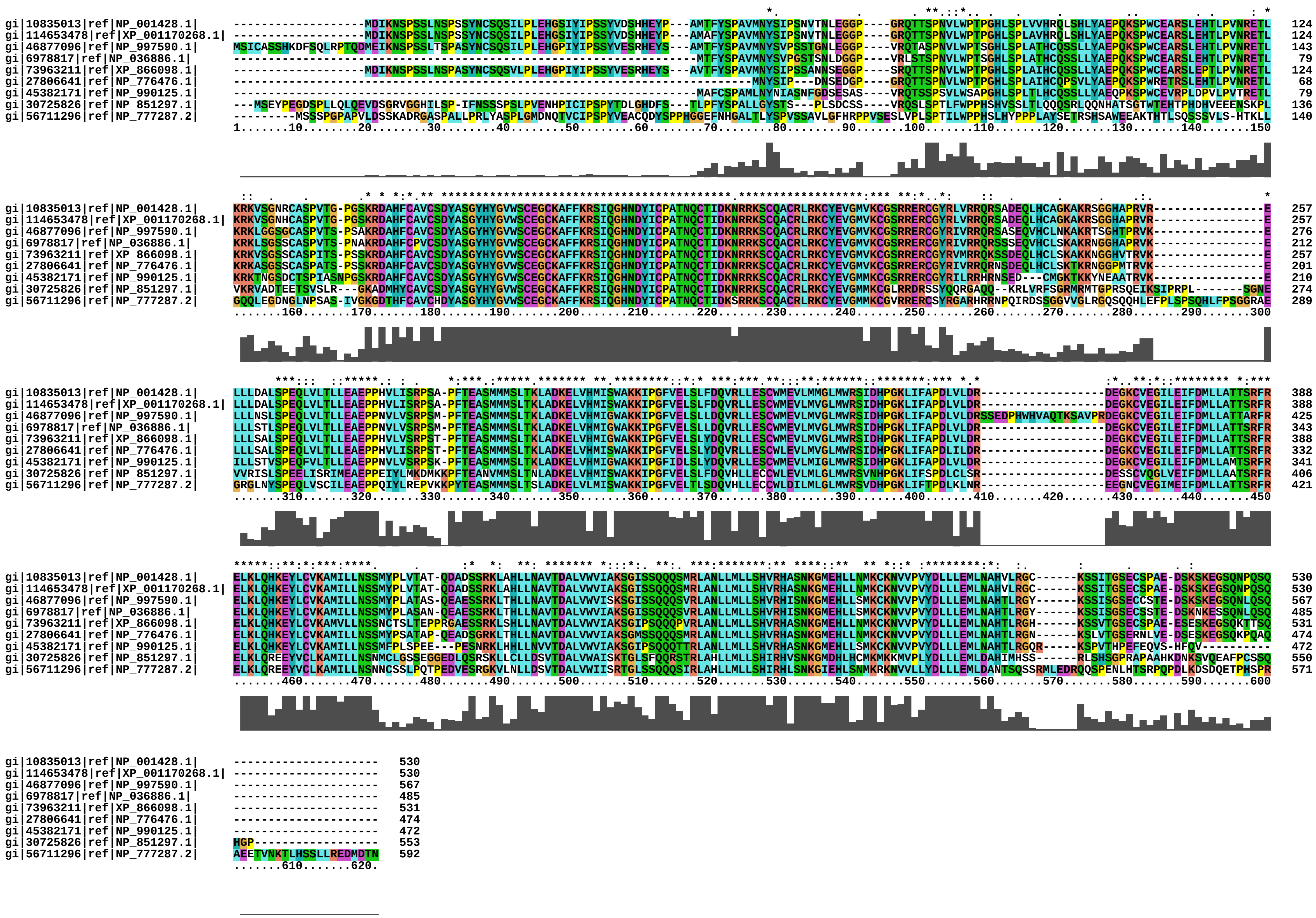

```
                                                                                                                 *.           .       . **.::*.. .   .     .         ..        . .     : *
gi|10835013|ref|NP_001428.1|        -------------------MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYP---AMTFYSPAVMNYSIPSNVTNLEGGP----GRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETL   124
gi|114653478|ref|XP_001170268.1|    -------------------MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYP---AMAFYSPAVMNYSIPSNVTNLEGGP----GRQTTSPNVLWPTPGHLSPLAVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETL   124
gi|46877096|ref|NP_997590.1|        MSICASSHKDFSQLRPTQDMEIKNSPSSLTSPASYNCSQSILPLEHGPIYIPSSYVESRHEYS---AMTFYSPAVMNYSVPSSTGNLEGGP----VRQTASPNVLWPTSGHLSPLATHCQSSLLYAEPQKSPWCEARSLEHTLPVNRETL   143
gi|6978817|ref|NP_036886.1|         -------------------------------------------------------------------MTFYSPAVMNYSVPGSTSNLDGGP----VRLSTSPNVLWPTSGHLSPLATHCQSSLLYAEPQKSPWCEARSLEHTLPVNRETL    79
gi|73963211|ref|XP_866098.1|        -------------------MDIKNSPSSLNSPASYNCSQSVLPLEHGPIYIPSSYVESRHEYS---AVTFYSPAVMNYSIPSSANNSEGGP----SRQTTSPNVLWPTPGHLSPLAIHCQSSLLYAEPQKSPWCEARSLEPTLPVNRETL   124
gi|27806641|ref|NP_776476.1|        ---------------------------------------------------------------------------MNYSIP---DNSEDGP----GRQTTSPNVLWPTPGHLSPLAIHCQPSVLYAEPQKSPWRETRSLEHTLPVNRETL    68
gi|45382171|ref|NP_990125.1|        -------------------------------------------------------------------MAFCSPAMLNYNIASNFGDSESAS----VRQTSSPSVLWSAPGHLSPLTLHCQSSLLYAEQPKSPWCEVRPLDPVLPVTRETL    79
gi|30725826|ref|NP_851297.1|        ---MSEYPEGDSPLLQLQEVDSGRVGGHILSP-IFNSSSPSLPVENHPICIPSPYTDLGHDFS---TLPFYSPALLGYSTS---PLSDCSS----VRQSLSPTLFWPPHSHVSSLTLQQQSRLQQNHATSGTWTEHTPHDHVEEENSKPL   136
gi|56711296|ref|NP_777287.2|        ---------MSSSPGPAPVLDSSKADRGASPALLPRLYASPLGMDNQTVCIPSPYVEACQDYSPPHGGEFNHGALTLYSPVSSAVLGFHRPPVSESLVPLSPTILWPPHSLHYPPPLAYSETRSHSAWEEAKTHTLSQSSSVLS-HTKLL   140
                                    1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                     ::  .    .       .* * *:*.** ******************************************.******************:*** **:*..*:    ::  .      .     .    .:.                *
gi|10835013|ref|NP_001428.1|        KRKVSGNRCASPVTG-PGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVR----------------E   257
gi|114653478|ref|XP_001170268.1|    KRKVSGNHCASPVTG-PGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVR----------------E   257
gi|46877096|ref|NP_997590.1|        KRKLGGSGCASPVTS-PSAKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRIVRRQRSASEQVHCLNKAKRTSGHTPRVK----------------E   276
