```
gi|4507751|ref|NP_001062.1|        --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|114672493|ref|XP_001150558.1|   --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|83716002|ref|NP_001032905.1|    --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|57100565|ref|XP_533309.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|73961995|ref|XP_849163.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|46358062|ref|NP_067263.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|9507217|ref|NP_062052.1|        --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|118086858|ref|XP_419147.2|      --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|18859519|ref|NP_571835.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|30690081|ref|NP_195183.2|       MRCLQN--------SAKTLPLAFKS-------------ALLPLS-------------------------------------------QRWFCKFSPKPSSLTN------------------------------   39
gi|15227185|ref|NP_179230.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|115485535|ref|NP_001067911.1|   MTWPNKRYYLLPSLLSIRTKSLKKKRKENPPFHTNLYSPPSQFPICSGGGERDTAAAAALRRTRPGGARRGTDTSTTLPFLSFLTPQPPTPDPRPPSRFIRAASIPSRRLESNRRIQMLVAEVFRAGAYISRFSRHACQVARFSGISC   150
gi|115488458|ref|NP_001066716.1|   MPVPNP-----------HSPGLSGKN------------PMPVPMSDGNG----------------YARR-----------------------ATHFFRKSNILILRLQS--------------------------------------   47
gi|11878473|ref|XP_311491.3|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|17137556|ref|NP_477367.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|50302825|ref|XP_451349.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|45188092|ref|NP_984315.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|83578104|ref|NP_014717.2|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|19115217|ref|NP_594305.1|       -----------------------------------------------------------------------------------MSQPLHARFATRAVKNPMILEKERQLTDSKYHILVAATGSVAAIKL   46
gi|39944952|ref|XP_362013.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|85089414|ref|XP_957941.1|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|71993377|ref|NP_491532.3|       --------------------------------------------------------------------------------------------------------------------------------------------------------
gi|124505475|ref|XP_001351479.1|   -------------------------------------------------------------------------------------------------------------------------------------------MMEQVCDV   8
                                   1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

```
gi|4507751|ref|NP_001062.1|        ----------------------------------------------------------------------------------------------------------------------------------------
gi|114672493|ref|XP_001150558.1|   ----------------------------------------------------------------------------------------------------------------------------------------
