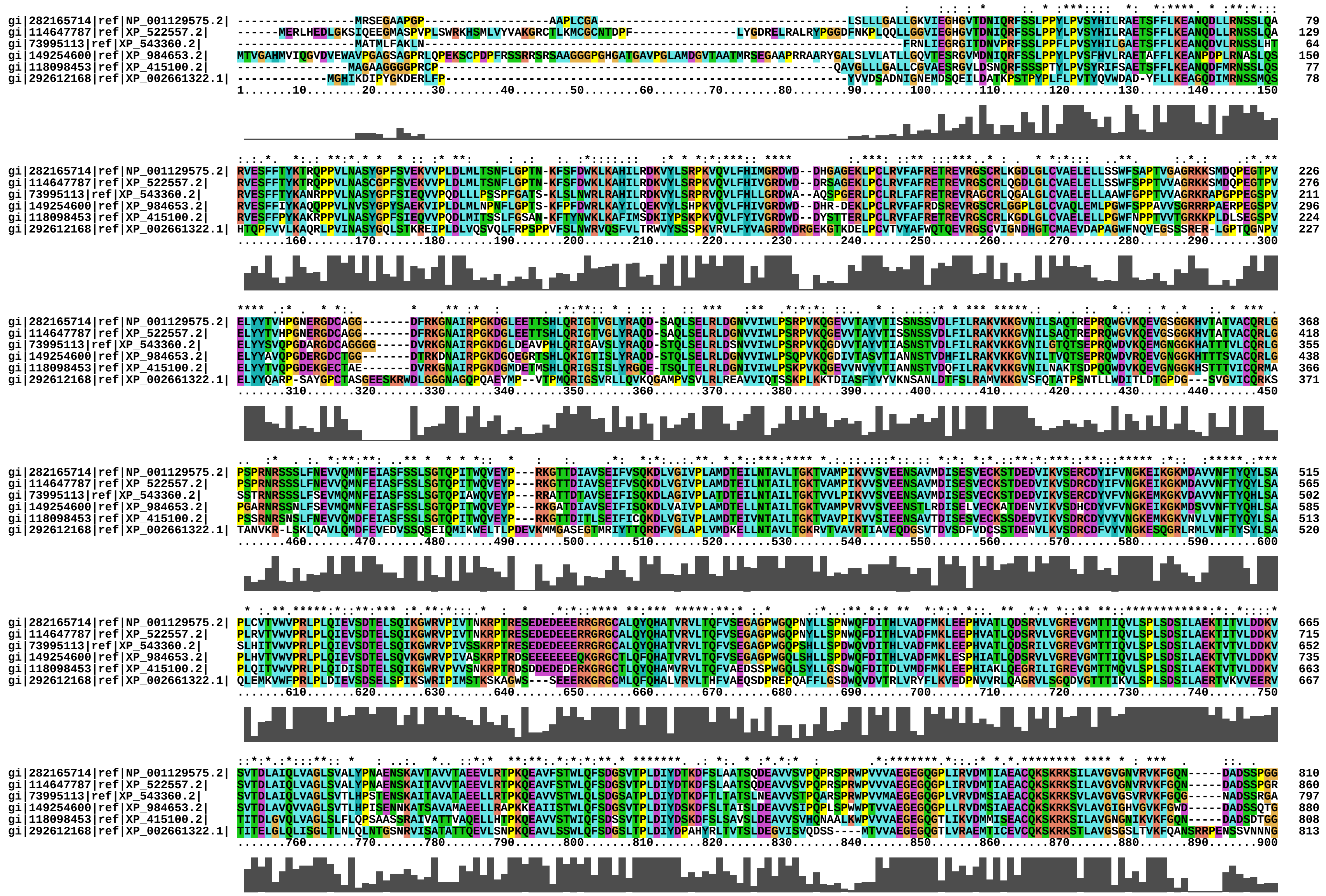
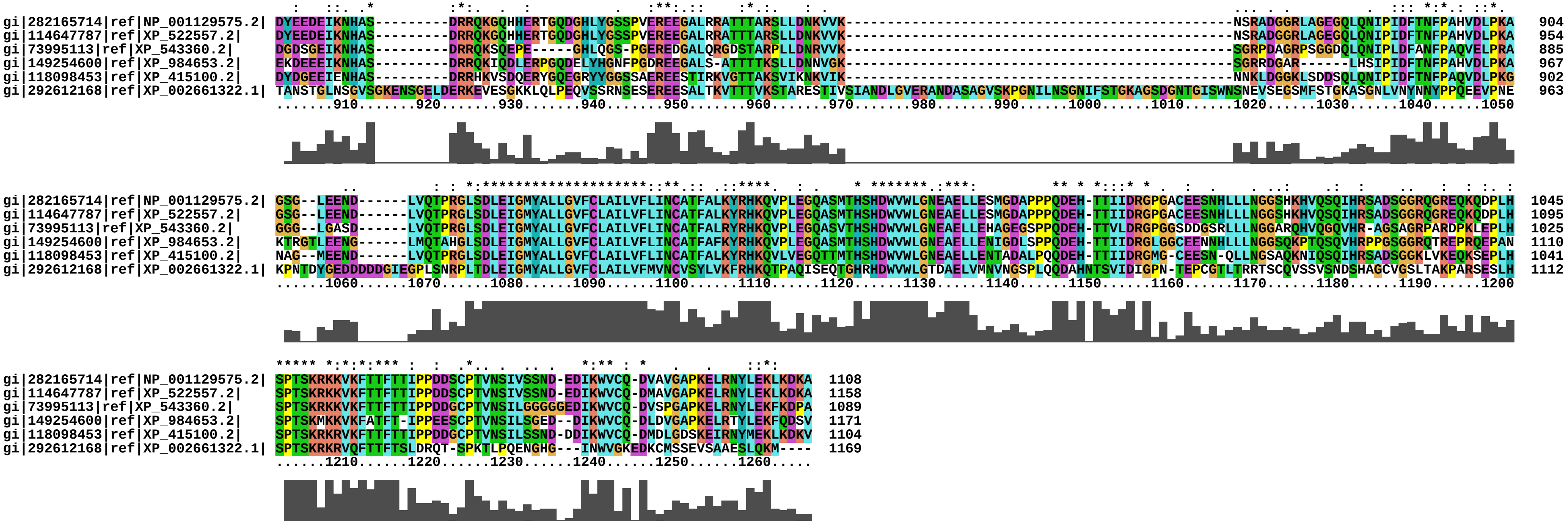


```
                                                                                                                                  :    :.: : *     :. * :***::::  *:  *:****. * :**:*:::
gi|282165714|ref|NP_001129575.2|  -----------------MRSEGAAPGP------------------AAPLCGA------------------------------------LSLLLGALLGKVIEGHGVTDNIQRFSSLPPYLPVSYHILRAETSFFLKEANQDLLRNSSLQA     79
gi|114647787|ref|XP_522557.2|     ------MERLHEDLGKSIQEEGMASPVPLSWRKHSMLVYVAKGRCTLKMCGCNTDPF---------------LYGDRELRALRYPGGDFNKPLQQLLGGVIEGHGVTDNIQRFSSLPPYLPVSYHILRAETSFFLKEANQDLLRNSSLQA    129
gi|73995113|ref|XP_543360.2|      -----------------MATMLFAKLN---------------------------------------------------------------------FRNLIEGRGITDNVPRFSSLPPFLPVSYHILGAETSFFLKEANQDVLRNSSLHT     64
gi|149254600|ref|XP_984653.2|     MTVGAHMVIQGVDVEWAVPGAGSAGPRLQPEKSCPDPFRSSRRSRSAAGGGPGHGATGAVPGLAMDGVTAATMRSEGAAPRRAARYGALSLVLATLLGQVTESRGVMDNIQRFSSLPPYLPVSFHVLRAETAFFLKEANPDPLRNASLQS    150
