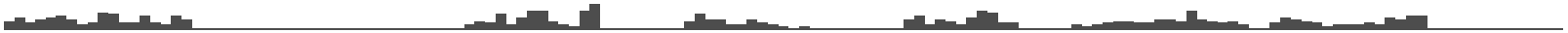
```
gi|158293720|ref|XP_315060.4|     ------------------------------------------------------------------------------------------MKKVVAARRPV---------------LGELGNKVLRNASQ    25
gi|158293718|ref|XP_315059.4|     ------------------------------------------------------------------------------------------MKKVVAARRPV---------------LGELGNKVLRNASQ    25
gi|24658583|ref|NP_726246.1|      ------------------------------------------------------------------------------------------MAALEKNASENFKQVQLKKLT---------------VPSMEATTKRAALG    35
gi|51762951|ref|XP_485921.1|      ------------------------------------------------------------------------------------------MALRVTRNTKINAENKAK---------------VSMAGAKRVPVTVT    32
gi|28195398|ref|NP_758505.2|      ------------------------------------------------------------------------------------------MALRVTRNTKINAENKAK---------------VSMAGAKRVPVTVT    32
gi|25282457|ref|NP_741988.1|      ------------------------------------------------------------------------------------------MALRVTRNTKINTENKAK---------------VSMAGAKRVPVAV-    31
gi|14327896|ref|NP_114172.1|      ------------------------------------------------------------------------------------------MALRVTRNSKINAENKAK---------------INMAGAKRVPTAPA    32
gi|114599953|ref|XP_517728.2|     MNVSYLNRTQGLECKKRRAFQAEESKGSPPIAELLVGGALAALLSRWPLQLPKSAGAEADHAGSSRRAAAERLLVSAGSRSLAGRVSGVLLLPAELLPGEEEAMALRVTRNSKINAENKAK---------------INMAGAKRVPTAPA   135
gi|73988334|ref|XP_851164.1|      ------------------------------------------------------------------------------------------MALRVTRNTKVNVENKAK---------------IGMAGAKRVPLASA    32
gi|73949659|ref|XP_850398.1|      ------------------------------------------------------------------------------------------MALRVTRNTKVNVENKAK---------------IGMAGAKRVPLASA    32
gi|114052292|ref|NP_001039337.1|  ------------------------------------------------------------------------------------------MALRITRNTKISAENKAK---------------ISMAGAKRVPVAAV    32
gi|20373137|ref|NP_571588.1|      ------------------------------------------------------------------------------------------MMALRVTRNTRLASS-----------------------ENQNALPGKAV    26
gi|15239938|ref|NP_196233.1|      ------------------------------------------------------------------------------------------MATRANV-PEQVRGAPLVD---------------GLKIQNKNGA-VKS    31
gi|22330995|ref|NP_187759.2|      ------------------------------------------------------------------------------------------MATGPVVHPQPVRGDP---------------------IDLKNAA-AKN    26
gi|15235573|ref|NP_195465.1|      ------------------------------------------------------------------------------------------MMTSRSIVPQQSTDDVVV-------------------VDGKNVAKGRN    29
gi|145615516|ref|XP_360272.2|     ------------------------------------------------------------------------------------------MPPARTARGQLVSNENDEN---------------AGSTRMTRTKAKAA    33