gi|83716002|ref|NP_001032905.1|    ----------------------------------------------------------------------------------------------------------------------------------------
gi|57100565|ref|XP_533309.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|73961995|ref|XP_849163.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|46358062|ref|NP_067263.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|9507217|ref|NP_062052.1|        ----------------------------------------------------------------------------------------------------------------------------------------
gi|118086858|ref|XP_419147.2|      ----------------------------------------------------------------------------------------------------------------------------------------
gi|18859519|ref|NP_571835.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|30690081|ref|NP_195183.2|       -------------------IFKVSISTMANTLNGNVIMTSKPQSTYQVVVAATKEMGIGKDGKLPWNLPTDLKFFKDLTLSTSDSAKKNAVVMGRKTWESIPKKYRPLSGRLNVVLSRSSGFDIANTENVVTCSSIDSALDLLAAPP   167
gi|15227185|ref|NP_179230.1|       --------------MATTTLNDSVT--TTLASEPQRTYQVVVAATKEMGIGKDGKLPWNLPTDLKFFKDITLTTSDSSKKNAVVMGRKTWESIPIKYRPLSGRLNVVLTRSGGFDIANTENVVTCSSVDSALDLLAAPP   123
gi|115485535|ref|NP_001067911.1|   APISQFRRPQSLEGSRKLRSCCFIQTRLIAMATTLS-NGVSQNGPQRNYQVVVAATRDMGIGKDGVLPWKLLGDLKFFKELTVTTADPVKKNAVIMGRKTWESLPKARPLPGRLNIILRSGSFEFATVENVVICGSMNSALELLSSTP   299
gi|115488458|ref|NP_001066716.1|   --------LKYLEFRDKLNFSRFHKSQVIVMSTNVN-NGNSESNLKRSYQVVVSATRDMGIGKDGTLPWKLPGDLKFFKDITVTTSDPSKKNAVVMGRKTWESIPLKFRPLPGRLNVILTRSGSFDFATAENVVIGSLDSALQLLATTP   188
gi|11878473|ref|XP_311491.3|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|17137556|ref|NP_477367.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|50302825|ref|XP_451349.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|45188092|ref|NP_984315.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|83578104|ref|NP_014717.2|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|19115217|ref|NP_594305.1|       TLIVKSLLTYKGVDVQVVLTDPARNFVEKEDLIALGVNVYNNADDWKNWDGLECPITHIELRRWAHLLLIAPLSANTMAKMANGLCDNLLTSLIRAWAPLKPILLAPAMNTLMWTNPITQEHLSAISRIYKNSEFIMPIEKVLACGDIGM   196
gi|39944952|ref|XP_362013.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|85089414|ref|XP_957941.1|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|71993377|ref|NP_491532.3|       ----------------------------------------------------------------------------------------------------------------------------------------
gi|124505475|ref|XP_001351479.1|   FDIYAICACCKVESKNEGKKNEVFNNYTFRGLGNKGVLPWKCNSLDMKYFCAVTTYVNESKYEKLKYKRCKYLNKETVDNVNDMPNSKKLQNVVVMGRTSWESIPKKFKPLSNRINVILSRTLKKE-DFDEDVYIINKVEDLIVLLG---   154
                                   .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

```
                                                                                                                                                                