gi|118098453|ref|XP_415100.2|     ----------------MAGAAGGGGPRCP---------------------------------------------------------QAVGLLLGALLCGVAESRGVLDSNQRFSSSPTYLPVSYRIFSAETSFFLKEANQDFMRNSSLQS     77
gi|292612168|ref|XP_002661322.1|  -------------MGHIKDIPYGKDERLFP----------------------------------------------------------YVVDSADNIGNEMDSQEILDATKPSTPYPLFLPVTYQVWDAD-YFLLKEAGQDIMRNSSMQS     78
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                  :.:.*.  *:.: **:*.* *  * :: :* **:   . : .:   :. :*::::.::   :* * *:*:***:: ****        :.***: ::** :::***..* : .  * *:*:::  ..**.     :.*.:    :*. **
gi|282165714|ref|NP_001129575.2|  RVESFFTYKTRQPPVLNASYGPFSVEKVVPLDLMLTSNFLGPTN-KFSFDWKLKAHILRDKVYLSRPKVQVLFHIMGRDWD--DHGAGEKLPCLRVFAFRETREVRGSCRLKGDLGLCVAELELLSSWFSAPTVGAGRKKSMDQPEGTPV    226
gi|114647787|ref|XP_522557.2|     RVESFFTYKTRQPPVLNASCGPFSVEKVVPLDLMLTSNFLGPTN-KFSFDWKLKAHILRDKVYLSRPKVQVLFHIVGRDWD--DRSAGEKLPCLRVFAFRETREVRGSCRLQGDLGLCVAELELLSSWFSPPTVVAGRKKSMDQPEGTPV    276
