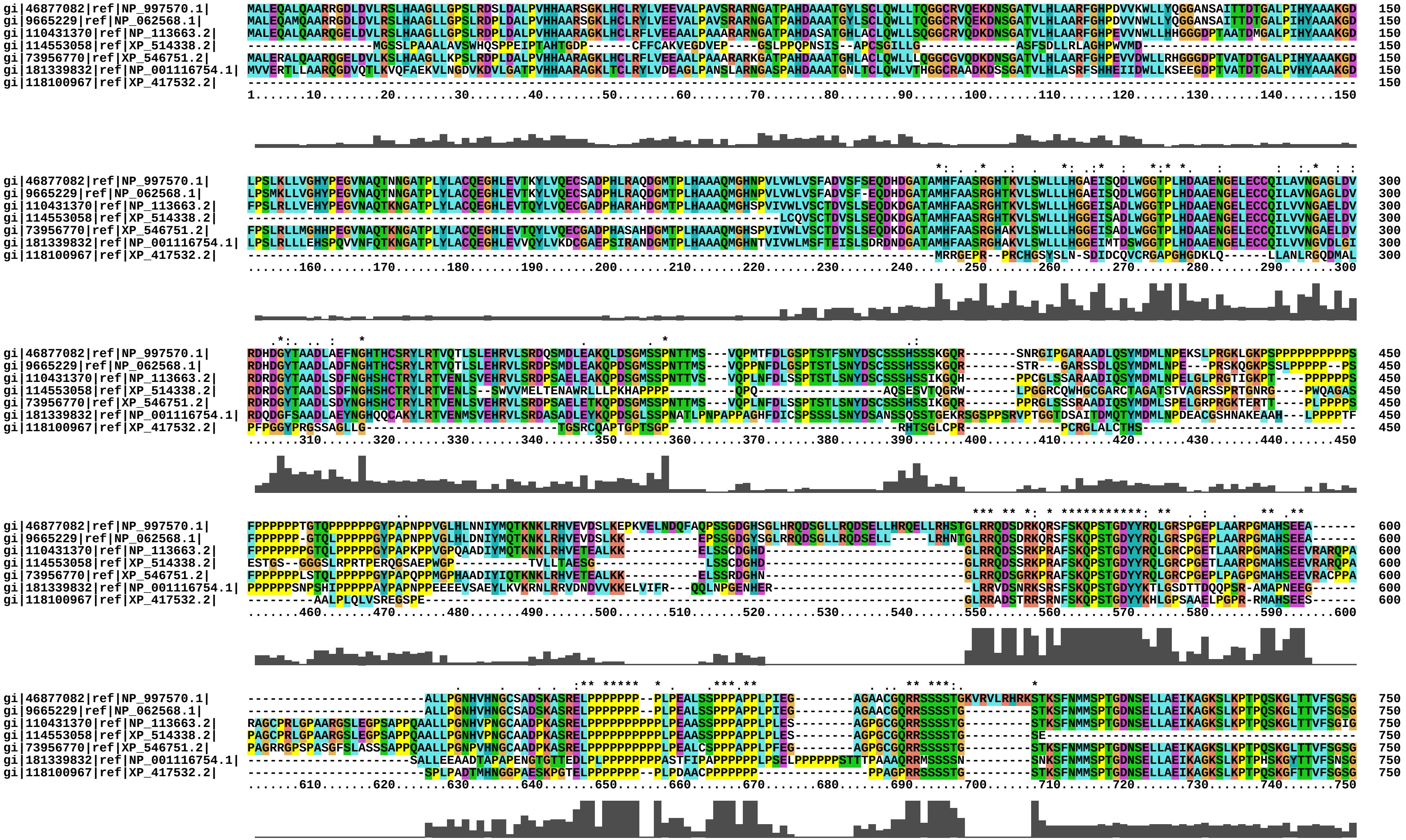

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gi|46877082|ref|NP_997570.1|      MALEQALQAARRGDLDVLRSLHAAGLLGPSLRDSLDALPVHHAARSGKLHCLRYLVEEVALPAVSRARNGATPAHDAAATGYLSCLQWLLTQGGCRVQEKDNSGATVLHLAARFGHPDVVKWLLYQGGANSAITTDTGALPIHYAAAKGD   150
gi|9665229|ref|NP_062568.1|       MALEQAMQAARRGDLDVLRSLHAAGLLGPSLRDPLDALPVHHAARSGKLHCLRYLVEEVALPAVSRARNGATPAHDAAATGYLSCLQWLLTQGGCRVQEKDNSGATVLHLAARFGHPDVVNWLLYQGGANSAITTDTGALPIHYAAAKGD   150
gi|110431370|ref|NP_113663.2|     MALEQALQAARQGELDVLRSLHAAGLLGPSLRDPLDALPVHHAARAGKLHCLRFLVEEAALPAAARARNGATPAHDASATGHLACLQWLLSQGGCRVQDKDNSGATVLHLAARFGHPEVVNWLLHHGGGDPTAATDMGALPIHYAAAKGD   150
gi|114553058|ref|XP_514338.2|     -----------------MGSSLPAAALAVSWHQSPPEIPTAHTGDP------CFFCAKVEGDVEP----GSLPPQPNSIS--APCSGILLG-------------ASFSDLLRLAGHPWVMD-----------------------------   150
gi|73956770|ref|XP_546751.2|      MALERALQAARQGELDVLKSLHAAGLLKPSLRDPLDALPVHHAARAGKLHCLRFLVEEAALPAAARARKGATPAHDAAATGHLACLQWLLLQGGCGVQDKDNSGATVLHLAARFGHPEVVDWLLRHGGGDPTVATDTGALPIHYAAAKGD   150
gi|181339832|ref|NP_001116754.1|  MVVERTLLAARQGDVQTLKVQFAEKVLNGDVKDVLGATPVHHAARAGKLTCLRYLVDEAGLPANSLARNGASPAHDAAATGNLTCLQWLVTHGGCRAADKDSSGATVLHLASRFSHHEIIDWLLKSEEGDPTVATDTGALPVHYAAAKGD   150
gi|118100967|ref|XP_417532.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                                                                                                               *: . .*  .:  .   *: .:*  :   *:* *.   :       :  :.*  : :
gi|46877082|ref|NP_997570.1|      LPSLKLLVGHYPEGVNAQTNNGATPLYLACQEGHLEVTKYLVQECSADPHLRAQDGMTPLHAAAQMGHNPVLVWLVSFADVSFSEQDHDGATAMHFAASRGHTKVLSWLLLHGAEISQDLWGGTPLHDAAENGELECCQILAVNGAGLDV   300
gi|9665229|ref|NP_062568.1|       LPSMKLLVGHYPEGVNAQTNNGATPLYLACQEGHLEVTKYLVQECSADPHLRAQDGMTPLHAAAQMGHNPVLVWLVSFADVSF-EQDHDGATAMHFAASRGHTKVLSWLLLHGAEISQDLWGGTPLHDAAENGELECCQILAVNGAGLDV   300
