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                                                 *                 :::    :* ****.*::.*.:  .    ***:: :   ::*:* *.:    ::::*    *..:: * .*       *   *   :::*: : **   : . *  *:.    :
gi|17137264|ref|NP_477196.1|      --------MSYVRQLKRQKMSQAKKF----GDGDPFNYQELNIIGEGAYGTVYRARDVITG-NIVALKKVRISLNENGVPMSTLREISLLKQLNASNHANIVKLYEVCQ--FLERDGQLLILLVFEHVEQDLSDLIDRLPKSGMSPPTIQ   150
gi|158294832|ref|XP_315841.3|     -------------------MNTS-------------NYEELGVIGTGAYGTVYRARDLKNAGTIVALKKVRVALTEDGVPMSTLREIFMLKQLDTFGHPNVVKLLDVCQGQRLEREGQLVLFLVFEHLDHDLDEYIKRLPPKGMPPATIQ   150
gi|223718134|ref|NP_001138778.1|  -------------------MEKDGL------CRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|114614484|ref|XP_001167181.1|  -------------------MEKDGL------CRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|73976283|ref|XP_852360.1|      -------------------MEKDGL------SRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIPASGVLRHLETFEHPSVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|119890699|ref|XP_589151.3|     -------------------MEKDGL------SRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|14149637|ref|NP_034003.1|      -------------------MEKDSL------SRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTSEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|62646797|ref|XP_342639.2|      -------------------MEKDSL------SRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|56118456|ref|NP_001007893.1|   -------------------MDKDGT------NLADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTSEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLDKVPEPGVPTETIK   150
gi|189532619|ref|XP_001345361.2|  -------------------MDKE---------SSTQQYEPVAEIGEGAYGKVYKARDLKNGGRFVALKRVRVQTEEEGMPLSTIREVAVLRQLESFEHPNVVRLFDVCTVSRTDRETKLT--LVFEHVDQDLTTYLEKAPDPGVPPETIK   150
gi|17551220|ref|NP_510256.1|      MCENLYGEEYKMEILRLQKMMNNMTCGQMAKPLTMKDFQIHQALGKGAYGNVYRVRSLHDG-KDYALKQIMISSKNEGIPQSVLREITVMKHLARKAHPNIISLKSVFHQLDPVR-AILKINMIMERCDWDLHTFLRNIPR-GVPEQQAK   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|17137264|ref|NP_477196.1|      RLSRELLTGVDFLHSHRIIHRDLKPQNLLVSSQGHLKIADFGLAKTYGSEMKLTS-VVVTLWYRAPEVLLAQPYNSTVDIWSAACIIFEMFNRRALFPGTSEKNQLDRIFELTGRPTEQQWPQTISVALEHFPQRHPKRPKDFCPHLCKY   300
gi|158294832|ref|XP_315841.3|     RLSREMLTGIDFLHSHRIIHRDLKPQNLLISSDGHLKLADFGLAKTYDFEMKLTT-VVVTLWYRAPEVLLGEAYNSSVDIWSAGCIIAEMFQRQALFPGTAEGNQLERIFELTGRPSEAQWPRGISIVRENFRSTQRREPREFCPKLCDN   300
gi|223718134|ref|NP_001138778.1|  DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDEL   300
gi|114614484|ref|XP_001167181.1|  DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDEL   300
gi|73976283|ref|XP_852360.1|      DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSPQPIEKFVTDIDEQ   300
gi|119890699|ref|XP_589151.3|     DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRLAFHSKSPQPIEKFVTDIDEQ   300
gi|14149637|ref|NP_034003.1|      DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDIIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDEL   300
gi|62646797|ref|XP_342639.2|      DMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAELFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDEL   300
gi|56118456|ref|NP_001007893.1|   DMMLQLFRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTS-VVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGNSDVDQLGKIFDVIGLPEEEDWPNDVALPRNAFASRPAQPIEKFVPDIDDM   300
gi|189532619|ref|XP_001345361.2|  DMMYQLLQGLDFLHSHRVVHRDLKPQNILVTSGGQIKLADFGLARIYSFQMALTSVVVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRRPLFRGNSDVDQLGKIFDVVGVPSPEDWPQEVGLPQSAFSPRPAQPIENLVPDMDEL   300
gi|17551220|ref|NP_510256.1|      HVTAQIVRALDFLHTHSIIHRDLKPQNILLNRDQTVKLADFGLSKEYSNTTAFTT-LVVTLWYRSPEVLLQSYYNSTVDMWALGCIVSEIYCRQPLFVGQNEAEQLTDIFKKMGTPVGKDWPSESVIARDSFPQYRPTNLKDLSPQMSKQ   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|17137264|ref|NP_477196.1|      ADDLLNKMLSYDLHLRPSALACLEHDYFQ-----QEPL----------------   355
gi|158294832|ref|XP_315841.3|     ANDLLKSMLAFSRHERPSARQCLNHAYFK-----QEPMPT---------------   355
gi|223718134|ref|NP_001138778.1|  GKDLLLKCLTFNPAKRISAYSALSHPYFQDLERCKENLDSHLPPSQNTSELNTA-   355
gi|114614484|ref|XP_001167181.1|  GKDLLLKCLTFNPAKRISAYSALSHPYFQDLERCKENLDSHLPPSQNTSELNTA-   355
gi|73976283|ref|XP_852360.1|      GKDLLLKCLTFNPAKRISAYSALSHPYFHDLERCKENLDSHLPPSQNSSEMNTA-   355
gi|119890699|ref|XP_589151.3|     GKDLLLKCLTFNPAKRISAYSALSHPYFHDLERRKENLDSHLPPSQNSSEMNTA-   355
gi|14149637|ref|NP_034003.1|      GKDLLLKCLTFNPAKRISAYGALNHPYFQDLERYKDNLNSHLPSNQSTSELNTA-   355
gi|62646797|ref|XP_342639.2|      GKDLLLKCLTFNPAKRISAYGALNHPYFQDLERYKDNLHSHLSSSQSTSELNTA-   355
gi|56118456|ref|NP_001007893.1|   GKDLLLKCLAFNPAKRISAYAALSHPYFHDLEKCKENLDSHMSSSQNSSEVNAS-   355
gi|189532619|ref|XP_001345361.2|  GKSLLLS----------------------LDSTSKSLYAQPFPSKKPSLEERAA   355
gi|17551220|ref|NP_510256.1|      AIEFVQQCLRYDHSKRLSARGALSHPFLKPAVATKSRVLKQINFNK--------   355
                                  .......310.......320.......330.......340.......350.....
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