gi|73995113|ref|XP_543360.2|      RVESFFTYKANRPPVLNASYGPFSIEQVVPQDLLLPSSPFGATS-KLSLNWRLRAHILRDKVYLSRPRVQVLFHLLGRDWA--AQSPGERLPCLRLFAFRETREVRAGCRLQGALGLCVAELELLAAWFGPPTVVAGRKRAPGPPEGSPV    211
gi|149254600|ref|XP_984653.2|     RVESFFIYKAQQPPVLNVSYGPYSAEKVIPLDLMLNPNFLGPTS-KFPFDWRLKAYILQEKVYLSHPKVQVLFHIVGRDWD--DHR-DEKLPCLRVFAFRDSREVRGSCRLGGPLGLCVAQLEMLPGWFSPPAVVSGRRRPAERPEGSPV    296
gi|118098453|ref|XP_415100.2|     RVESFFPYKAKRPPVLNASYGPFSIEQVVPQDLMITSSLFGSAN-KFTYNWKLKAFIMSDKIYPSKPKVQVLFYIVGRDWD--DYSTTERLPCLRVFAFRETREVRGSCRLKGDLGLCVAELELLPGWFNPPTVVTGRKKPLDLSEGSPV    224
gi|292612168|ref|XP_002661322.1|  HTQPFVVLKAQRLPVINASYGQLSTKREIPLDLVQSVQLFRPSPPVFSLNWRVQSFVLTRWVYSSSPKVRVLFYVAGRDWDRGEKGTKDELPCVTVYAFWQTQEVRGSCVIGNDHGTCMAEVDAPAGWFNQVEGSSSRER-LGPTQGNPV    227
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                  **** .:* .  * *:.        *   .** :*  :      . :*:**:: * : :: :  :: ***   :**  .*:*:*: ::..  * : ..:.:* * *** *****.:  . . :.  *.:  : * .*   :. * *** .