gi|4507751|ref|NP_001062.1|        ----------------------------------------------------------------------------MPVAGSELPRRPLPPAAQERDAEPRPPP---------------------------------------    27
gi|114672493|ref|XP_001150558.1|   ----------------------------------------------------------------------------MPVAGSELPRRPLPPAAQERDAEPRPP----------------------------------------    27
gi|83716002|ref|NP_001032905.1|    ----------------------------------------------------------------------------MPAAGSEPSRPPSPPGVQEQSAEPRPPPPP-------------------------------------    30
gi|57100565|ref|XP_533309.1|       ----------------------------------------------------------------------------MPAPGSELQRPPSPPAAQKPRARPQPPP---------------------------------------    28
gi|73961995|ref|XP_849163.1|       ----------------------------------------------------------------------------MPAPGSELQRPPSPPAAQKPRARPQPPP---------------------------------------    28
gi|46358062|ref|NP_067263.1|       ----------------------------------------------------------------------------MLVVGSELQSDAQQLSAEAPR---------------------------------------------    21
gi|9507217|ref|NP_062052.1|        ----------------------------------------------------------------------------MLVEGSELQSGAQQPRTEAPQ---------------------------------------------    21
gi|118086858|ref|XP_419147.2|      ----------------------------------------------------------------------------MPAAEE------PSSGLEG----------------------------------------------    13
gi|18859519|ref|NP_571835.1|       ----------------------------------------------------------------------------MPDTAVEVTNGHCVNGESKKEETNGGKKEFS-----------------------------------    31
gi|30690081|ref|NP_195183.2|       FSLSIEKVFVIGGGDILREALNKPSCEAIHITEIDTSIDCDTFIPTVDTSAYQPWCSSFPICENGLRFSFTTHVRVKSSSAGEASDES-----DGSKVLQVDWKKFSSVLPKMI-------------------------------   276
gi|15227185|ref|NP_179230.1|       YCLSIERVFVIGGGDILREALNRPSCDAIHLTEIDTSVDCDTFIPAIDTSVYQPWSSSFPVTENGLRFCFTTFVRVKSS-ADESSDES-----NGSQSLQFDGKKF-LFLPKMV-------------------------------   230
gi|115485535|ref|NP_001067911.1|   YCLSIEKVFVIGGGQVLRESLNGPSCEAVHLTDIQSSIECDTFIPPIDLSVFQPWYSSLPVWESSNIRHSFVTYVRVRKTMAETHDSNGKESANDGIKSDKFETENF-SFLPKLI-------------------------------   412
gi|115488458|ref|NP_001066716.1|   YCLTVEKTFIIGGGEILRQSLNAPACEAIHLTDIESSIECDTFIPPIDLSMFHPWYSSFPVVENGIKHSFISFVRVTKSIAEANDSSGKELTGNDSKKVKFEIENF-SFLPKMI-------------------------------   301
gi|11878473|ref|XP_311491.3|       ----------------------------------------------------------------------------MEGENG--NVVKKD----------------------------------------------------    12
gi|17137556|ref|NP_477367.1|       -------------------MVLTPTKDGP-----------------------------------------------DQESMPLPADNGESPSKQQA---------------------------------------------    30