gi|32423039|ref|XP_331957.1|      ------------------------------------------------------------------------------------------MPNLRTRNPRSLANENDEN---------------STATTTRMIRAKAA    33
gi|19111963|ref|NP_595171.1|      ------------------------------------------------------------------------------------------MTTRRLTRQHLLANTLGNN---------------DENHPSNHIARAKS    33
gi|50307537|ref|XP_453748.1|      ------------------------------------------------------------------------------MSKDKYD-----RSLKN--LNMLRRPVLNNVTNTTES---------------TFGKVLRQAKSRLQ    44
gi|45184922|ref|NP_982640.1|      ------------------------------------------------------------------------MSSVNKENYRGVPSGRGMKNPVLAGAKRAVLNNVTNTTLSQEAANSNAHSGSGYTNSFGKVLRQAKSKLQ    70
gi|6325376|ref|NP_015444.1|       ------------------------------------------------------------------------------MSNPIENTENSQNTSSSRFLRNVQRLALNNVTNTTFQK-------------SNANNPALTNFKSTLN    54
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

```
gi|158293720|ref|XP_315060.4|     DLLGKGVEKGAALKNAN------------------------PTLKNIKPRVDTRWRK----ADTAAAAVVVPKKVVT-------RSDSQKVAVEPKPSANADAVKVHVQLNKGNEVKHVALKREDSQLSLRTLAKQ-------------   126
gi|158293718|ref|XP_315059.4|     DLLGKGVEKGAALKNAN------------------------PTLKNIKPRVDTRWRK----ADTAAAAVVVPKKVVT-------RSDSQKVAVEPKPSANADAVKVHVQLNKGNEVKHVALKREDSQLSLRTLAKQ-------------   126
gi|24658583|ref|NP_726246.1|      DLQNRGISRPIAAKDAAQKDSKD---------------LKLTDALRNAKARVDSHWKKQPLGSTNGNGNGAVPPKVNEGGVSAFLRSNSVRNRVPTK--TTVEPTKVTVKSSSSENVNEPTLKREDSNLSKKSLTKLRAALAKPVMGVSG   168
gi|51762951|ref|XP_485921.1|      AASKPGLRPRTALGDIGNK--------------------------VSEELQARVPLKR--------EAKTLGTGKGTV---------KALPKPVEKVP-----VCEPEVELAEPEPEPELEHVREEKLSPEPILVDN-------------   121
gi|28195398|ref|NP_758505.2|      AASKPGLRPRTALGDIGNK--------------------------VSEELQARVPLKR--------EAKTLGTGKGTV---------KALPKPVEKVP-----VCEPEVELAEPEPEPELEHVREEKLSPEPILVDN-------------   121
gi|25282457|ref|NP_741988.1|      AASKPLLRSRTALGDIGNK--------------------------VSE--QSRIPLKK--------ETKKLGSGTVTV---------KALPKPVDKVP-----VCEPEVELDEPEPEP----VMEVKHSPEPILVDT-------------   114
gi|14327896|ref|NP_114172.1|      ATSKPGLRPRTALGDIGNK--------------------------VSEQLQAKMPMKK--------EAKPSATGKVID---------KKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEP--VKEEKLSPEPILVDT-------------   124
gi|114599953|ref|XP_517728.2|     ATSKPGLRPRTALGDIGNK--------------------------VSEQLQAKMPMKK--------EAKPSATGKVID---------KKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEP--VKEEKLSPEPILVDT-------------   227
gi|73988334|ref|XP_851164.1|      AASKPGLRPRTALGDIGNK--------------------------VSEQPQAKLPLKK--------EAKTAVPGKVIA---------KKIPKPLEKAP--------EPVPVPEPELEPEP--VKEEKLSPEPILVDT-------------   116
