```
gi|18858119|ref|NP_572332.1|      ------------------------------------------------------------------------------------------------------------
gi|158301201|ref|XP_320934.4|     ------------------------------------------------------------------------------------------------------------
gi|33468885|ref|NP_033916.1|      ------------------------------------------------------------------------------------------------------------
gi|51948388|ref|NP_001004208.1|  ------------------------------------------------------------------------------------------------------------
gi|7656952|ref|NP_055227.1|      ------------------------------------------------------------------------------------------------------------
gi|114565466|ref|XP_514016.2|    MNFDNSMYRCNISITWANSPSPGLKHNLQKKLLADSNRCLGRSIKLSARYVTSQGSLPWTIWPGHEANAAPPPTAASDDATTSELIDRERTKAGDSLVNFRLGLRRSGGEQDITLLGLPVRSRDLSVARRFGRRAEPDSAGRGGVGLGSA   150
gi|57088975|ref|XP_537183.1|      ------------------------------------------------------------------------------------------------------------
gi|77736602|ref|NP_001029981.1|  ------------------------------------------------------------------------------------------------------------
gi|50751150|ref|XP_422279.1|     ------------------------------------------------------------------------------------------------------------
gi|47086265|ref|NP_998052.1|     ------------------------------------------------------------------------------------------------------------
gi|18397342|ref|NP_564346.1|     ------------------------------------------------------------------------------------------------------------
gi|115440029|ref|NP_001044294.1| ------------------------------------------------------------------------------------------------------------
gi|124806625|ref|XP_001350775.1| ------------------------------------------------------------------------------------------------------------
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                                                                                                                  :  *: *:  :       .:   :       :
gi|18858119|ref|NP_572332.1|      ------------------------------------------------------------------------------------MS---LEQLKSDVAELAAFLQQAKGARVKDVLTTAKAEAEREIVN-LELKAKIAAER-------   53
gi|158301201|ref|XP_320934.4|     ------------------------------------------------------------------------------------MSREAIENLTLDLEEMRKLAGSAQRSRVQQMLAIDIRKLETDIQRQRDLLAAQAASSE--QTVA   62
gi|33468885|ref|NP_033916.1|      ------------------------------------------------------------------------------------MA-SVLEELQKDLEEVKVLLEKSTRKRLRDTLTSEKSKIETELKNKMQQKSQKKPE-----LDN   58
gi|51948388|ref|NP_001004208.1|  ------------------------------------------------------------------------------------MA-SALEELQKDLEEVKVLLEKSTRKRLRDTLTNEKSKIETELRNKMQQKSQKKPE-----FDN   58