gi|110431370|ref|NP_113663.2|     FPSLRLLVEHYPEGVNAQTKNGATPLYLACQEGHLEVTQYLVQECGADPHARAHDGMTPLHAAAQMGHSPVIVWLVSCTDVSLSEQDKDGATAMHFAASRGHTKVLSWLLLHGGEISADLWGGTPLHDAAENGELECCQILVVNGAELDV   300
gi|114553058|ref|XP_514338.2|     ------------------------------------------------------------------------LCQVSCTDVSLSEQDKDGATAMHFAASRGHTKVLSWLLLHGGEISADLWGGTPLHDAAENGELECCQILVVNGAELDV   300
gi|73956770|ref|XP_546751.2|      FPSLRLLMGHHPEGVNAQTKNGATPLYLACQEGHLEVTQYLVQECGADPHASAHDGMTPLHAAAQMGHSPVIVWLVSCTDVSLSEQDKDGATAMHFAASRGHAKVLSWLLLHGGEISADLWGGTPLHDAAENGELECCQILVVNGAELDV   300
gi|181339832|ref|NP_001116754.1|  LPSLRLLLEHSPQVVNFQTKNGATPLYLACQEGHLEVVQYLVKDCGAEPSIRANDGMTPLHAAAQMGHNTVIVWLMSFTEISLSDRDNDGATAMHFAASRGHAKVLSWLLLHGGEIMTDSWGGTPLHDAAENGELECCQILVVNGVDLGI   300
gi|118100967|ref|XP_417532.2|     ---------------------------------------------------------------------------------------------MRRGEPR--PRCHGSYSLN-SDIDCQVCRGAPGHGDKLQ------LLANLRGQDMAL   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                     .*:. .. :   *                             .        . *                                .:
gi|46877082|ref|NP_997570.1|      RDHDGYTAADLAEFNGHTHCSRYLRTVQTLSLEHRVLSRDQSMDLEAKQLDSGMSSPNTTMS---VQPMTFDLGSPTSTFSNYDSCSSSHSSSKGQR-------SNRGIPGARAADLQSYMDMLNPEKSLPRGKLGKPSPPPPPPPPPPS   450
gi|9665229|ref|NP_062568.1|       RDHDGYTAADLADFNGHTHCSRYLRTVQTLSLEHRVLSRDPSMDLEAKQPDSGMSSPNTTMS---VQPPNFDLGSPTSTLSNYDSCSSSHSSSKGQR-------STR---GARSSDLQSYMDMLNPE---PRSKQGKPSSLPPPPP--PS   450
gi|110431370|ref|NP_113663.2|     RDRDGYTAADLSDFNGHSHCTRYLRTVENLSVEHRVLSRDPSAELEAKQPDSGMSSPNTTVS---VQPLNFDLSSPTSTLSNYDSCSSSHSSIKGQH-------PPCGLSSARAADIQSYMDMLNPELGLPRGTIGKPT----PPPPPPS   450
gi|114553058|ref|XP_514338.2|     RDRDGYTAADLSDFNGHSHCTRYLRTVENLS--SWVVMELTENAWRLLLPKHAPPPP---------QPQ-----------------AQSESVTQGRW-------LPGGRCQWHGCGARCTAGATSTVAGRSSPRTGNRG----PWQAGAS   450
gi|73956770|ref|XP_546751.2|      RDRDGYTAADLSDYNGHSHCTRYLRTVENLSVEHRVLSRDPSAELETKQPDSGMSSPNTTMS---VQPLNFDLSSPTSTLSNYDSCSSSHSSIKGQR-------PPRGLSSSRAADIQSYMDMLSPELGRPRGKTERTT----PLPPPPS   450
