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                                 *****:******:*..********:*******:*.***** *.:*    *:* :. **:*  *.* :.*   :..***...  :**. : :**:.. ::    :  :  *:**:    :  :  : *:* .:*************.
gi|23503237|ref|NP_061825.2|     MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYP-APYGPGPGQDKGFATSSYYPPAGGGYGR---AAPCDYGPAPAFYREKESACALSGADEQP-PFHPEPRKSDCAQ--DKSVFGETEEQKCSTPVYPWMQRMNSCNSSSFG   143
gi|114666344|ref|XP_001172963.1| MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYP-APYGPGPGQDKGFATSSYYPPAGGGYGR---AAPCDYGPAPAFYREKESACALSGADEQP-PFHPEPRKSDCAQ--DKSVFGETEEQKCSTPVYPWMQRMNSCNSSSFG   143
gi|21886813|ref|NP_032295.1|     MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYP-APYGPGPGQDKGFAASSYYPPAGGGYGR---AAPCDYGPAPAFYREKDAACALSGADEPP-PFHPEPRKSDCAQ--DKSVFGETEEQKCSTPVYPWMQRMNSCNSSSFG   143
gi|62656892|ref|XP_573182.1|     MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYP-APYGPGPGQDKGFAASSYYPPAGGGYGR---AAPCDYGPAPAFYREKDAACALSGADEPP-PFHPEPRKSDCAQ--DKSVFGETEEQKCSTPVYPWMQRMNSCNSSSFG   143
gi|194676061|ref|XP_887495.3|    MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYP-APYGPGPGQDKGFAASSYYPPAGGGYGR---AAPCDYGPAPAFYREKESACALSGADEPP-PFHPEPRKSDCAQ--DKSVFGEAEEQKCSTPVYPWMQRMNSCNSE---   140
gi|18858839|ref|NP_571194.1|     MSSYFLNSTFPVTLPGGQESFLGQIPLYSSGYTDPLRHYPGAAYGGSSVQEKAYP-SSFYQQANGAYSRATAAGPCDYATA-SFYREKDPACALASIEEHSFVLSQDHRKTDCTGSTGKSIYPEADEQKPSAPVYPWMQRMNSCNGT-FG   147
gi|125831460|ref|XP_001335190.1| MSSYFVNSTFPVSLPGGQESFLGQIPLYSSGYTDSLRHYPSATFGATNVQDKVYT-SSYYQQAGGVFGRSGSTSACDYSTP-NIYRSADRSCAIGSLEDSL-VLTQDQCKTDCTEQGTERYF--STEDKPCTPVYPWMQRMNSCNGMP-G   144
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                  *:*.* :*** *.********:*********:**:*****:*****************: *   .    *     .
gi|23503237|ref|NP_061825.2|     PSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKESKLLSASQLS---AEEEEEKQAE--------   224
gi|114666344|ref|XP_001172963.1| PSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKESKLLSASQLS---AEEEEEKQAE--------   224
gi|21886813|ref|NP_032295.1|     PSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKESKLLSASQLS---AEEEEEKPAE--------   224
gi|62656892|ref|XP_573182.1|     PSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKESKLLSASQLS---AEEEEEKPAE--------   224
gi|194676061|ref|XP_887495.3|    -DGKRSRTAYTRQQVLELEKEFHYNRYLTRRRRVEIAHALCLSERQIKIWFQNRRMKWKKDHKLPNTKIRSGGTAGSAGGPPGRPNGGPPAL   231
gi|18858839|ref|NP_571194.1|     NAGRRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKENKLINCSQTS---GEEEEEKRTE--------   228
gi|125831460|ref|XP_001335190.1| STGRRGRQTYTRFQTLELEKEFHFNRYLTRRRRIEISHALCLTERQIKIWFQNRRMKWKKENKAVNSAKVS---DEEDGGKAG---------   224
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240..
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