gi|73949659|ref|XP_850398.1|      AASKPGLRPRTALGDIGNK--------------------------VSEQPQAKLPLKK--------EAKTAVPGKVIA---------KKIPKPLEKAP--------EPVPVPEPELEPEP--VKEEKLSPEPILVDT-------------   116
gi|114052292|ref|NP_001039337.1|  ATSKPGLRPRTALGDIGNK--------------------------VSEQPQAKLPLKK--------EAKTLASGKVTA---------KKVPKPLEKAP--------VPVPEPQPEPEPEPEPHVKEDKLSPEPILVDT-------------   118
gi|20373137|ref|NP_571588.1|      VANKPGLRPRAALGEIGN---------------------------NPQTRQALKK--------KEVKVAP---------------AAEVVVEKAP---------VVQQPKKDSPK----VQHG----VKVVSEP-------------    93
gi|15239938|ref|NP_196233.1|      RRALGDIGNLVSVPGVQGGKA---------------------QPPINRPITRSFRAQ------LLANAQLERKPINGDNKVPALGPKRQPLAARNPEAQRAVQKKNLVVKQQ-TKPVEVIETKKEVTK--KEVAMSPK----------   139
gi|22330995|ref|NP_187759.2|      RRALGDIGNVDSLIGVEGGK--------------------------LNRPITRNFRAQ------LLENAQVAAA---ANKKAPILDG-----VTKKQEVVRAVQKKARGDKREPSKPIEVIVISPDTN----EVAKAKE-----------   121
gi|15235573|ref|NP_195465.1|      RQVLGDIGNVVRGNYPKNNEP---------------------EKINHRPRTRSQNPT------LLVEDNLKKP------------------VVKRN----AVPKPKKVAGKP--KVVDVIEISSDSDEELGLVAAREKK----------   117
gi|145615516|ref|XP_360272.2|     ALNVDELALPTKQLQTKKG--------------------------VAGKPAPTTRTTRNALGDVSNVTKVD-AGRKAVGGKAGAVAKAAAPAGVQK----SSARTAPT-RSALSSKPANVTNGNAEKQSGRGTLSKRK--APAQAAANN-   148
gi|32423039|ref|XP_331957.1|      TLHVDELSMPAKTMQTKKTTI---------------------STTTAATAARTVGKRNALGDVSNVTKVEVAGTKKAIAKPGLVSKAAQPSGIQKKTTTATSRTATTARRALSNKEPNKTVG---PSAGAGTIPAKRKPPPSTSKLAP-   157
gi|19111963|ref|NP_595171.1|      SLHSSENSLVNGKKATVSS------------------------------TNVPKKRHALDDVSNFHNKE------------GVPLASKNTNVRH-----TTASVST-RRALEEKSIIPATD------DEPASKKRRQPSVFNSSVPS-   126
gi|50307537|ref|XP_453748.1|      NSRTNN--LPQGTANSYSNTKPAPLRDDIMVPEDKENYNPLAKIDEREELDSNLVHNHKSLGTQKHVTIDERQEIIGYSHLDTEKSAPSSSTYSSEHTENDGVHDVNPNVQRSDNEADFKMQTTNAFHENVNDGSDATDDASSGSKSSNE   192
gi|45184922|ref|NP_982640.1|      SARVAGSLIPQMKREGLASSQ-----------EDKENVVPTGVAPAAVAAAAAAAQMAPAIAKPILQSISEESHQECQSLLKDGGSDEGASTVSTKSSDTELAPSSSSSLQSAPANSEEPVVLESGTQLVERRRPQTLNTTLTGSVAS--   207
gi|6325376|ref|NP_015444.1|       SVKKEGSRIPQFTRESVSRST------------------------AAQEEKRTLKENGIQLPKNNLLDDK-----------ENQDPSSQQFGALTSIKEGRAELPANISLQESSSAKEIIQH---------------DPLKGVGSS--   150
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```



```
                                                                                                                          ::.  *  :     **. ::: :   :          :    ::  : * :* :*: .:: :* *  :*  ::: ::**
gi|158293720|ref|XP_315060.4|       ----------------NRKAQPKSAPSSGTSSSDE---------HEIVSISKKPEKVEAHSQKLLENIENIDANDGWNPMLVAEYVNDIYNYLNELESRPGYALCENFLDGHKEITHKMRTILIDWINEVHYQFKLDIDTYHMTVSLIDR   251
gi|158293718|ref|XP_315059.4|       ----------------NRKAQPKSAPSSGTSSSDE---------HEIVSISKKPEKVEAHSQKLLENIENIDANDGWNPMLVAEYVNDIYNYLNELESRPGYALCENFLDGHKEITHKMRTILIDWINEVHYQFKLDIDTYHMTVSLIDR   251
