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                                 :  :.  :*:******:**:.         . .*:*:***: * **:***::****:**:.. .     *.* :::        : ::**.*. ***: ::                          :.:  *:  .:
gi|34556205|ref|NP_904326.1|     ----MENFQKVEKIGEGTYGVVYKAKNKLT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|41054836|ref|NP_955795.1|     ----MENFQKVEKIGEGTYGVVYKAKNKLT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|62460564|ref|NP_001014934.1|  ----MENFQKVEKIGEGTYGVVYKAKNKLT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|16936528|ref|NP_001789.2|     ----MENFQKVEKIGEGTYGVVYKARNKLT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|114644318|ref|XP_522432.2|    ----MENFQKVEKIGEGTYGVVYKARNKLT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|73968301|ref|XP_848347.1|     ----MENFQKVEKIGEGTYGVVYKAKNKVT---GEVVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLLDVIHTEN----KLYLVFEFLHQDLKKFMDASALTG------------------IPLPLIKSYLFQLLQGLA   116
gi|50811836|ref|NP_998571.1|     ----MESFQKVEKIGEGTYGVVYKAKNKVT---GETVALKKIRLDTETEGVPSTAIREISLLKELNHPN----IVKLRDVIHTEN----KLYLVFEFLHQDLKRFMDSTSVSG------------------ISLPLVKSYLFQLLQGLA   116
gi|50304029|ref|XP_451964.1|     MS-ELTNYKRLEKVGEGTYGVVYKAVDLR--HQNRVVAMKKIRLESEDEGVPSTAIREISLLKELKDDN----IVRLYDIVHSDA---HKLYLVFEFLDLDLKRYMESIPKDQP------------------LGGNIIKKFMMQLCKGIA   122
gi|45187931|ref|NP_984154.1|     MS-DLTNYKRLEKVGEGTYGVVYKAVDLR--HGQRIVALKKIRLESEDEGVPSTAIREISLLKELKDDN----IVRLYDIVHSDA---HKLYLVFEFLELDLKRYMESVPKDQP------------------LGDKIIKKFMMQLCKGIA   122
gi|6319636|ref|NP_009718.1|      MSGELANYKRLEKVGEGTYGVVYKALDLRPGQGQRVVALKKIRLESEDEGVPSTAIREISLLKELKDDN----IVRLYDIVHSDA---HKLYLVFEFLDLDLKRYMEGIPKDQP------------------LGADIVKKFMMQLCKGIA   125
gi|39951439|ref|XP_363436.1|     ----MENYQKLEKIGEGTYGVVYKARDLL--NGGRIVAMKKIRLEAEDEGVPSTAIREISLLKEMRDPN----IVRLFNIVHTDG---TKLYLVFEFLDLDLKKYMEALPVADGGRGKALPEGTGPQLSRLGLGDTMIKKFMSQLCDGVR   137
gi|32419969|ref|XP_330428.1|     ----MENYQKLEKIGEGTYGVVYKARDLA--NSGRIVALKKIRLEAEDEGVPSTAIREISLLKEMRDPN----IVRLLNIVHADGGQGHKLYLVFEFLDLDLKKYMEALPVSDGGRGKALPEGTGAGLHNLGLGEDIIKKFMSQLCEGVR   140
gi|19112421|ref|NP_595629.1|     ----MENYQKVEKIGEGTYGVVYKARHKL---SGRIVAMKKIRLEDESEGVPSTAIREISLLKEVNDENNRSNCVRLLDILHAES----KLYLVFEFLDMDLKKYMDRISETGATS----------------LDPRLVQKFTYQLVNGVN   123
gi|115450343|ref|NP_001048772.1| ----MEQYEKEEKIGEGTYGVVYRARDKVTN---ETIALKKIRLEQEDEGVPSTAIREISLLKEMHHGN----IVRLHDVIHSEK----RIYLVFEYLDLDLKKFMDSCPEFA------------------KNPTLIKSYLYQILRGVA   116
gi|114443903|ref|NP_001045731.1| ----MEQYEKVEKIGEGTYGVVYKGKHRHTN---ETIALKKIRLEQEDEGVPSTAIREISLLKEMQHRN----IVRLQDVVHKEK----CIYLVFEYLDLDLKKHMDSSPDF------------------KNHRIVKSFLYQILRGIA   115
gi|18408696|ref|NP_566911.1|     ----MDQYEKVEKIGEGTYGVVYKARDKVTN---ETIALKKIRLEQEDEGVPSTAIREISLLKEMQHSN----IVKLQDVVHSEK----RLYLVFEYLDLDLKKHMDSTPDFS-----------------KDLHMIKTYLYQILRGIA   116
gi|124513848|ref|XP_001350280.1| ----MEKYHGLEKIGEGTYGVVYKAQNNYG----ETFALKKIRLEKEDEGIPSTTIREISILKELKHSN----IVKLYDVIHTKK----RLVLVFEHLDQDLKKLLDVCEGG-------------------LESVTAKSFLLQLLNGIA   114
gi|17738075|ref|NP_524420.1|     MTTILDNFQRAEKIGEGTYGIVYKARSNST---GQDVALKKIRLEGETEGVPSTAIREISLLKNLKHPN----VVQLFDVVISGN----NLYMIFEYLNMDLKKLMDKKKDV------------------FTPQLIKSYMHQILDAVG   119