gi|6978817|ref|NP_036886.1|         KRKLSGSSCASPVTS-PNAKRDAHFCPVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRIVRRQRSSSEQVHCLSKAKRNGGHAPRVK----------------E   212
gi|73963211|ref|XP_866098.1|        KRKVSGSSCASPITS-PSSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRVMRRQKSSDEQLHCLSKAKKNGGHVTRVK----------------E   257
gi|27806641|ref|NP_776476.1|        KRKASGSSCASPATS-PSSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRIVRRQRNSDEQLHCLSKTKRNGGPMTRVK----------------E   201
gi|45382171|ref|NP_990125.1|        KRKTNGSDCTSPIASNPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMMKCGSRRERCGYRILRRHRNSED---CMGKTKKYNEAATRVK----------------E   210
gi|30725826|ref|NP_851297.1|        VKRVADTEETSVSLR---GKADMHYCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMMKCGLRRDRSSYQQRGAQQ--KRLVRFSGRMRMTGPRSQEIKSIPRPL-------SGNE   274
gi|56711296|ref|NP_777287.2|        GQQLEGDNGLNPSAS-IVGKGDTHFCAVCHDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKSRRKSCQACRLRKCYEVGMMKCGVRRERCSYRGARHRRNPQIRDSSGGVVGLRGQSQQHLEFPLSPSQHLFPSGGRAE   289
                                    .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                          ***:::  ::*****.: : .    *:***.:*****.******* **.********::*:* ***:***.**:::**:******::*******:*** *.*                  :*..**:*::******** *:***
gi|10835013|ref|NP_001428.1|        LLLDALSPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDR------------------DEGKCVEGILEIFDMLLATTSRFR   388
gi|114653478|ref|XP_001170268.1|    LLLDALSPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDR------------------DEGKCVEGILEIFDMLLATTSRFR   388
gi|46877096|ref|NP_997590.1|        LLLNSLSPEQLVLTLLEAEPPNVLVSRPSM-PFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRSSEDPHWHVAQTKSAVPRDEGKCVEGILEIFDMLLATTARFR   425
gi|6978817|ref|NP_036886.1|         LLLSTLSPEQLVLTLLEAEPPNVLVSRPSM-PFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDR------------------DEGKCVEGILEIFDMLLATTSRFR   343
gi|73963211|ref|XP_866098.1|        LLLSALSPEQLVLTLLEAEPPHVLVSRPST-PFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLYDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDR------------------DEGKCVEGILEIFDMLLATTSRFR   388
gi|27806641|ref|NP_776476.1|        LLLSALSPEQLVLTLLEAEPPHVLISRPST-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLYDQVRLLESCWLEVLMVGLMWRSIDHPGKLIFAPDLILDR------------------DEGKCVEGILEIFDMLLATTSRFR   332
gi|45382171|ref|NP_990125.1|        ILLSTVSPEQFVLTLLEAEPPNVLVSRPSK-PFTEASMMMSLTKLADKELVHMIGWAKKIPGFIDLSLYDQVRLLESCWMEVLMIGLMWRSIDHPGKLIFAPDLVLDR------------------DEGKCVEGILEIFDMLLAMTSRFR   341
gi|30725826|ref|NP_851297.1|        VVRISLSPEELISRIMEAEPPEIYLMKDMKKPFTEANVMMSLTNLADKELVHMISWAKKIPGFVELSLFDQVHLLECCWLEVLMLGLMWRSVNHPGKLIFSPDLCLSR------------------DESSCVQGLVEIFDMLLAATSRFR   406