gi|24658583|ref|NP_726246.1|        --IRREPVAVSRKEATKKELPETKKDSLEVKKDATRMPLIRGNSAVTTTTSTMPTTMSLSSKRLAGIEDIDANDKENLVLVSEYVNDIYDYLYQVELEQ--PIHKDHLAGQKEVSHKMRAVLIDWINEVHLQFHLAAETFQLAVAIIDR   314
gi|51762951|ref|XP_485921.1|        -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VSDVDADDGADPNLCSEYVKDIYAYLRQLEEEQ--SVRPKYLQG-REVTGNMRAILIDWLIQVQMKFRLLQETMYMTVSIIDR   229
gi|28195398|ref|NP_758505.2|        -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VSDVDADDGADPNLCSEYVKDIYAYLRQLEEEQ--SVRPKYLQG-REVTGNMRAILIDWLIQVQMKFRLLQETMYMTVSIIDR   229
gi|25282457|ref|NP_741988.1|        -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VSDVDADDGGDPNLCSEYVKDIYAYLRQLEEEQ--SVRPKYLLG-REVTGNMRAILIDWLIQVQMKFRLLQETMYMTVSIIDR   222
gi|14327896|ref|NP_114172.1|        -------------------ASPSPMETSG-------------------CAPAEEDLCQAFSDVILA-VNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQ--AVRPKYLLG-REVTGNMRAILIDWLVQVQMKFRLLQETMYMTVSIIDR   232
gi|114599953|ref|XP_517728.2|       -------------------PSPSPMETSG-------------------CAPAEEDLCQAFSDVILA-VNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQ--AVRPKYLLG-REVTGNMRAILIDWLVQVQMKFRLLQETMYMTVSIIDR   335
gi|73988334|ref|XP_851164.1|        -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQ--AVKPKYLLG-REVTGNMRAILIDWLVQVQMKFRLLQETMYMTVSIIDR   224
gi|73949659|ref|XP_850398.1|        -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQ--AVKPKYLLG-REVTGNMRAILIDWLVQVQMKFRLLQETMYMTVSIIDR   224
gi|114052292|ref|NP_001039337.1|    -------------------PSPSPMETSG-------------------CAPAEEYLCQAFSDVILA-VSDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQ--AVKPKYLMG-REVTGNMRAILIDWLVQVQIKFRLLQETMYMTVSIIDR   226
gi|20373137|ref|NP_571588.1|        -------------------SSPVPMETSG-------------------CAS--DDLCQAFSDVLLN-IKDVDADDYDNPMLCSEYVKDIYLYLRQLETEQ--AVRPKYLAG-KEVTGNMRAILIDWLVQVQIKFRLLQETMYMTVAIIDR   199
gi|15239938|ref|NP_196233.1|        --------------------NKK-VTYSS-------------------VLSARSKAACGIVNKP--KIIDIDESDKDNHLAAVEYVDDMYSFYKEVEKES---QPKMYMHIQTEMNEKMRAILIDWLLEVHIKFELNLETLYLTVNIIDR   244
gi|22330995|ref|NP_187759.2|        --------------------NKKKVTYSS-------------------VLDARSKAAS--------KTLDIDYVDKENDLAAVEYVEDMYIFYKEVVNES---KPQMYMHTQPEIDEKMRSILIDWLVEVHVKFDLSPETLYLTVNIIDR   221
gi|15235573|ref|NP_195465.1|        ------------------ATKKKATTYTS-------------------VLTARSKAACGLEKKQKEKIVDIDSADVENDLAAVEYVEDIYSFYKSVESEW---RPRDYMASQPDINEKMRLILVEWLIDVHVRFELNPETFYLTVNILDR   227
gi|145615516|ref|XP_360272.2|       --IKEESTLEGEPARKQARVAATAAVDTKRAAP---AKELKCVEPELKPTREFIRDPRLLAGEVPPGVIDLSMDDYDDPLMVAEYAEEIFSYMLNLELSS--MPNPNYMDHQDDVEWKTRGILIDWLIEVHTRFHLVPETLFLAVNIVDR   291
gi|32423039|ref|XP_331957.1|        --IKESAPVENEPARKKIHVEEPEKKKVSRTEAKENDAPSKAVKPMAEPPAPVVRDVVPVQSVYPPGVKDLDTEDLEDPLMVAEYATEIFEYLRDLECKS--VPNPQYMSHQDDLEWKTRGILIDWLIEVHTRFHLLPETLFLAVNIIDR   303