gi|282165714|ref|NP_001129575.2|  ELYYTVHPGNERGDCAGG-------DFRKGNAIRPGKDGLEETTSHLQRIGTVGLYRAQD-SAQLSELRLDGNVVIWLPSRPVKQGEVVTAYVTISSNSSVDLFILRAKVKKGVNILSAQTREPRQWGVKQEVGSGGKHVTATVACQRLG    368
gi|114647787|ref|XP_522557.2|     ELYYTVHPGNERGDCAGG-------DFRKGNAIRPGKDGLEETTSHLQRIGTVGLYRAQD-SAQLSELRLDGNVVIWLPSRPVKQGEVVTAYVTISSNSSVDLFILRAKVKKGVNILSAQTREPRQWGVKQEVGSGGKHVTATVACQRLG    418
gi|73995113|ref|XP_543360.2|      ELYYSVQPGDARGDCAGGGG-----DVRKGNAIRPGKDGLDEAVPHLQRIGAVSLYRAQD-STQLSELRLDSNVVIWLPSRPVKQGDVVTAYVTIASNSTVDLFILRAKVKKGVNILGTQTSEPRQWDVKQEMGNGGKHATTTVLCQRLG    355
gi|149254600|ref|XP_984653.2|     ELYYAVQPGDERGDCTGG-------DTRKDNAIRPGKDGQEGRTSHLQKIGTISLYRAQD-STQLSELRLDGNVVIWLPSQPVKQGDIVTASVTIANNSTVDHFILRAKVKKGVNILTVQTSEPRQWDVRQEVGNGGKHTTTSVACQRLG    438
gi|118098453|ref|XP_415100.2|     ELYYTVQPGDEKGECTAE-------DVRKGNAIRPGKDGMDETMSHLQRIGSISLYRGQE-TSQLTELRLDGNIVIWLPSKPVKQGEVVNVYVTIANNSTVDQFILRAKVKKGVNILNAKTSDPQQWDVKQEVGNGGKHSTTTVICQRMA    366
gi|292612168|ref|XP_002661322.1|  ELYYQARP-SAYGPCTASGEESKRWDLGGGNAGQPQAEYMP--VTPMQRIGSVRLLQVKQGAMPVSVLRLREAVVIQTSSKPLKKTDIASFYVYVKNSANLDTFSLRAMVKKGVSFQTATPSNTLLWDITLDTGPDG---SVGVICQRKS    371
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                  ..  :*  . :. *:**:**: ..** *  * * *::  *   :   :.    .*:  *:*:..:.**. *.*::***:**** *.:.::.:::*::.:: *:*: *:*.::**:*:***::**:::***** :*::  :*****.:***
gi|282165714|ref|NP_001129575.2|  PSPRNRSSSLFNEVVQMNFEIASFSSLSGTQPITWQVEYP---RKGTTDIAVSEIFVSQKDLVGIVPLAMDTEILNTAVLTGKTVAMPIKVVSVEENSAVMDISESVECKSTDEDVIKVSERCDYIFVNGKEIKGKMDAVVNFTYQYLSA    515
gi|114647787|ref|XP_522557.2|     PSPRNRSSSLFNEVVQMNFEIASFSSLSGTQPITWQVEYP---RKGTTDIAVSEIFVSQKDLVGIVPLAMDTEILNTAILTGKTVAMPIKVVSVEENSAVMDISESVECKSTDEDVIKVSDRCDYIFVNGKEIKGKMDAVVNFTYQYLSA    565
gi|73995113|ref|XP_543360.2|      SSTRNRSSSLFSEVMQMNFEIASFSSLSGTQPIAWQVEYP---RRATTDTAVSEIFISQKDLAGIVPLATDTEILNTAILTGKTVVLPIKVVSVEENSAVMDISESVECKSTDEDVIKVSERCDYVFVNGKEMKGKVDAVVNFTYQHLSA    502
gi|149254600|ref|XP_984653.2|     PGARNRSSNLFSEVMQMNFEIASFSSLSGTQPITWQVEYP---RKGATDIAVSEIFISQKDLVAIVPLAMDTELLNTAILTGKTVAMPVRVVSVEENSTLRDISELVECKATDENVIKVSDHCDYVFVNGKEIKGKMDSVVNFTYQHLSA    585