gi|56711296|ref|NP_777287.2|        GRGLNYSPEQLVSCILEAEPPQIYLREPVKKPYTEASMMMSLTSLADKELVLMISWAKKIPGFVELTLSDQVHLLECCWLDILMLGLMWRSVDHPGKLIFTPDLKLNR------------------EEGNCVEGIMEIFDMLLATTSRFR   421
                                    .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                    *****::**:*:***:****.     .      :*  *:  **: ******* *:::*:. **:. ***:*******:** ****::**  ** *::* :********:*:  :.       :      .      . :
gi|10835013|ref|NP_001428.1|        ELKLQHKEYLCVKAMILLNSSMYPLVTAT-QDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRGC------KSSITGSECSPAE-DSKSKEGSQNPQSQ   530
gi|114653478|ref|XP_001170268.1|    ELKLQHKEYLCVKAMILLNSSMYPLVTAT-QDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRGC------KSSITGSECSPAE-DSKSKEGSQNPQSQ   530
gi|46877096|ref|NP_997590.1|        ELKLQHKEYLCVKAMILLNSSMYPLATAS-QEAESSRKLTHLLNAVTDALVWVISKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEMLNAHTLRGY------KSSISGSECCSTE-DSKSKEGSQNLQSQ   567
gi|6978817|ref|NP_036886.1|         ELKLQHKEYLCVKAMILLNSSMYPLASAN-QEAESSRKLTHLLNAVTDALVWVIAKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEMLNAHTLRGY------KSSISGSECSSTE-DSKNKESSQNLQSQ   485
gi|73963211|ref|XP_866098.1|        ELKLQHKEYLCVKAMVLLNSSNCTSLTEPPRGAESSRKLSHLLNAVTDALVWVIAKSGIPSQQQPVRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHTLRGH------KSSVTGSECSPAE-ESESKEGSQKTTSQ   531
gi|27806641|ref|NP_776476.1|        ELKLQHKEYLCVKAMILLNSSMYPSATAP-QEADSGRKLTHLLNAVTDALVWVIAKSGMSSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHTLRGN------KSLVTGSERNLVE-DSESKEGSQKPQAQ   474
gi|45382171|ref|NP_990125.1|        ELKLQHKEYLCVKAMILLNSSMFPLSPEE---PESNRKLHHLLNVVTDALVWVIAKSGIPSQQQTTRLANLLMLLSHVRHASNKGMEHLLSMKCKNVVPVYDLLLEMLNAHTLRGQR-----KSPVTHPEFEQVS-HFQV----------   472
gi|30725826|ref|NP_851297.1|        ELKLQREEYVCLKAMILLNSNMCLGSSEGGEDLQSRSKLLCLLDSVTDALVWAISKTGLSFQQRSTRLAHLLMLLSHIRHVSNKGMDHLHCMKMKKMVPLYDLLLEMLDAHIMHSS------RLSHSGPRAPAAHKDNKSVQEAFPCSSQ   550
gi|56711296|ref|NP_777287.2|        ELKLQREEYVCLKAMILLNSNNCSSLPQTPEDVESRGKVLNLLDSVTDALVWIISRTGLSSQQQSIRLAHLLMLLSHIRHLSNKGIEHLSNMKRKNVVLLYDLLLEMLDANTSQSSRMLEDRQQSPENLHTSRPQPDLKDSDQETPHSPR   571
                                    .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

gi|10835013|ref|NP_001428.1|        --------------------   530
gi|114653478|ref|XP_001170268.1|    --------------------   530
gi|46877096|ref|NP_997590.1|        --------------------   567
gi|6978817|ref|NP_036886.1|         --------------------   485
gi|73963211|ref|XP_866098.1|        --------------------   531
gi|27806641|ref|NP_776476.1|        --------------------   474
gi|45382171|ref|NP_990125.1|        --------------------   472
gi|30725826|ref|NP_851297.1|        HGP-----------------   553
gi|56711296|ref|NP_777287.2|        AEETVNKTLHSSLLREDMTN   592
                                    .......610.......620.
```