gi|7656952|ref|NP_055227.1|      ------------------------------------------------------------------------------------------MASEELQKDLEEVKVLLEKATRKRVRDALTAEKSKIETEIKNKMQQKSQKKAEL----LDN   57
gi|114565466|ref|XP_514016.2|    RRGRVGGARLGGLCVLAVGGGGGCLAKVRDPSRAGGGPRSCAGSVWAQAAAPRLVWVGVCARFEGSARGFLFLPLRGCSSGLRPDPAP-MASEELQKDLEEVKVLLEKATRKRVRDALTAEKSKIETEIKNKMQQKSQKKAEL----LDN  295
gi|57088975|ref|XP_537183.1|      ------------------------------------------------------------------------------------MA-SALEELQKDLEEVKVLLEKANRKRVRDALTVEKSKIETEIKNKMQQKSQRKAEL----LDN   59
gi|77736602|ref|NP_001029981.1|  ------------------------------------------------------------------------------------MS-SALEELQKDLEEVKVLLEKATRKRVRDALTAEKSKIETEMKNKMQQKSQRKAEL----TEN   59
gi|50751150|ref|XP_422279.1|     ------------------------------------------------------------------------------------MA-AAREELQKDLEEVKELLAKATRKRLRDVLMMEKHKLELEIKNQPLPKPK---DV----IEE   56
gi|47086265|ref|NP_998052.1|     ------------------------------------------------------------------------------MDIN-ELIAGLETDLKEITSLQEKCERQRVRDILTQEQKKIEKELAQKRQQKQQ---------QEK   56
gi|18397342|ref|NP_564346.1|     ------------------------------------------------------------------------------------------MAEEVGLDLEELRQLQNIAKRPRVLNLINSEISNLEKLRDSAVSSNAKPKVPVTVPAPVS   60
gi|115440029|ref|NP_001044294.1| ------------------------------------------------------------------------------------------------MSADELRLDLEELRRLEGLAKRPRVLSALANEIRAVDAKLAKATEPQAPQAVAAGSPPVVA   61
gi|124806625|ref|XP_001350775.1| ------------------------------------------------------------------------------------MTTEEKINNLNDDLEELNTLLLSVKRENVKAKIQECIENINGEIIKLKINKNQMPNKITETKVQ-   64
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

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                                                  :  :.*:*.  .  :.::: : .*.    :.:   :   .:.   . ::. * .   . :*   *     .   :*   : :   *     .*  :    .   . .          :*   ::.::::: .*
gi|18858119|ref|NP_572332.1|      ---QATGSSEAKRYLHELTDYGWDQSAKFVKLFITLNGVQGCTEENVTVTYTPNSLQLHVRDLQGKDFGLTVNNLLHSIDVEKSYRKIKTDMVAIYLQKVED-KHWDVLTAIQKRLKQKKDSELSK----DGDNPESALVNIMKKMYNDG   195
gi|158301201|ref|XP_320934.4|     RPVQTSVPGDVRRYQVELKEYAWDQSDKFIKIFVTVNGVQQVPEDNVNVEFTENSFQLVISDLNNKDYIFVVNNLLNSIDAEKSYRRVKSDMVAIYLAKQGP-AKWAHLTLTAKRLQDLKDERMSDGKKATSDDPSAGLMNIMQQLYESG   211
gi|33468885|ref|NP_033916.1|      EKPAAVVAPLTTGYTVKISNYGWDQSDKFVKIYITLTGVHQVPTENVQVHFTERSFDLLVKNLNGKNYSMIVNNLLKPISVESSSKKVKTDTVIILCRKKAENTRWDYLTQVEKECKEKEKPSYDTEA-----DPSEGLMNVLKKIYEDG   203
gi|51948388|ref|NP_001004208.1|  EKPAAVVAPLTTGYTVKISNYGWDQSDKFVKIYITLTGVHQVPAENVQVHFTERSFDLLVKNLNGKNYSMIVNNLLKPISVESSSKKVKTDTVIILCRKKAENTRWDYLTQVEKECKEKEKPSYDTEA-----DPSEGLMNVLKKIYEDG   203
gi|7656952|ref|NP_055227.1|      EKPAAVVAPITTGYTVKISNYGWDQSDKFVKIYITLTGVHQVPTENVQVHFTERSFDLLVKNLNGKSYSMIVNNLLKPISVEGSSKKVKTDTVLILCRKKVENTRWDYLTQVEKECKEKEKPSYDTET-----DPSEGLMNVLKKIYEDG   202
