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                                  :* * : : *  :* :*:::*::***** : ***:******:*********: * *************:* ******:* *  *.: ** *:: ** *:. :**:***:::* .* ::*. ****.*:.*** : ..*:****
gi|61744424|ref|NP_001012982.1|  -------MKKLMVVLSLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGHLLCGGVLIHPLWVLTAAHCKKPNLQVFLGKHNLRQRESSQEQSSVVRAVIHPDYDAASHDQDIMLLRLARPAKLSELIQPLPLERDCSANTTSCHILGW   150
gi|73947861|ref|XP_533605.2|     -----MGMKTLIVAVILMAAAWAEEQNKVLHGGPCEQTSHPYQAALYTSGHLLCGGVLIHPLWVLTAAHCKKPNLQVYLGKHNLQQRESFQEQSSVVRAVAHPGYNAATHDQDIMLLRLARPAKFSERIQPLSLEQDCSANHSSCHILGW   150
gi|155372007|ref|NP_001094610.1| -----MAVKMLVIALVLVAAAQAEEKDKVLHGGPCEQTSHPYQAALYTAGHLLCGGVLIHPLWVLTAAHCKKPNLQVFLGKHNLQQREFFQEESSVIRTVAHPGYNAATHDQDIMLLRLSRPPRLSDHIQPLALERDCSANHTSCHILGW   150
gi|6755180|ref|NP_035307.1|      -------MKMLALCLVLAKSAWSEEQEKVVHGGPCLKDSHPFQAALYTSGHLLCGGVLIDPQWVLTAAHCKKPNLQVILGKHNLRQTETFQRQISVDRTIVHPRYNPETHDNDIMMVHLKNPVKFSKKIQPLPLKNDCSEENPNCQILGW   150
gi|9506997|ref|NP_062048.1|      MPTKMLTVKTLALCLILAKSAWSEDQDKVVHGGPCLKNSHPFQAALYTSGHLLCGGVLVGPQWVLTAAHCKKPNLEVYLGKHNLRQTETFQRQISVDRTIVHPRYNPQTHDNDIMMVHLKRPVKFSQRIQPLPLKKDCSEKNPDCQILGW   150
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                                  **  :*::*:***** ::**.**:*::***.:**:.*:**** : *:**************.:***:****::************:** : .**:. :: :
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gi|73947861|ref|XP_533605.2|     GKTADGDFPNTIQCAYIHLVPREECERAYPSQITQNMVCAGDEKYGKDSCQGDSGGPLVCGDRLRGLVSWGNVPCGSKEKPGVYTDVCRYGHWIRKTIQAN--   253
gi|155372007|ref|NP_001094610.1| GKMADGEYPDTIQCAYVHLVSREKCDHAYPGQITQNMVCAGDEKHGKDSCQGDSGGPLVCGDRLRGLVSWGNVPCGSKEKPGVYTDVCRYGHWIQRVIQAN--   253
gi|6755180|ref|NP_035307.1|      GKMENGDFPDTIQCADVHLVPREQCERAYPGKITQSMVCAGDMKEGNDSCQGDSGGPLVCGGRLRGLVSWGDMPCGSKEKPGVYTDVCTHIRWIQNILRNKWL   253
gi|9506997|ref|NP_062048.1|      GKMENGEFPDTIQCADVQLVSREECERAYPGKITRSMVCAGDKREGNDSCQGDSGGPLVCGGHLRGIVSWGDMPCGSKEKPGVYTDVCTHIRWIQNIIRNK--   253
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