gi|50302825|ref|XP_451349.1|       ----------------------------------------------------------------------MTLSD--------RNVKRVKLEAV------------------------------------------------    16
gi|45188092|ref|NP_984315.1|       -----------------------------------------------------------MSWRSLKDPTYARQAHYIYQLILQRNMGLPNLKMDSVKSDTRSSV-------------------------------------    45
gi|83578104|ref|NP_014717.2|       ----------------------------------------------------------------------------MTMDGK--------------------------------------------------------------    6
gi|19115217|ref|NP_594305.1|       GGMAEWRNIVGRVADKLQLEQKSVLPNAVKNIDGQDDDSEQTAAFEEYDDDDDDDVDDNEQSNSMIETSANADITPKASLLPSTTESSISKDHETSQAPLGSESVDTQASENVTTKPEPPVP-----------------------   319
gi|39944952|ref|XP_362013.1|       ----------------------------------------------------------------------------MADAGAKPAQNG----------------------------------------------------    12
gi|85089414|ref|XP_957941.1|       ---------------------------------------------------------------------------MTVTTSEPVAPAQSQSQTSSRTNPT-----------------------------------------    25
gi|71993377|ref|NP_491532.3|       ----------------------------------------------------------------------------MNKENIIADAPSDVVKTVQQQVH---------------------------------------------    23
gi|124505475|ref|XP_001351479.1|   -KLNYYKCFIIGGSVVYQEFLEKKLIKKIYFTRINSTYECDVFFPEINENEYQIISVSDVYTSNNTTLDFIIYKKTNNKMLNEQNCIKGEEKNNDMPLKNDDKDTCHMKKLTEFYKNVDKYKINYENDDDDEEEDDFVYFNFNKEKEEKN   303
                                   .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450


                                            *  **     *:  *    :  ***  .*   * *.      ::  :                              :*****:::  :.: *****: . *.  . *   .::**: *. * :**
gi|4507751|ref|NP_001062.1|        ------------------HGELQYLGQIQHILRCGVRKDDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSTREEGDLGPV   134
gi|114672493|ref|XP_001150558.1|   ------------------HGELQYLGQIEHILRCGVRKDDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSTREEGDLGPV   134
gi|83716002|ref|NP_001032905.1|    ------------------HGELQYLGQIEHILRCGFRRDDRTGTGTLSVFG-MQARYNLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSDRAEGDLGPV   137
gi|57100565|ref|XP_533309.1|       ------------------HGELQYLRQVEHILSCGARKHDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSRGVKIWDANGSRDFLDSLGFANREEGDLGPI   135
gi|73961995|ref|XP_849163.1|       ------------------HGELQYLRQVEHILRCGFKKEDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSRGVKIWDANGSRDFLDSLGFSARQEGDLGPV   135
gi|46358062|ref|NP_067263.1|       ------------------HGELQYLRQVEHIMRCGFKKEDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSARQEGDLGPV   128
gi|9507217|ref|NP_062052.1|        ------------------HGELQYLRQVEHIMRCGFKKEDRTGTGTLSVFG-MQARYSLRD--------------------EFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSARQEGDLGPV   128