gi|19111963|ref|NP_595171.1|        --LPQHLSTKSHSVSTHG-VDAFHKDQATIPKKLKKDVDERVVS---KDIPKLHRDS--VESPESQDWDDLDAEDWADPLMVSEYVVDIFEYLNELEIET--MPSPTYMDRQKELAWKMRGILTDWLIEVHSRFRLLPETLFLAVNIIDR   266
gi|50307537|ref|XP_453748.1|        CPAVNVGNSLAPMPIDENANNSASSVELRAKQLQVEDSKKRPISTVVEQTLPKKFKVCEKG--KEYEWEDLDEEDINDPFMVSEYVTDIFEYLHRLEMMT--LPNRHELFKHANIQQN-RDILVNWMVKIHNKFGLLPETLYLALNIMDR   337
gi|45184922|ref|NP_982640.1|        --SSDCTTSTGQLTESTAGELTTTQNQLRPSVAVAESKKKRPISTIVEPEELKKFKISDQG--NQCEWEDLDAEDINDPFMVSEYVNDIFEYLHKLEVMT--LPNRHDLFKHANIQQN-RDILVNWMVKIHNKFGLLPETLYLALNIMDR   350
gi|6325376|ref|NP_015444.1|         ------TEVVHNSVENEKLHPARSQLQVRNTESETDSGKKRPISTIVEQELPKKFKVCDENGKEEYEWEDLDAEDVNDPFMVSEYVNDIFEYLHQLEVIT--LPKKEDLYQHRNIHQN-RDILVNWLVKIHNKFGLLPETLYLAINIMDR   291
                                    .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
```

```
                                    ::              ***** :.:::::****:  * : .:   ::      :*   *  :.  :.  :   *     ** *  *        . : ::: *:  :..       **  .::    :    :                 *  .: .:
gi|158293720|ref|XP_315060.4|       YLQTMKTVPKKKLQLVGVTAMFIASKYEELFPPEIQDFVYITDDTYQKYQILEMEKEMVRTLDFNLGKPLPTHFLRRFSKAAKASDVNHVLAKYLIELASVDYST-AHYKPSEIAAAALYISLYLFPLTSNGGNGTSAIIWTKTLEHYTH   400
gi|158293718|ref|XP_315059.4|       YLQTMKTVPKKKLQLVGVTAMFIASKYEELFPPEIQDFVYITDDTYQKYQILEMEKEMVRTLDFNLGKPLPTHFLRRFSKAAKASDVNHVLAKYLIELASVDYST-AHYKPSEIAAAALYISLYLFPLTCNGGNGTSAIIWTKTLEHYTH   400
gi|24658583|ref|NP_726246.1|        YLQVVKDTKRTYLQLVGVTALFIATKYEELFPPAIGDFVFITDDTYTARQIRQMELQIFKAIDCNLSRPLPIHFLRRYSKAAGAEDEHHTMSKYFIELASVDYEM-ATYRPSEIAAASLFLSLHLLNGNHRAGTGFNDRHWTPTLTFYSR   463
gi|51762951|ref|XP_485921.1|        FMQNS-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAYVTNNTYTKHQIRQMEMKILRVLNFSLGRPLPLHFLCRASKVGEVDVEQHTLAKYLMELSMLDYDM-VHFAPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   367
gi|28195398|ref|NP_758505.2|        FMQNS-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTNNTYTKHQIRQMEMKILRVLNFSLGRPLPLHFLRRASKVGEVDVEQHTLAKYLMELSMLDYDM-VHFAPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   367
gi|25282457|ref|NP_741988.1|        FMQDS-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTNNTYTKHQIRQMEMKILRVLNFSLGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELSMLDYDM-VHFAPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   360
gi|14327896|ref|NP_114172.1|        FMQNN-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELTMLDYDM-VHFPPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   370
gi|114599953|ref|XP_517728.2|       FMQNN-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELTMLDYDM-VHFPPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   473