gi|118098453|ref|XP_415100.2|     PSSRNRSNSLFNEVVQMDFEIASFSSLSGTQPITWQVEYP---RKGTTDITLSEIFICQKDLVGIVPLAMDTEIVNTAILTGKTVAVPIKVVSIEENSAVTDISESVECKSSDEDVIKVSDRCDYVYVNGKEMKGKVNVLVNFTYQYLSA    513
gi|292612168|ref|XP_002661322.1|  TANVKR-LSKLQAVLQMDFEVEDVSSQSEIQMIKWELTLPDEVKMMGASEGTMRIYTTQRDFVGLAPLVMDKELLNTAVLTGKRVTVAVRTIAVEQDGSVTDVSDFVDCSSTDENVLKVSDRCDFVYVNGKESQGRLRMLVNFTYSYLSA    520
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                                   * :.**.*****:*::**:*** :*.**:*:::.*  :  *   .*:*::**** **:*** *****:**:* :.*     .:*..:**.*:* **  *:*:*.*::. ** .*:* *::** **::************:*:.*::::*
gi|282165714|ref|NP_001129575.2|  PLCVTVWVPRLPLQIEVSDTELSQIKGWRVPIVTNKRPTRESEDEDEEERRGRGCALQYQHATVRVLTQFVSEGAGPWGQPNYLLSPNWQFDITHLVADFMKLEEPHVATLQDSRVLVGREVGMTTIQVLSPLSDSILAEKTITVLDDKV    665
gi|114647787|ref|XP_522557.2|     PLRVTVWVPRLPLQIEVSDTELSQIKGWRVPIVTNKRPTRESEDEDEEERRGRGCALQYQHATVRVLTQFVSEGAGPWGQPNYLLSPNWQFDITHLVADFMKLEEPHVATLQDSRVLVGREVGMTTIQVLSPLSDSILAEKTITVLDDKV    715
gi|73995113|ref|XP_543360.2|      SLHITVWVPRLPLQIEVSDTELSQIKGWRVPIVSSKRPTRESEDEDEEERRGRGCALQYQHATVRVLTQFVSEGAGPWGQPSHLLSPDWQVDITHLVADFMKLEEPHVATLQDSRILVGREVGMTTIQVLSPLSDSILAEKTVTVLDDKV    652
gi|149254600|ref|XP_984653.2|     PLHVTVWVPRLPLQIEVSDTELSQVKGWRVPIVASKRPTRDSEEEEEEEQKGRGCTLQFQHATVRVLTQFVSEGAGPWGQLSHLLSPDWQFDITHLVADFMKLESPHIATLQDSRVLVGREVGMTTIQVLSPLSDSILAEKTVTVLDDKV    735
gi|118098453|ref|XP_415100.2|     PLQITVWVPRLPLQIDISDTELSQIKGWRVPVVSNKRPTRDSDDEDEDERKGRGCTLQYQHAMVRVLTQFVAEDSSPWGQLSYLLGSDWQFDITDLVMDFMKLEEPHIAKLQEGRILIGREVGMTTMQVLSPLSDSILAEKTVTVLDDKV    663
gi|292612168|ref|XP_002661322.1|  QLEMKVWFPRLPLDIEVSDSELSPIKSWRIPIMSTKSKAGWS---SEEERKGRGCMLQFQHALVRVLTHFVAEQSDPREPQAFFLGSDWQVDVTRLVRYFLKVEDPNVVRLQAGRVLSGQDVGTTTIKVLSPLSDSILAERTVKVVEERV    667
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

                                  ::*:*.:*:::**:: *   : ..:.  *.. ::*:*  **:**:.*:*:*:**.* *******. .: *:. * :*.*:*  :       .*:*******.*::.:* *.*.******** **** * : ***  .     ::. .