gi|181339832|ref|NP_001116754.1|  RDQDGFSAADLAEYNGHQQCAKYLRTVENMSVEHRVLSRDASADLEYKQPDSGLSSPNATLPNPAPPAGHFDICSPSSSLSNYDSANSSQSSTGEKRSGSPPSRVPTGGTDSAITDMQTYMDMLNPDEACGSHNAKEAAH---LPPPPTF   450
gi|118100967|ref|XP_417532.2|     PFPGGYPRGSSAGLLG--------------------------TGSRCQAPTGPTSGP-------------------------------RHTSGLCPR-------------PCRGLALCTHS-----------------------------   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                                      ..                                                                            *** ** *: * ***********: **  . :   .   ** .**
gi|46877082|ref|NP_997570.1|      FPPPPPPTGTQPPPPPPGYPAPNPPVGLHLNNIYMQTKNKLRHVEVDSLKEPKVELNDQFAQPSSGDGHSGLHRQDSGLLRQDSELLHRQELLRHSTGLRRQDSDRKQRSFSKQPSTGDYYRQLGRSPGEPLAARPGMAHSEEA------   600
gi|9665229|ref|NP_062568.1|       FPPPPPP-GTQLPPPPPGYPAPNPPVGLHLDNIYMQTKNKLRHVEVDSLKK----------EPSSGDGYSGLRRQDSGLLRQDSELL-----LRHNTGLRRQDSDRKQRSFSKQPSTGDYYRQLGRSPGEPLAARPGMAHSEEA------   600
gi|110431370|ref|NP_113663.2|     FPPPPPPPGTQLPPPPPGYPAPKPPVGPQAADIYMQTKNKLRHVETEALKK----------ELSSCDGHD---------------------------GLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLAARPGMAHSEEVRARQPA   600
gi|114553058|ref|XP_514338.2|     ESTGS--GGGSLRPRTPERQGSAEPWGP----------TVLLTAESG---------------LSSCDGHD---------------------------GLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLAARPGMAHSEEVRARQPA   600
gi|73956770|ref|XP_546751.2|      FPPPPPPLSTQLPPPPPGYPAPQPPMGPHAADIYIQTKNKLRHVETEALKK----------ELSSRDGHN---------------------------GLRRQDSGRKPRAFSKQPSTGDYYRQLGRCPGEPLPAGPGMAHSEEVRACPPA   600
gi|181339832|ref|NP_001116754.1|  PPPPPPSNPSHIPPPPPAYPAPNPPEEEEVSAEYLKVKRNLRRVDNDVVKKELVIFR---QQLNPGENHER---------------------------LRRVDSNRKSRSFSKQPSTGDYYKTLGSDTTDQQPSR-AMAPNEEG------   600
gi|118100967|ref|XP_417532.2|     ---------AALPLQLVSREGSPE-------------------------------------------------------------------------GLRRADSTRRSRNFSKQPSTGDYYKHLGPSAAELPGPR-RMAHSEES------   600