gi|73988334|ref|XP_851164.1|        FMQNN-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRSLNFGLGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELSMLDYDM-VHFPPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   362
gi|73949659|ref|XP_850398.1|        FMQNN-CVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRSLNFGLGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELSMLDYDM-VHFPPSQIAAGAFCLALKILDNGE----------WTPTLQHYLS   362
gi|114052292|ref|NP_001039337.1|    FMQDT-YVPKKMLQLVGVTAMFVASKYEEMYPPEIGDFAFVTDNTYTKFQIRQMEMKILRALNFSLGRPLPLHFLRRASKIGEVDVELHTLAKYLMELTMLDYDM-VHFPPSQIAAGAFCLALKVLDNGE----------WTPTLQHYLS   364
gi|20373137|ref|NP_571588.1|        FLQDH-PVPKKQLQLVGVTAMFIASKYEEMYPPEIADFAFVTDRAYTTSQIREMEMKVLRVLNFGFGRPLPLQFLRRASKIGDVTAEHHTLAKYFLELTMVDYDM-VHYPPSQMASAAYALTLKVFNCGD----------WTPTLQHYMG   337
gi|15239938|ref|NP_196233.1|        FLSVK-AVPKRELQLVGISALLIASKYEEIWPPQVNDLVYVTDNAYSSRQILVMEKAILGNLEWYLTVPTQYVFLVRFIKASMSDPEMENMVHFLAELGMMHYDT-LTFCPSMLAASAVYTARCSLNKSP---------AWTDTLQFHTG   383
gi|22330995|ref|NP_187759.2|        FLSLK-TVPRRELQLVGVSALLIASKYEEIWPPQVNDLVYVTDNSYNSRQILVMEKTILGNLEWYLTVPTQYVFLVRFIKASGSDQKLENLVHFLAELGLMHHDS-LMFCPSMLAASAVYTARCCLNKTP---------TWTDTLKFHTG   360
gi|15235573|ref|NP_195465.1|        FLSVK-PVPRKELQLVGLSALLMSAKYEEIWPPQVEDLVDIADHAYSHKQILVMEKTILSTLEWYLTVPTHYVFLARFIKASIADEKMENMVHYLAELGVMHYDTMIMFSPSMVAASAIYAARSSLRQVP---------IWTSTLKHHTG   367
gi|145615516|ref|XP_360272.2|       FLSEK-VVQLDRLQLVGITAMFIASKYEEVMSPHVTNFRHVTDDGFSESEILSAERFILSTLNYDLSYPNPMNFLRRVSKADNYDTPCRTIGKYLMEISLLDHRF-LQYRPSLVAASAMALSRIILDRGE----------WDKTISYYSG   429
gi|32423039|ref|XP_331957.1|        FLSEK-VVQLDRLQLVGITAMFVASKYEEVLSPHIANFRHVADDGFTEAEILSAERFILSTLNYDLSYPNPMNFLRRISKADNYDIQSRTLGKYLMEISLLDHRF-MPYRPSHVAAAAMYLARLILGRGE----------WDKTIAYYAG   441
gi|19111963|ref|NP_595171.1|        FLSLR-VCSLNKLQLVGIAALFIASKYEEVMCPSVQNFVYMADGGYDEEEILQAERYILRVLEFNLAYPNPMNFLRRISKADFYDIQTRTVAKYLVEIGLLDHKL-LPYPPSQQCAAAMYLAREMLGRGP----------WNRNLVHYSG   404
gi|50307537|ref|XP_453748.1|        FLCKE-LVQLEKLQLVGTACLFIASKYEEVYSPSVKHFAYETDGACDEEEIKEGEKFILKTLEFNLNYPNPMNFLRRISKADDYDIQSRTLAKYLLEISIVDFKF-IGILPSLCAAASMFLSRKMLGKGQ----------WDGNLIHYSG   475
gi|45184922|ref|NP_982640.1|        FLGKE-LVQLEKLQLVGTACLFIASKYEEVYSPSVKHFAYETDGACDEEEIKEGEKFILKTLQFNLNYPNPMNFLRRISKADDYDIQSRTLAKYLLEISVVDFKF-IGILPSLCAAASMFLSRKMLGKGK----------WDGNLIHYSG   488
gi|6325376|ref|NP_015444.1|         FLGKE-LVQLDKLQLVGTSCLFIASKYEEVYSPSIKHFASETDGACTEDEIKEGEKFILKTLKFNLNYPNPMNFLRRISKADDYDIQSRTLAKFLLEISLVDFRF-IGILPSLCAAAAMFMSRKMLGKGK----------WDGNLIHYSG   429
                                    .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
```

```
                                  :    :    . :                    **
gi|158293720|ref|XP_315060.4|     -YNVKYLAPIVQRLANVIKAVPKMM--EKKQKSCWLKYSSSKFLKISTHSKLKGTEMDTLAEGKLIF-----------------------------   464