gi|118086858|ref|XP_419147.2|      -----------------GEPQYLQQVRHILQHGHRKEDRTGTGTISVFG-MQARYSLRD----------------------QFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSAKGVKIWDANGSREFLDKQGFCTREEGDLGPV   119
gi|18859519|ref|NP_571835.1|       ---------------LFCDERGYLSLVEFILQNGAKKGDRTGTGVISVFG-TQARYSLRD--------------------QFPLLTTKRVFWKGILEELLWFIKGSTNAKDLSEKGVRIWDANGSREFLDKNGFTDREEGDLGPV   140
gi|30690081|ref|NP_195183.2|       ---------------FDRHEEYLYLNLVKEIISNGNLKDDRTGTGTLSKFG-CQMKFNLRR--------------------NFPLLTTKRVFWRGVVEELLWFISGSTNAKVLQEKGIRIWDGNASRAYLDGIGLTEREEGDLGPV   386
gi|15227185|ref|NP_179230.1|       ---------------FDQHEEFLYLNMVEDIISNGNVKNDRTGTGTLSKFG-CQMRFNLRR--------------------SFPLLTTKRVFWRGVVEELLWFISGSTNAKVLQEKGIHIWDGNASREYLDGIGLTEREEGDLGPV   340
gi|115485535|ref|NP_001067911.1|   ---------------FDRHEEYHYLNLVEDIIRSGAQKNDRTGTGTLSKFG-CQMRFNLRN--------------------SFPLLTTKRVFWRGVVEELLWFISGSTSAKVLQEKGIHIWDGNASREYLDSVGLAHREEGDLGPV   522
gi|115488458|ref|NP_001066716.1|   ---------------FERHEEYQYLNLVQDIIRNGAKKNDRTGTGTLSKFG-CQMRFNLRR--------------------NFPLLTTKRVFWRGVVEELLWFISGSTNAKVLQEKGIHIWDGNASRQYLD--------------   396
gi|11878473|ref|XP_311491.3|       ---------------NGNEEEQAYLQLIRDIINKGSKRLDRTGVGTILSIFG-AQMRFSLRDG--------------------IIPLLTTKKVFFRGVAEELLWFIKGSTNVKDLQAKGVKIWDGNSTREYLDSCGFDREEGDLGPV   123
gi|17137556|ref|NP_477367.1|       ---------------PVNRDEMHYLDLLRHIIANGEQRMDRTEVGTLSVFG-SQMRFDMRN--------------------SFPLLTTKRVFFRAVAEILLWFVAGKTDAKLLQAKNVHIWDGNSSRREFLDKMGFTGRAVGDLGPV   140
gi|50302825|ref|XP_451349.1|       ------------------NAEEQQYLDLCERIINEGEFRPDRTGTGTYSLFAPPQLRFNLSNDT-------------------FPLLTTKRVFTKGIILELLWFVAGCTDGKKLSEQGREYLDSLGLIDRREGDLGPV   126
gi|45188092|ref|NP_984315.1|       ------------------NAEEQQYLDLCKRIIEHGEFRPDRTGTGTYSLFAPPQLRFDLSGDK-------------------FPLLTTKRVFTRGIILELLWFIAGCTDGKKLSEQGVKIWEGNSREYLDSLGLHDRREGDLGPV   155
gi|83578104|ref|NP_014717.2|       ------------------NKEEEQYLDLCKRIIDEGEFRPDRTGTGTLSLFAPPQLRFDLANLL-------------------FPLLTTKRVFTRGIILELLWFLAGDTDANLLSEQGVKIWDGNSREYLDKMGFKDRHEGDLGPV   116
gi|19115217|ref|NP_594305.1|       --------FTSSEYRNTEEEQYLNLIRYILENGQSRPDRTGTGTRSVFAPPQLRFSLRNNI--------------------LPLLLTTKRVLRGVLEELLWFIHGDTNANHLSEKGIHIWDGNSREFLDSRGLTDRVGDLGPI   436
gi|39944952|ref|XP_362013.1|       ------------------TERHEEYQYLDLVREILDNGEHRPDRTGTGTYSIFAPRPLKFSLNKDG-------------------TPILPLLTTKRVFSRAVILELLWFVSGATSAKPLSDAGVKIWDGNGSREFLDGLGLQHREVGDLGPV   127
gi|85089414|ref|XP_957941.1|       --------------SKRHEEYQYLDLVRQILDEGELREDRTGTGTYSIFAPTPLKFALSRPSSSSPSSQGVKSSSTTLSAQGVKIWDGNGSRAFLDMLGLSHRKEGDLGPV   159
gi|71993377|ref|NP_491532.3|       ------------------LNQDEYKYLKQVEQILREGTRRDDRTGTGTISIFG-MQSKYCLRNG--------------------TIPLLTTKRVYWKGVLEELLWFISGSTDGKLLMEKNVKIWEKNGDRAFLDNLGFTSREEGDLGPV   133
gi|124505475|ref|XP_001351479.1|   KNSIHPNDFQIYNSLKYKYHPEYQYLNIIYDIMMNGNKQSDRTGVGVLSKFG-YIMKFDLSQ--------------------YFPLLTTKRVFLFLRGIIEELLWFIRGETNGNTLLNKNVRIWEANGTREFLDNRKLFHREVNDLGPI   429
