----------------------------------------ELE   300
gi|109458606|ref|XP_574426.2|   ------------------------------LQDPDEEIAKIDKTVKSQDSSQP------------------------------WDDDSACVDPCSFIPTPNKEEDN-----------------------------------------ELE   300
gi|71897105|ref|NP_001026529.1| ------------------------------LQDPDEEIAKIEMSRKKQYENQL------------------------------SWNN-INKDPHMLIPTPDKDDD------------------------------------------PVG   300
gi|18858511|ref|NP_571070.1|    ------------------------------LQDPDEEVTEMTR--KKQCASQAC-----------------------------WNPDTGYTSPCRRIPTPDEVEEPVA-------------------------------------FGSVG   300
gi|24584476|ref|NP_723926.1|    QGNLSSVASSVYTSPVVSVDGQSTQELLSIRSSPAEDLSEAPHSPLPDSPDSPPSPDRGSKQTPVVVRYAAEQVVTSTVVTQKTEDDDLLDDSCEDYSYDEDDEDDVEEEDDDVEIYSSTISPASSGCSQQQAVNGERTPGLPKHQEQIH   300
gi|71981558|ref|NP_001021028.1| -----------------------KSSSSDNLAESEESHEMVRLEERQDIEEEIEDDFD-------------------------DEEEDVVNDKEEYEEIESEDEDDYPVQNE---------------------------------GFAVT   300
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                            .            .      ..  .**  :  :::          : .** :: . * :*:**::****  **:****:*. *:.**::     :  .  :**:* :.**:*:* *******  :**::**.* :  :
gi|17318559|ref|NP_001229.1|    YPNSTCKPRIIAP--------SRGSPLPVLSWANREEVWKIMLNKEK--TYLRDQHFLEQHPLLQPKMRAILLDWLMEVCEVYKLHRETFYLAQDFFDRYMATQ-ENVVKTLLQLIGISSLFIAAKLEEIYPPKLHQFAYVTDGACSGDE   450
gi|114676470|ref|XP_512559.2|   YPNSTCKPRIIAP--------SRGSPLPVLSWANREEVWKIMLNKEK--TYLRDQHFLEQHPLLQPKMRAILLDWLMEVCEVYKLHRETFYLAQDFFDRYMATQ-ENVVKTLLQLIGISSLFIAAKLEEIYPPKLHQFAYVTDGACSGDE   450
gi|73948568|ref|XP_541724.2|    YPSSVCGPQSFMP--------SRASPLPLLNWANRDEVWKIMLNKEK--TYLRDKHFMQRHPLLQPKMRAILLDWLMEVCEVYKLHRETFYLAQDFFDRYMATQ-QNIVKTLLQLIGISSLFIAAKLEEIYPPKLHQFAYVTDGACSGEE   450
gi|119910263|ref|XP_612960.3|   YPHAAYKPQRSTPSS------SRASPLPVLNWANREEVWKIMLNKEK--TYLRDKHLMQRHPLLQPKMRAILLDWLMEVCEVYKLHRETFYLAQDFFDRYMATQ-QNVVKTLLQLIGISSLFIAAKLEEIYPPKLHQFAYVTDGACSGDE   450
gi|110227586|ref|NP_031659.2|   YPRTAFQPRKIRP--------PRASPLPVLNWGNREEVWRIMLNKEK--TYLRDEHFLQRHPLLQARMRAVLLDWLMEVCEVYKLHRETFYLAQDFFDRYMASQ-HNIIKTLLQLIGISALFIASKLEEIYPPKLHQFAYVTDGACSGDE   450
gi|109458606|ref|XP_574426.2|   YPKTAFQPRKIRP--------PRASPLPVLNWGNREEVWRIMLNKEK--TYLRDEHFLQRHPLLQARMRAVLLDWLMEVCEVYKLHRETFYLAQDFFDRYMASQ-QNIIKTLLQLIGISALFIASKLEEIYPPKLHQFAYVTDGACSGDE   450