gi|282165714|ref|NP_001129575.2|  SVTDLAIQLVAGLSVALYPNAENSKAVTAVVTAEEVLRTPKQEAVFSTWLQFSDGSVTPLDIYDTKDFSLAATSQDEAVVSVPQPRSPRWPVVVAEGEGQGPLIRVDMTIAEACQKSKRKSILAVGVGNVRVKFGQN-----DADSSPGG    810
gi|114647787|ref|XP_522557.2|     SVTDLAIQLVAGLSVALYPNAENSKAITAVVTAEEVLRTPKQEAVFSTWLQFSDGSVTPLDIYDTKDFSLAATSQDEAVVSVPQPRSPRWPVVVAEGEGQGPLIRVDMTIAEACQKSKRKSILAVGVGNVRVKFGQN-----DADSSPGR    860
gi|73995113|ref|XP_543360.2|      SVTDLAIQLVAGLSVTLHPSTENSKAITAVATAEELLRTPKQEAVVSTWLQLSDGSATPLDIYDTKDFTLTATSLNEAVVSTPQARSPRWPVVMAEGEGQGPLVRVDMSIAEACQKSKRKSVLAVGVGSVRVKFGQG-----NADSSRGA    797
gi|149254600|ref|XP_984653.2|     SVTDLAVQVVAGLSVTLHPISENNKATSAVAMAEELLRAPKKEAIISTWLQFSDGSVTPLDIYDSKDFSLTAISLDEAVVSIPQPLSPWWPTVVAEGEGQGPLLRVDMSIAEACQKSKRKSVLAVGIGHVGVKFGWD-----DADSSQTG    880
gi|118098453|ref|XP_415100.2|     TITDLGVQLVAGLSLFLQPSAASSRAIVATTVAQELLHTPKQEAVVSTWIQFSDSSVTPLDIYDSKDFSLSAVSLDEAVVSVHQNAALKWPVVVAEGEGQGTLIKVDMMISEACQKSKRKSILAVGNGNIKVKFGQN-----DADSDTGG    808
gi|292612168|ref|XP_002661322.1|  TITELGLQLISGLTLNLQLNTGSNRVISATATTQEVLSNPKQEAVLSSWLQFSDGSLTPLDIYDPAHYRLTVTSLDEGVISVQDSS----MTVVAEGEGQGTLVRAEMTICEVCQKSKRKSTLAVGSGSLTVKFQANSRRPENSSVNNNG    813
                                  .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
```



```
                                   :   ::. .*         :*:.  .  :          .   :**:.::    :*.:.   : .                                                 ... . .         .  ::: *:*.: ::*.
gi|282165714|ref|NP_001129575.2| DYEEDEIKNHAS---------DRRQKGQHHERTGQDGHLYGSSPVEREEGALRRATTTARSLLDNKVVK-----------------------------------------------NSRADGGRLAGEGQLQNIPIDFTNFPAHVDLPKA   904
gi|114647787|ref|XP_522557.2|    DYEEDEIKNHAS---------DRRQKGQHHERTGQDGHLYGSSPVEREEGALRRATTTARSLLDNKVVK-----------------------------------------------NSRADGGRLAGEGQLQNIPIDFTNFPAHVDLPKA   954
gi|73995113|ref|XP_543360.2|     DGDSGEIKNHAS---------DRRQKSQEPE-----GHLQGS-PGEREDGALQRGDSTARPLLDNRVVK-----------------------------------------------SGRPDAGRPSGGDQLQNIPLDFANFPAQVELPRA   885
gi|149254600|ref|XP_984653.2|    EKDEEEIKNHAS---------DRRQKIQDLERPGQDELYHGNFPGDREEGALS-ATTTTKSLLDNNVGK-----------------------------------------------SGRRDGAR------LHSIPIDFTNFPAHVDLPKA   967
gi|118098453|ref|XP_415100.2|    DYDGEEIENHAS---------DRRHKVSDQERYGQEGRYYGGSSAEREESTIRKVGTTAKSVIKNKVIK-----------------------------------------------NNKLDGGKLSDDSQLQNIPIDFTNFPAQVDLPKG   902