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                                                              .     .    . .  :** *****  * .    .***.**               . .. ** ***:.         *
gi|46877082|ref|NP_997570.1|      ------------------------ALLPGNHVHNGCSADSKASRELPPPPPPP--PLPEALSSPPPAPPLPIEG--------AGAACGQRRSSSSTGKVRVLRHRKSTKSFNMMSPTGDNSELLAEIKAGKSLKPTPQSKGLTTVFSGSG   750
gi|9665229|ref|NP_062568.1|       ------------------------ALLPGNHVHNGCSADSKASRELPPPPPPP--PLPEALSSPPPAPPLPIEG--------AGAACGQRRSSSSTG---------STKSFNMMSPTGDNSELLAEIKAGKSLKPTPQSKGLTTVFSGSG   750
gi|110431370|ref|NP_113663.2|     RAGCPRLGPAARGSLEGPSAPPQAALLPGNHVPNGCAADPKASRELPPPPPPPPPPLPEAASSPPPAPPLPLES--------AGPGCGQRRSSSSTG---------STKSFNMMSPTGDNSELLAEIKAGKSLKPTPQSKGLTTVFSGIG   750
gi|114553058|ref|XP_514338.2|     PAGCPRLGPAARGSLEGPSAPPQAALLPGNHVPNGCAADPKASRELPPPPPPPPPPLPEAASSPPPAPPLPLES--------AGPGCGQRRSSSSTG---------SE------------------------------------------   750
gi|73956770|ref|XP_546751.2|      PAGRRGPSPASGFSLASSSAPPQAALLPGNPVHNGCAADPKASRELPPPPPPPPPPLPEALCSPPPAPPLPFEG--------AGPGCGQRRSSSSTG---------STKSFNMMSPTGDNSELLAEIKAGKSLKPTPQSKGLTTVFSGSG   750
gi|181339832|ref|NP_001116754.1|  ----------------------SALLEEAADTAPAPENGTGTTEDLPLPPPPPPPPASTFIPAPPPPPPLPSELPPPPPPSTTTPAAAQRRMSSSSN---------SNKSFNMMSPTGDNSELLAEIKAGKSLKPTPHSKGYTTVFSNSG   750
gi|118100967|ref|XP_417532.2|     ------------------------SPLPADTMHNGGPAESKPGTELPPPPPPP--PLPDAACPPPPPPP---------------PPAGPRRSSSSTG---------STKSFNMMSPTGDNSELLAEIKAGKSLKPTPQSKGFTTVFSGSG   750
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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gi|46877082|ref|NP_997570.1|     QPASQPESP----------------QPLVSPAPSRTRSPTPPASGSQPLLNGSVVPAPPATPAPG----------VHLDVEALIPTLDEQGRPIPEWKRQVMVRKLQQKMQEEEEQRRKEEEEEARLASLPAWRRDILRKKLEEEREQKR   900
gi|9665229|ref|NP_062568.1|      QPASQPESP----------------QPAVSPGPSRARSPTPPASGPQPLLNGSIVPAPPATLAPG----------VHLDVEALIPTLDEQGRPIPEWKRQVMVRKLQQKMQEEEEQRRKEEEEEARLASLPAWRRDILRKKLEEEREQKR   900