gi|71897105|ref|NP_001026529.1| VDYSHFIHLNVAS--------TRSSPLPILGWANRDDVWKNMINKEE--TYVRDKLYMQRHPLLQPKMRTILLDWLMEVCEVYKLYRETFYLAQDFFDRFMATQ-QNVVKTLLQLIGISSLFIAAKLEEIYPPKLHQFAYVTDGACTEDE   450
gi|18858511|ref|NP_571070.1|    FTQYASESIFITP--------TRSTPLPALCWASKDEVWNNLLGKDK--LYLRDTRVMERHPNLQPKMRAILLDWLMEVCEVYKLHRETFYLGQDYFDRFMATQ-ENVLKTTLQLIGISCLFIAAKMEEIYPPKVHQFAYVTDGACTEDD   450
gi|24584476|ref|NP_723926.1|    HPVSDLMINMRTPMSPAVENGLRQCPLPALAWANAADVWRLMCHRDEQDSRLRSISMLEQHPGLQPRMRAILLDWLIEVCEVYKLHRETFYLAVDYLDRYLHVA-HKVQKTHLQLIGITCLFVAAKVEEIYPPKIGEFAYVTDGACTERD   450
gi|71981558|ref|NP_001021028.1| KRLMNDEHMVTAP--------TFLSTAKCDGIGSPTKVWSLMVKRDE--IPRATRFLLGNHPDMDDEKRRILIDWMMEVCESEKLHRETFHLAVDYVDRYLESSNVECSTDNFQLVGTAALFIAAKYEEIYPPKCIDFAHLTDSAFTCDN   450
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                * . * :::: : * :.*:*   **. *:*:                        .  .:     ::: .::**:  :::    :.*  :**:.:     .     : :*     ::   .:: *.   : :              .
gi|17318559|ref|NP_001229.1|    ILTMELMIMKALKWRLSPLTIVSWLNVYMQVAYLN----------------DLHEVLLPQYPQQIFIQIAELLDLCVLDVDCLEFPYGILAASALYH-FSSSELMQKVSGYQWCDIENCVKWMVPFAMVIRETG------------SSKL   600
gi|114676470|ref|XP_512559.2|   ILTMELMIMKALKWRLSPLTIVSWLNVYMQVAYLN----------------DLHEVLLPQYPQQIFIQIAELLDLCVLDVDCLEFPYGILAASALYH-FSSSELMQKVSGYQWCDIENCVKWMVPFAMVIRETG------------SSKL   600
gi|73948568|ref|XP_541724.2|    ILSMELIIMKALKWHLSPLTIVSWLNVYMQVAYLN----------------DLYEVLLPQYPQQIFIQIAELLDLCVLDVGCLEFPYGVLAASALYH-FSSSELMQKVSGYQWCDIEKCVKWMVPFAMVIRETG------------SSKL   600
gi|119910263|ref|XP_612960.3|   ILTMELIIMKALKWHLSPLTIVSWLNVYMQVAYLN----------------DVYEVLLPQYPQQIFIQIAELLDLCVLDVGCLEFSYGVLAASALYH-FSSSELMQKVSGYQWCDIEKCVKWMVPFAIVIRETG------------SSKL   600
gi|110227586|ref|NP_031659.2|   ILTMELMMMKALKWRLSPLTIVSWLNVYVQVAYVN----------------DTGEVLMPQYPQQVFVQIAELLDLCVLDVGCLEFPYGVLAASALYH-FSSLELMQKVSGYQWCDIEKCVKWMVPFAMVIREMG------------SSKL   600
gi|109458606|ref|XP_574426.2|   ILTMELMMMKALKWRLSPLTIVSWLNVYVQVAYVN----------------DTGEVLMPQYPQQVFVQIAELLDLCVLDVGCLEFPYGVLAASALYH-FSSLELMQKVSGYQWCDIEKCVKWMVPFAMVIREMG------------SSKL   600
gi|71897105|ref|NP_001026529.1| ILSMELIIMKALNWNLNPLTVVSWLNIYMQVAYLN----------------ELYEVLLPQYPQQIFVQIAELLDLCVLDIGCLEYTYGVLAASALYH-FSSSELMQKVSGYEWCEIEECVKWMVPFAMAIREVG------------SSKL   600
gi|18858511|ref|NP_571070.1|    ILSMEIIIMKELNWSLSPLTPVAWLNIYMQMAYLK----------------ETAEVLTAQYPQATFVQIAELLDLCILDVRSLEFSYSLLAASALFH-FSSLELVIKVSGLKWCDLEECVRWMVPFAMSIREAG------------SSAL   600