                                   .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
```
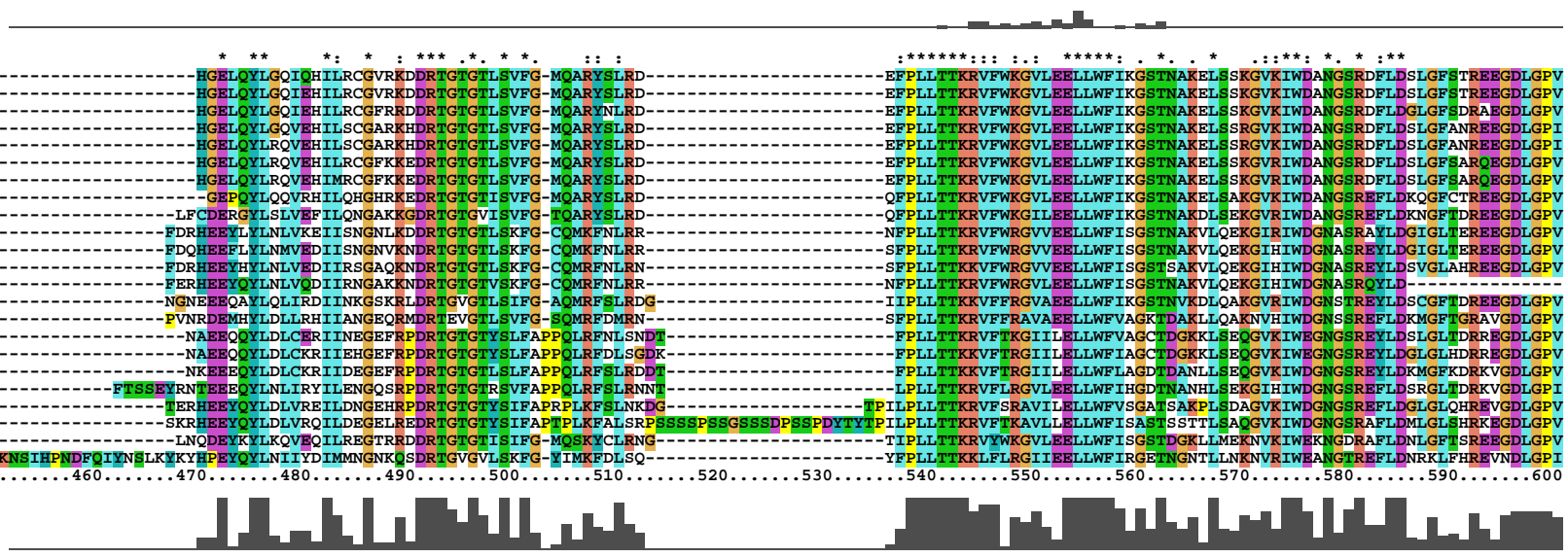
```
                                              *    :* .:*.*** ::  :: .* .**:::..**   :  *.***** :.**:*                          .* . :**** *:******;***.::* ::*   .  .. : *. *:
gi|4507751|ref|NP_001062.1|       YGFQWRHFGAEYRDMESDYSGQGVDQLQRVIDTIKTNPDDRRIIMCAWNPRDLPLMALPPCHALCQFYVVN-----------------------------SELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDA  255
gi|114672493|ref|XP_001150558.1|  YGFQWRHFGAEYRDMESDYSGQGVDQLQRVIDTIKSNPDDRRIIMCAWNPRDLPLMALPPCHALCQFYVVN-----------------------------SELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDA  255
gi|83716002|ref|NP_001032905.1|   YGFQWRHFGAEYKDMDSEYSGQGVDQLQKVIDTIKTNPNDRRIILCAWNPKDLPLMALPPCHALCQFYVVN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITDLKPGDFVHTLGDA  258
gi|57100565|ref|XP_533309.1|      YGFQWRHFGAEYKDKDSDYSGQGVDQLQKVIDTIKTNPDDRRIILCGWNPKDLPLMALPPCHALCQFYVVN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDA  256
gi|73961995|ref|XP_849163.1|      YGFQWRHFGAEYKDKDSDYSGQGVDQLQKVIDTIKTNPDDRRIILCGWNPKDLPLMALPPCHALCQFYVVN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDA  256
gi|46358062|ref|NP_067263.1|      YGFQWRHFGAEYKDMDSDYSGQGVDQLQKVIDTIKTNPDDRRIIMCAWNPKDLPLMALPPCHALCQFYVVN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLQPGDFVHTLGDA  249
gi|9507217|ref|NP_062052.1|       YGFQWRHFGAEYKDMDSDYSGQGVDQLQKVIDTIKTNPDDRRIIMCAWNPKDLPLMALPPCHALCQFYVVN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLQPGDFVHTLGDA  249
gi|118086858|ref|XP_419147.2|     YGFQWRHFGADYKDMHTDYSNQGVDQLQKVIEMIKTNPDDRRIIMCAWNPKDISLMALPPCHALCQFYVLN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYSLLTYMIAHVTGLKPGEFIHTLGDA  240
gi|18859519|ref|NP_571835.1|      YGFQWRHFGAEYKDMHTDYSGEGVDQLQKVIDTIKSNPEDRRIIMCAWNPKDLPLMALPPCHALCQFYVSN-----------------------------GELSCQLYQRSGDIGLGVPFNIASYALLTYMIAHITGLKPGDFVHTLGDA  261
gi|30690081|ref|NP_195183.2|      YGFQWRHFGAKYTDMHADYTGQGFDQLLDVINKIKNNPDDRRIIMSAWNPSDLKLMALPPCHMFAQFYVAN-----------------------------GELSCQMYQRSADMGLGVPFNIASYSLLTCILAHVCDLVPGDFIHVIGDA  507
gi|15227185|ref|NP_179230.1|      YGFQWRHFGAKYTDMHADYTGGFDQLVDVIDKIKNNPDDRRIIMSAWNPSDLKLMALPPCHMFAQFYVAE-----------------------------GELSCQMYQRSADMGLGVPFNIASYSLLTCMLAHVCDLVPGDFIHVLGDA  461
gi|115485535|ref|NP_001067911.1|  YGFQWRHFGAEYTDMHADYTGKGFDQLMDVIDKIKNNPDDRRIILSAWNPSDLKKMALPPCHMFAQFYVES-----------------------------GELSCQMYQRSADMGLGVPFNIASYSLLTCMIAVCGLSPGEFVHVIGDA  643
gi|115488458|ref|NP_001066716.1|  ----------RVTDMHADYVGKGFDQLMDVIDKIKNNPDDRRIILSAWNPTDLKKMALPPCHMFAQFYVEN-----------------------------GELSCQMYQRSADMGLGVPFNIASYSLLTCMIAQVCDLSPGDFIHVIGDA  507