gi|110431370|ref|NP_113663.2|    QPAFQPDSP----------------LPSVSPALSPVRSPTPPAAGFQPLLNGSLVPVPPTTPAPG----------VQLDVEALIPTHDEQGRPIPEWKRQVMVRKMQLKMQEEEEQRRKEEEEEARLASMPAWRRDLLRKKLEEEREQKR   900
gi|114553058|ref|XP_514338.2|    ------------------------------------------------------------------------------------------------------------------------------------------------------   900
gi|73956770|ref|XP_546751.2|     QPISQPDLP----------------LPQASPAPSRARSPTPPAAGPQPLLNGSVAPAPPATPAPG----------VQLDVEALIPTHDEQGRPIPEWKRQVMVRKLQLKMQEEEEQRRKEEEEEARLASMPAWRRDLLRKKLEEEREQRR   900
gi|181339832|ref|NP_001116754.1| TPGNNGESPSSPPEPLPKPNDTQSAKPESPPPACPPTPPNPTASRSSPQNLSTSQSSDQLTAAVNGNTSVVQNKTSVVDVESLVPTHDEQGRAIPEWKRQVMVRKLQVKMQEEEENKRKAEEEAARLASLPAWRRDIMKKKLEEEK----   900
gi|118100967|ref|XP_417532.2|    QAGANADSP-----------------ASSPSPTRTPTPPATPEAGGPPRCMAGGSPEPVLNGSSPVPGP---GAMAPPDVEALVPSHDEQGRPNPEWKRQVMVRKLQLRLQVGSEDHR-EKEEEARLASMPAWRRDILRKKLEEEREQKR   900
                                 .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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gi|46877082|ref|NP_997570.1|     KEEERQKLEEIQRAKEQSEKLRTLGYDEAKLAPWQRQVILKKGEIPK------   953
gi|9665229|ref|NP_062568.1|      KEEERQKLEEIQRAKEQSEKLRTLGYDEAKLAPWQRQVILKKGEIPK------   953
gi|110431370|ref|NP_113663.2|    KEEERQKQEELRREKEQSEKLRTLGYDESKLAPWQRQVILKKGDIAKY-----   953
gi|114553058|ref|XP_514338.2|    -----------------------------------------------------   953
gi|73956770|ref|XP_546751.2|     KEEERQKQEELQREKEQSEKLRTLGYDETKLAPWQRQIILKKGDIAKY-----   953
gi|181339832|ref|NP_001116754.1| KDEEQRRMEKESEEKSELERLRTLGYDETKLAPWQKQIILKKGDIAKQ-----   953
gi|118100967|ref|XP_417532.2|    KEQEKQKREEEEKEKEQSEKLRTLGYDETKLVLNTYFTTSMYLSVSCSQLVCP   953
                                 .......910.......920.......930.......940.......950...
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