gi|24584476|ref|NP_723926.1|    ILNHEKILLQALDWDISPITITGWLGVYMQLNVNNRTPASFSQIGRQKSAEADDAFIYPQFSGFEFVQTSQLLDLCTLDVGMANYSYSVLAAAAISH-TFSREMALRCSGLDWQVIQPCARWMEPFFRVISQKAPYLQLNEQNEQVSNKF   600
gi|71981558|ref|NP_001021028.1| IRTMEVLIVKYIGWSLGPITSIQWLSTYLQLLGTGKK--------NKSDHYEEQNMYVPELLRSEYLEMCKILDFLLFEIDSFTFSYRTIAAAVLFVNYEPTCAVEKATGFMQAQLEKVIEYVEPVCRAFAKQR------------QLLD   600
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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                                           .:  :* * **.:                  : .     .           * *
gi|17318559|ref|NP_001229.1|       KH---FRGVADEDAHNIQTHRDSLDLLDK-------ARAKKAMLSEQNRAS-PLPSGLLTPPQSGKKQS-------------SGPEMA------------------------------   718
gi|114676470|ref|XP_512559.2|      KH---FRGVADEDAHNIQTHRDSLDLLDK-------ARAKKAMLSEQNRASSPLPSGLLTPPQSGKKQS-------------SGPEMA------------------------------   718
gi|73948568|ref|XP_541724.2|       KH---FRGVPAEDAHNIQTHINSLDLLDK-------AQAKKAILSEQNRIS-PPPTGVLTPPQSSKKQS-------------SGQDTA------------------------------   718
gi|119910263|ref|XP_612960.3|      KH---FRGVPAEDAHNIQTHINSLDLLDK-------AQAKKAILSEENRIS-PLPTGVLTPPQSSKKQS-------------SGQGSA------------------------------   718
gi|110227586|ref|NP_031659.2|      KH---FRGVPMEDSHNIQTHTNSLDLLDK-------AQAKKAILSEQNRIS-PPPSVVLTPPPSSKKQS-------------SEQETE------------------------------   718
gi|109458606|ref|XP_574426.2|      KH---FRGVPMEDSHNIQTHTNSLDLLDK-------AQAKKAILSEQNRIS-PPPSGVLTPPHSSKKQS-------------SEQETE------------------------------   718
gi|71897105|ref|NP_001026529.1|    KH---FRGIAPEDLHNIQTHINSLDLLDK-------AQAKQAILAEQNRTS-PFPTGVLTPPQSSKKQP-------------AGLKPI------------------------------   718
gi|18858511|ref|NP_571070.1|       KT---FKGIAADDMHNIQTHVPYLEWLGK-------VHSYQLVDIESSQRS-PVPTGVLTPPPSSEKPE-------------STIS--------------------------------   718
gi|24584476|ref|NP_723926.1|       GLGLICPNIVTDDSHIIQTHTTTMDMYDEVLMAQDAAHAMRARIQASPATALRAPESLLTPPASSHKPDEYLGDEGDETGARSGISSTTTCCNTAASNKGGKSSSNNSVTSCSSRSNP   718
gi|71981558|ref|NP_001021028.1|    DVIPKHESIKSDDSHNIQVYVK--------------RSSMEPIVKSERERIQHLKARRLHPQRLF-----------------------------------------------------   718
                                   .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710........
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