gi|158293718|ref|XP_315059.4|     -YNVKYLAPIVQRLANVIKAVPKMM--DKKVKYPWLKYSSSKFQCISTHPKLKGSEIEELLNNELRC-----------------------------   464
gi|24658583|ref|NP_726246.1|      -YSAAHLRPITRLIAKLARDAP-----QAKLKAIYNKYQGSKFQKIALRTELTGALMDSIVGQSQRK-----------------------------   524
gi|51762951|ref|XP_485921.1|      -YSEDSLLPVMQHLAKNVVMVNCG---LTKHMTFKNKYAASKHAKISTLAQLNSALVQNLSKAVTKAYLQWTATSADAVGTMCRLYIGYLPCLLALQ   460
gi|28195398|ref|NP_758505.2|      -YSEDSLLPVMQHLAKNVVMVNCG---LTKHMTVKNKYAASKHAKISTLAQLNCTLVQNLSKAVTKA-----------------------------   430
gi|25282457|ref|NP_741988.1|      -HTEESLLPVMQHLAKNIVMVNRG---LTKHMTIKNKYATSKHAKISTLAQLNCTLVQNLSKAVTKA-----------------------------   423
gi|14327896|ref|NP_114172.1|      -YTEESLLPVMQHLAKNVVMVNQG---LTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV-----------------------------   433
gi|114599953|ref|XP_517728.2|     -YTEESLLPVMQHLAKNVVMVNQG---LTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV-----------------------------   536
gi|73988334|ref|XP_851164.1|      -YTEESLLNVMQHLAKNIVMVNRG---LTKHMTIKNKYAASKHAKISTLAQLNSALVQDLAKAVAKV-----------------------------   425
gi|73949659|ref|XP_850398.1|      -YTEESLLNVMQHLAKNIVMVNRG---LTKHMTIKNKYAASKHAKISTLAQLNSALVQDLAKAVAKV-----------------------------   425
gi|114052292|ref|NP_001039337.1| -YTEESLLVVMQHLAKNVVMVNRG---LTKHMTIKNKYATSKHAKISTLAQLNSALVQDLAKAVAKV-----------------------------   427
gi|20373137|ref|NP_571588.1|      -YTEDELVPVMQHIAKNVVRVNEG---LSKHLAVKNKYSSQKQMRIATISQLKSSLIKDLAKQIS----------------------------   398
gi|15239938|ref|NP_196233.1|      -YTESEIMDCSKLLAFLHSRCGE-----SRLRAVYKKYSKAENGGVAMVSPAKSLLSAAADWKKPVSS-----------------------------   445
gi|22330995|ref|NP_187759.2|      -YSESQLMDCSKLLAFIHSKAGE-----SKLRGVLKKYSKLGRGAVALISPAKSLMSSAP-----------------------------------   414
gi|15235573|ref|NP_195465.1|      -YSETQLMDCAKLLAYQQWKQQEEGSESSTKGALRKKYSKDERFAVALIPPAKALLTGTESA----------------------------------   428
gi|145615516|ref|XP_360272.2|     -YNEDDVEPVVNLMVDYLSRPVIH-------EAFFKKYASKKFFKA-----------------------------IDQL---------------   471
gi|32423039|ref|XP_331957.1|      -YTEEEIEPVFHLMVDYLARPVIH-------EAFFKKYGSKKFLKASILTRQWAKKNAVLYGVVDAEIPLDKLKDRPVDQLP---------------   515
gi|19111963|ref|NP_595171.1|      -YEEYQLISVVKKMINYLQKPVQH-------EAFFKKYASKKFMKASLFVRDWIKKNSIPLGDDADEDYTFHKQKRIQHDMKDEEW-----------   482
gi|50307537|ref|XP_453748.1|     GYTKDELAPVCNMVMEYLVQPVVH-------DELFKKYASRRFMKASVISRQWAKKVM--------------SHNYDIMTLHDSE------------   539
gi|45184922|ref|NP_982640.1|     GYSTTELAPICNMLMDYLVQPVVH-------DELFKKYASRRFMKASVISRQWAKKVM--------------TRSYDIMTLHETQTEY---------   555
gi|6325376|ref|NP_015444.1|      GYTKEELAPVCHMIMDYLVSPIVH-------DEFHRKYQSRRFMKASIISVQWALKVR--------------KNGYDIMTLHE--------------   491
                                 .......610.......620.......630.......640.......650.......660.......670.......680.......690.......
```