gi|114565466|ref|XP_514016.2|    EKPAAVVAPITTGYTVKISNYGWDQSDKFVKIYITLTGVHQVPTENVQVHFTERSFDLLVKNLNGKSYSMIVNNLLKPISVEGSSKKVKTDTVLILCRKKVENTRWDYLTQVEKECKEKEKPSYDTET-----DPSEGLMNVLKKIYEDG   440
gi|57088975|ref|XP_537183.1|      EKPAAVVAPITTGYTVKISNYGWDQSDKFVKIYITLTGVHQVPTENVQVHFTERSFDLLVKNLNGKSYSMIVNNLLKPISVEGSSKKVKTDTVLILCRKKAENTRWDYLTQVEKECKEKEKPSYDTET-----DPSEGLMNVLKKIYEDG   204
gi|77736602|ref|NP_001029981.1|  EKPAAVVAPITTGYTVKISNYGWDQSDKFVKIYITLPGVHQVPAESVQVNFTERSFDLLVKNLNGKSYSMIVNNLLKPISVEGSSKKVKTDTVLILCRKKAENTRWDYLTQVEKECKEKEKPSYDTET-----DPSEGLMNVLKKIYEDG   204
gi|50751150|ref|XP_422279.1|     EKSS------LGGYTVKINNYGWDQSDKFIKIYVSLNGVQKLPAENVQVNFTERSFDLLVKNLNGKNYTMTFNNLLKPISVEGSSRKIKTDTVLVMCKKKRE-EKWECLTQVEKESKEKEKAAYDTS------DPSEGLMNLLKKMYAEG   193
gi|47086265|ref|NP_998052.1|      KESGDKTETTVKGYTVKINNYGWDQSDKFVKIYITLKGVHTIPAENVESSFTERGFNTLVKDLDGKNHQMTINNLLFPIIAAESSKKIKTDMVLIMCKKKSA-KKWDCLTQVEKQSKEKDKPSMGENA-----DPSEGLMSVLKKIYTDG   200
gi|18397342|ref|NP_564346.1|      SSGK--PVSSSALNYVTLGTFSWDQDNDKVKMYISLEGVD---EDKVQAEFKPMSLDIKIHDVQGKNYRCAIPKLCKEIMPEKCKVLVKPKRIVITMVKSSR-GNWLDIHHKED---KIKP-SLEKEK-----DPMAGIMGMMKNLYEDG   195
gi|115440029|ref|NP_001044294.1| AAAAPAPAAAAGVSYVTLGSFSWDQDAEKIKIYVFLEGVE---QDKVETTFKPMSVDTKFHDVKGKNYRCAIPKLHKEIVPEKCKVLVKPTKIIVTLYKASK-GNWLDLHFKED---KFKP-SMAKEK-----DPMSGIMDLMKNMYEEG   198
gi|124806625|ref|XP_001350775.1| -------LNDPIVSYNSVQSFAWNQERNKVTIFLTVKNVHTVGEEKISTVFEERSFEIKMNDVDKKHYRFCIKKLCDKIIPNKCSFKVKKDSVHVTLVKQEN-KHWENLHFKESPMSKIKPPSMDEQA-----EPSAMLMNMMKQLYQEG   201
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                  * . *: * *** ::.
gi|18858119|ref|NP_572332.1|      DSKTKQMIAKAWTESQDKAKLGKETGGGLDSFDDL--------------------   230
gi|158301201|ref|XP_320934.4|     DPETKRMINKAWHESQTKQKMPTLE-----------------------------   236
gi|33468885|ref|NP_033916.1|      DDDMKRTINKAWVESREKQAR-EDTEF---------------------------   229
gi|51948388|ref|NP_001004208.1|  DDDMKRTINKAWVESREKQAR-EDTEF---------------------------   229
gi|7656952|ref|NP_055227.1|      DDDMKRTINKAWVESREKQAK-GDTEF---------------------------   228
gi|114565466|ref|XP_514016.2|    DDDMKRTINKAWVESREKQAK-GDTEF---------------------------   466
gi|57088975|ref|XP_537183.1|      DDDMKRTINKAWVESREKQAK-GDTEF---------------------------   230
gi|77736602|ref|NP_001029981.1|  DDDMKRTINKAWVESREKQAK-GDTDF---------------------------   230
gi|50751150|ref|XP_422279.1|     DDEMKRTINKAWVESREKQSK-GDIPMDI--------------------------   221
gi|47086265|ref|NP_998052.1|      DDEMKRTINKAWVESQEKKAKPDDFDF---------------------------   227
gi|18397342|ref|NP_564346.1|      DEEMKKTIAKAWTDARSGKAADPLKGL---------------------------   222
gi|115440029|ref|NP_001044294.1| DEDMKRTIAKAWSDARSGKTADSVRGLP---------------------------   226
gi|124806625|ref|XP_001350775.1| DSDMKRTIAKAWCEANEKKSDFSVIIYVIIYILYFFLRNMYLCLTTKIYYHFDEA   256
                                  .......460.......470.......480.......490.......500.....
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