gi|292612168|ref|XP_002661322.1| TANSTGLNSGVSGKENSGELDERKEVESGKKLQLPEQVSSRNSESEREESALTKVTTTVKSTARESTIVSIANDLGVERANDASAGVSKPGNILNSGNIFSTGKAGSDGNTGISWNSNEVSEGSMFSTGKASGNLVNYNNYPPQEEVPNE   963
                                 .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050

                                         ..         : : *:********************::**.:: .::****.  : .    * *******.:***:         ** * *:::* * .  :  .    . ..:    .:  :    ..   :  : :. :
gi|282165714|ref|NP_001129575.2| GSG--LEEND------LVQTPRGLSDLEIGMYALLGVFCLAILVFLINCATFALKYRHKQVPLEGQASMTHSHDWVWLGNEAELLESMGDAPPPQDEH-TTIIDRGPGACEESNHLLLNGGSHKHVQSQIHRSADSGGRQGREQKQDPLH  1045
gi|114647787|ref|XP_522557.2|    GSG--LEEND------LVQTPRGLSDLEIGMYALLGVFCLAILVFLINCATFALKYRHKQVPLEGQASMTHSHDWVWLGNEAELLESMGDAPPPQDEH-TTIIDRGPGACEESNHLLLNGGSHKHVQSQIHRSADSGGRQGREQKQDPLH  1095
gi|73995113|ref|XP_543360.2|     GGG--LGASD------LVQTPRGLSDLEIGMYALLGVFCLAILVFLINCATFALRYRHKQVPLEGQASVTHSHDWVWLGNEAELLEHAGEGSPPQDEH-TTVLDRGPGGSDDGSRLLLNGGARQHVQGQVHR-AGSAGRPARDPKLEPLH  1025
gi|149254600|ref|XP_984653.2|    KTRGTLEENG------LMQTAHGLSDLEIGMYALLGVFCLAILVFLINCATFAFKYRHKQVPLEGQASMTHSHDWVWLGNEAELLENIGDLSPPQDEH-TTIIDRGLGGCEENNHLLLNGGSQKPTQSQVHRPPGSGGRQTREPRQEPAN  1110
gi|118098453|ref|XP_415100.2|    NAG--MEEND------LVQTPRGLSDLEIGMYALLGVFCLAILVFLINCATFALKYRHKQVLVEGQTTMTHSHDWVWLGNEAELLENTADALPQQDEH-TTIIDRGMG-CEESN-QLLNGSAQKNIQSQIHRSADSGGKLVKEQKSEPLH  1041
gi|292612168|ref|XP_002661322.1| KPNTDYGEDDDDDGIEGPLSNRPLTDLEIGMYALLGVFCLAILVFMVNCVSYLVKFRHKQTPAQISEQTGHRHDWVWLGTDAELVMNVNGSPLQQDAHNTSVIDIGPN-TEPCGTLTRRTSCQVSSVSNDSHAGCVGSLTAKPARSESLH  1112
                                 ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200

                                 ***** *:*:*:*** :  :  .*.. .  .. .   *:** : *   .   .    ::*:
gi|282165714|ref|NP_001129575.2| SPTSKRKKVKFTTFTTIPPDDSCPTVNSIVSSND-EDIKWVCQ-DVAVGAPKELRNYLEKLKDKA  1108
gi|114647787|ref|XP_522557.2|    SPTSKRKKVKFTTFTTIPPDDSCPTVNSIVSSND-EDIKWVCQ-DMAVGAPKELRNYLEKLKDKA  1158
gi|73995113|ref|XP_543360.2|     SPTSKRKKVKFTTFTTIPPDDGCPTVNSILGGGGGEDIKWVCQ-DVSPGAPKELRNYLEKFKDPA  1089
gi|149254600|ref|XP_984653.2|    SPTSKMKKVKFATFT-IPPEESCPTVNSILSGED--DIKWVCQ-DLDVGAPKELRTYLEKFQDSV  1171
gi|118098453|ref|XP_415100.2|    SPTSKRKRVKFTTFTTIPPDDGCPTVNSILSSND-DDIKWVCQ-DMDLGDSKEIRNYMEKLKDKV  1104
gi|292612168|ref|XP_002661322.1| SPTSKRKRVQFTTFTSLDRQT-SPKTLPQENGHG---INWVGKEDKCMSSEVSAAESLQKM----  1169
                                 ......1210......1220......1230......1240......1250......1260.....
```