gi|158292393|ref|XP_562342.3|    -MQRVGVYDRVDKIGEGTYGVVYKAKDIRT---QNYVALKRIRLDNETEGIPSTAMREISLLKDLKHHS----IVELFDVVIIDA----SIYMVFEYLDMDLKKMLDRHKSS------------------FTPMLVKSYMHQMLDAIA   118
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 :** .*::**********::   . :*:.******:...*:* :***:********::*:* : *.. :* **:****:**                                  .:*.* ** *:: :**
gi|34556205|ref|NP_904326.1|     FCHSHRVLHRDLKPQNLLINA-EGSIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEMHLVCTQHHAKCCGEHRRNGRHSLCPLCSYLEVAASQGGGMTAVSAPHPVTRRALFPGDSEIDQLFRIFR   265
gi|41054836|ref|NP_955795.1|     FCHSHRVLHRDLKPQNLLINA-EGSIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEM-----------------------------------------------VTRRALFPGDSEIDQLFRIFR   217
gi|62460564|ref|NP_001014934.1|  FCHSHRVLHRDLKPQNLLINA-DGSIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEM-----------------------------------------------VTRRALFPGDSEIDQLFRIFR   217
gi|16936528|ref|NP_001789.2|     FCHSHRVLHRDLKPQNLLINT-EGAIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEM-----------------------------------------------VTRRALFPGDSEIDQLFRIFR   217
gi|114644318|ref|XP_522432.2|    FCHSHRVLHRDLKPQNLLINT-EGAIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEM-----------------------------------------------VTRRALFPGDSEIDQLFRIFR   217
gi|73968301|ref|XP_848347.1|     FCHSHRVLHRDLKPQNLLINA-EGAIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEMHLVCTQHHARCCGEHRRNGRHSLCPLCSYLEVAASQGGGMTAVSTPHPVTRRALFPGDSEIDQLFRIFR   265
gi|50811836|ref|NP_998571.1|     FCHSHRVLHRDLKPQNLLINA-QGEIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEM-----------------------------------------------ITRRALFPGDSEIDQLFRIFR   217
gi|50304029|ref|XP_451964.1|     YCHAHRIIHRDLKPQNLLINR-DGNLKLGDFGLARAFGVPLRAYTHEIVTLWYRAPEVLLGGKQYSTGVDVWSIGCIFAEM-----------------------------------------------CNRKPLFSGDSEIDQIFKIFR   223
gi|45187931|ref|NP_984154.1|     YCHAHRIIHRDLKPQNLLINR-NGNLKLGDFGLARAFGVPLRAYTHEIVTLWYRAPEVLLGGKQYSTGVDVWSIGCIFAEM-----------------------------------------------CNRKPLFSGDSEIDQIFKIFR   223
gi|6319636|ref|NP_009718.1|      YCHSHRILHRDLKPQNLLINK-DGNLKLGDFGLARAFGVPLRAYTHEIVTLWYRAPEVLLGGKQYSTGVDTWSIGCIFAEM-----------------------------------------------CNRKPIFSGDSEIDQIFKIFR   226
gi|39951439|ref|XP_363436.1|     YCHSHRILHRDLKPQNLLIDR-EGNLKLADFGLARAFGVPLRTYTHEVVTLWYRAPEILIGGRQYSTGVDMWSVGCIFAEM-----------------------------------------------CTRKPLFPGDSEIDEIFKIFR   238
gi|32419969|ref|XP_330428.1|     YCHSHRVLHRDLKPQNLLIDR-DGNLKLADFGLARAFGVPLRTYTHEVVTLWYRAPEILLGGRQYSTGVDMWSVGCIFAEM-----------------------------------------------CTRKPLFPGDSEIDEIFKIFR   241
gi|19112421|ref|NP_595629.1|     FCHSRRIIHRDLKPQNLLIDK-EGNLKLADFGLARSFGVPLRNYTHEIVTLWYRAPEVLLGSRHYSTGVDIWSVGCIFAEM-----------------------------------------------IRRSPLFPGDSEIDEIFKIFQ   224
gi|115450343|ref|NP_001048772.1| YCHSHRVLHRDLKPQNLLIDRRTNALKLADFGLARAFGIPVRTFTHEVVTLWYRAPEILLGSRQYSTPVDMWSVGCIFAEM-----------------------------------------------VNQKPLFPGDSEIDELFKIFR   218
gi|115443903|ref|NP_001045731.1| YCHSHRVLHRDLKPQNLLIDRRTNSLKLADFGLARAFGIPVRTFTHEVVTLWYRAPEILLGARHYSTPVDMWSVGCIFAEM-----------------------------------------------VNQKPLFPGDSEIDELFKIFS   217