gi|118781473|ref|XP_311491.3|     YGFQWRHFGATYKTCHDDYTGQGIDQLAEVIDKIKNNPYDRRIIMCAWNPSDIPNMALPPCHCLAQFYVSD-----------------------------GELSCQMYQRSADVGLGVPFNIASYSLLTHMIAHVTGLKAGEFIHTTGDT  244
gi|17137556|ref|NP_477367.1|      YGFQWRHFGAQYTCDDDYSGKGIDQLRQVIDTIRNNPSDRRIIMSAWNPLDIPKMALPPCHCLAQFYVSN-----------------------------GELSCQLYQRSCDMGLGVPFNIASYALLTHMIAHVTGLKPGDFVHTMGDT  263
gi|50302825|ref|XP_451349.1|      YGFQWRHFGAEYKTCDDDYSGQGVDQLKEIIHKLKTNPYDRRIILSAWNPNPDFPKMALPPCHVFSQFYVSFPKG-EGA----------------------KPRLSCVLYQRSCDMGLGVPFNIASYALLTKMIAMVCDMEPGEFIHTLGDA  254
gi|45188092|ref|NP_984315.1|      YGFQWRHFGAEYGTCDDDYTGKGVDQLRELIDKINKPYDRRIILSAWNPADFPKMALPPCHVLSQFYVSFGP-EGS----------------------KPKLSCQLYQRSCDMGLGVPFNIASYALLTKMIAMVCDMDAGEFIHTMGDA  282
gi|83578104|ref|NP_014717.2|      YGFQWRHFGAEYKTCDDDYTGQGIDQLRDVIDKIKNNPADFDKMALPPCHIFSQFYVSFPKEGEGSG-----------------------------KPRLSCQLYQRSCDMGLGVPFNIASYALLTRMIAKVVDMEPGEFIHTLGDA  246
gi|19115217|ref|NP_594305.1|      YGFQWRHFGAQYVDCTDYTNKGVDQLAQVISTLKLNPYDRRIILSAWNPLAIPEMALPPCHIFCQFYVSEPCK-PGG----------------------KPQLSSMMYQRSADMGLGVPFNIASYSLLTHMIAHMCGYEAAEFVHVMGDC  564
gi|39944952|ref|XP_362013.1|      YGFQWRHFGAEYTDCHADYTGQGVDQLAEVVHKLRTNPYDRRMVLSAWNPKDLKLMVLPPCHMFAQFYVSYPKAGSDSNGNGNTTEGADQTSSPS--KPKGHLHCQLYQRSCDMGLGVPFNIASYALLTHMIARATGLVPGSLTHVMGDA  275
gi|85089414|ref|XP_957941.1|      YGFQWRHFGAEYVDCETDYTGQGVDQLQRIIDTLRNNPYDRRILSAWNPKDMSQMVLPPCHMFAQFYVSYPGSRTRGGATQTQNKEGELDTPPKEKKPRGHLHCQLYQRSCDMGLGVPFNIASYALLTHMIAHVCDLVPGSLTHVMGDA  309
gi|71993377|ref|NP_491532.3|      YGFQWRHFGAKYVDCHTDYSGQGVDQLAEVIRQIKEQPDSRRIIMSAWNPSDLGQMVLPPCHTMCQFYVDN-----------------------------GELSCQLYQRSGDMGLGVPFNIASYGLLTHMIAKVCGLKPGTLVHTLGDA  254
gi|124505475|ref|XP_001351479.1|  YGFQWRHFGAEYTNMYDNYENKGVDQLKNIINLIKNDPTSRRILLCAWNVKDLDQMALPPCHILCQFYVFD-----------------------------GELSCIMYQRSGDMGLGVPFNIASYSIFTHMIAQVCNLQPAQFIHVLGNA  550
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750


                                  *:*  *:  *. *                                           : . *  :* :: :             ..:    : :                      :
gi|4507751|ref|NP_001062.1|       HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLRILR------KVEKIDDFKAEDFQIEG------YNPHPTIKMEMAV------  313
gi|114672493|ref|XP_001150558.1|  HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLKILR------KVEKIDDFKAEDFQIEG------YNPHPTIKMEMAV------  313
gi|83716002|ref|NP_001032905.1|   HIVLNHIEPLKTQALMELRGQSSRSLDGDGQAGTSRWAPVATDTERDRCCELQREPRPFPKLKILR------KVETIDDFQAEDFQIEG------YNPNPTIKMEMAV------  354
gi|57100565|ref|XP_533309.1|      HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLRILR------RVEKIDKFKAEDFQIEGSANFKNYTSAVNPKFEQAEEHQHS-  325
gi|73961995|ref|XP_849163.1|      HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLRILR------RVEKIDKFKAEDFQIEGSANFKNYTSAVNPKFEQAEEHQHS-  325
gi|46358062|ref|NP_067263.1|      HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLKILR------KVETIDDFKVEDFQIEG------YNPHPTIKMEMAV------  307