gi|18408696|ref|NP_566911.1|     YCHSHRVLHRDLKPQNLLIDRRTNSLKLADFGLARAFGIPVRTFTHEVVTLWYRAPEILLGSHHYSTPVDIWSVGCIFAEM-----------------------------------------------ISQKPLFPGDSEIDQLFKIFR   218
gi|124513848|ref|XP_001350280.1| YCHDRRVLHRDLKPQNLLINR-EGELKIADFGLARAFGIPVRKYTHEVVTLWYRAPDVLMGSKKYSTTIDIWSVGCIFAEM-----------------------------------------------VNGTPLFPGVSEADQLMRIFR   215
gi|17738075|ref|NP_524420.1|     FCHTNRILHRDLKPQNLLVDT-AGKIKLADFGLARAFNVPMRAYTHEVVTLWYRAPEILLGTKFYSTGVDIWSLGCIFSEM-----------------------------------------------IMRRSLFPGDSEIDQLYRIFR   220
gi|158292393|ref|XP_562342.3|    YCHLNRILHRDLKPQNLLIDR-EGHIKLADFGLARAVNFPIRVYTHEVVTLWYRAPEILLGTKFYCVGVDTWSLGCIFAEM-----------------------------------------------ILKRPLFPGDSEIDQLFKIFR   219
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|34556205|ref|NP_904326.1|     TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   346
gi|41054836|ref|NP_955795.1|     TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   298
gi|62460564|ref|NP_001014934.1|  TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   298
gi|16936528|ref|NP_001789.2|     TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   298
gi|114644318|ref|XP_522432.2|    TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   298
gi|73968301|ref|XP_848347.1|     TLGTPDEVVWPGVTS---MPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL---------------   346
gi|50811836|ref|NP_998571.1|     TLGTPDESIWPGVTS---MPDYKPSFPKWARQDLSKVVPPLDEDGRDLLGQMLTYDPNKRISAKNALVHRFFRDVTMPVPPLRL---------------   298
gi|50304029|ref|XP_451964.1|     VLGTPNERTWPDIIY---LPDFKTTFPKWNRRNLSEVIPSLDANGIDLLDKLITYDPIHRISAKRAVQHPYFKEE-----------------------   295
gi|45187931|ref|NP_984154.1|     LLGTPNESVWPDIVY---LPDFKPTFPKWQRRDLAQVVPSLNEHGLDLLDKLVTYDPIHRISAKRAVTHPYFKDE-----------------------   295
gi|6319636|ref|NP_009718.1|      VLGTPNEAIWPDIVY---LPDFKPSFPQWRRKDLSQVVPSLDPRGIDLLDKLLAYDPINRISARRAAIHPYFQES-----------------------   298
gi|39951439|ref|XP_363436.1|     LLGTPTEETWPSVTDEHIYPDFKPSFPKWQRDPNMKLCPGLNDAGLDLLEMMLVYDPAGRISAKQACNHPYFEDNTPAPPRR-----------------   320
gi|32419969|ref|XP_330428.1|     LLGTPTEDIWPGVTS---YPDFKASFPKWVRDYNVPLCQNLDDVGLELLESMLVYDPAGRISAKAACNHPYFEDYNPKPKSKYRDSSRYA---------   328
gi|19112421|ref|NP_595629.1|     VLGTPNEEVWPGVTL---LQDYKSTFPRWKRMDLHKVVPNGEEDAIELLSAMLVYDPAHRISAKRALQQNYLRDFH-----------------------   297
gi|115450343|ref|NP_001048772.1| VLGTPNEQSWPGVSS---LPDYKSAFPKWQAQDLATIVPTLDPAGLDLLSKMLRYEPNKRITARQALEHEYFKDLEMVQ-----------------------   294
gi|115443903|ref|NP_001045731.1| IMGTPNEETWPGVAS---LPDYISTFPKWPSVDLATVVPTLDSSGLDLLSKMLRLDPSKRINARAALEHEYFKDLEVA-----------------------   292
gi|18408696|ref|NP_566911.1|     IMGTPYEDTWRGVTS---LPDYKSAFPKWKPTDLETFVPNLDPDGVDLLSKMLLMDPTKRINARAALEHEYFKDLGGMP---------------------   294
gi|124513848|ref|XP_001350280.1| ILGTPNSKNWPNVTE---LPKYDPNFTVYEPLPWESFLKGLDESGIDLLSKMLKLDPNQRITAKQALEHAYFKENN-----------------------   288
gi|17738075|ref|NP_524420.1|     TLSTPDETNWPGVTQ---LPDFKTKFPRWEGTNMPQPIT--EHEAHELIMSMLCYDPNLRISAKDALQHAYFRNVQHVDHVALPVDPNAGSASRLTRLV   314
gi|158292393|ref|XP_562342.3|    QMGTPDETKWPGVSH---LSDYKESFPYWEPQPLPNEMQH-DLDAHTLFCELMHYDPTKRLSPKSAMSHSYFDNVSLVPPEL-----------------   297
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.........
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