gi|9507217|ref|NP_062052.1|       HIVLNHIEPLKIQ----------------------------------------------LQREPRPFPKLKILR------KVETIDDFKVEDFQIEG------YNPHPTIKMEMAV------  307
gi|118086858|ref|XP_419147.2|     HIVLNHVEPLKVQ----------------------------------------------LQREPRPLPKLRILR------KVEDISDFKAEDFQIED------YNPHPHIKMEMAV------  298
gi|18859519|ref|NP_571835.1|      HIYTNHIEPLKEQ----------------------------------------------IQREPRPFPKLRIKR------KVEQINDFCAEDFEIYD------YDPHPTIKMQMAV------  319
gi|30690081|ref|NP_195183.2|      HVVKNHVRPLQEQ----------------------------------------------LENPPKPFPVLKINP------EKKDIDSFVADDFELIG------YDPHKKIDMKMAV------  565
gi|15227185|ref|NP_179230.1|      HVVKTHVRPLQEQ----------------------------------------------LLNLPKPFPVMKINP------EKKQIDSFVASDFDLTG------YDPHKKIEMKMAV------  519
gi|115485535|ref|NP_001067911.1|  HVRTHVRALEEQ----------------------------------------------IQKLPKPFPVLKINP------LKKDIDSFVASDFKLV-----------AKLGPPVTM------  696
gi|115488458|ref|NP_001066716.1|  HVYRTHVEALEEQ----------------------------------------------MRKQPKPFFILKINP------VKKDIDSFVTSDFKLVR------YDPHHKIEMKMAQIQLEPF  571
gi|118781473|ref|XP_311491.3|     HIVLNHVDGLREQ----------------------------------------------IERTPKKFPTLVFKR------KVESIDNFTYDDFEILN------YNPQSAIKMKMAV------  302
gi|17137556|ref|NP_477367.1|      HIVLNHVEPLKEQ----------------------------------------------LERTPRPFPKLIIKR------QVQDIDDFRFEDFQIVD------YNPHPKIQMDMAV------  321
gi|50302825|ref|XP_451349.1|      HVVKDHVDALKTQ----------------------------------------------IAREPRAFPKKIKR---NVSDI---DDFKYEDFEITD------YNPHGKIQMKMSV------  312
gi|45188092|ref|NP_984315.1|      HVVSDHIAALKEQ----------------------------------------------IERVPREFPNLRIKR---KVTDI---DDFTLDDFEITD------YNPHPIRIQMNMSV------  340
gi|83578104|ref|NP_014717.2|      HVVKDHIDALKEQ----------------------------------------------ITRNPRPPKLKIKR---DVKDI---DDFKLTDFEIED------YNPHPIQMKMSV------  304
gi|19115217|ref|NP_594305.1|      HIYNDHLEALQTQ----------------------------------------------LERVPKAFPKLFFKR---DAKDIGSIDSFSVDDFAVEG------YNPYGPIKMKMSV------  625
gi|39944952|ref|XP_362013.1|      HVVADHVDALRTQ----------------------------------------------LEREPRPFPELEINRPEVPEGGDGVIDGWKLEDFVIKG------YDPHKAIAMKMSV------  339
gi|85089414|ref|XP_957941.1|      HVVLNHVDALRTQ----------------------------------------------LEREPREFPTLEIQR-----EKG-GSIDGWKAEDFVIKG------YEPHKTIAMEMSV------  368
gi|71993377|ref|NP_491532.3|      HVVSNHVDALKTQ----------------------------------------------LDREPYAFPKIRFTR---DVASIDDFTSDMIALDD------YKCHPKIPMDMAV------  312
gi|124505475|ref|XP_001351479.1|  HVINNHIDSLKTQ----------------------------------------------LNRIPYPFPTLKLNP------DIKNIEDFTISDFTIQN------YVHHEKISMDMAA------  608
                                  .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860....
```