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gi|4505205|ref|NP_002416.1|  --MMHLAFLVLLCLPVCSAVPLSGAAKEEDSNKDLAQOYLEKYINLEKDVKQ-FRRKDSNLIVKKIQGMOKFLGLEVTGKLDTDILEVMRKPRCGVDPVGHFSSFPQMPKWRKTHLYRIVNYPDLPRDAVDSAIEKALKVWEEVPLT 150
gi|114640098|ref|XP_001153881.1|  --MMHLAFLVLLCLPVCSAVPLSGAAKEEDSNRDLAQOYLEKYINLEKDVKQ-FRRKDSNLIVKKIQGMOKFLGLEVTGKLDTDILEVMRKPRCGVDPVGHFSSFPQMPKWRKTHLYRIVNHTPDLPRDAVDSAIEKALKVWEEVPLT 150
gi|9506899|ref|NP_062344.1|  --MEPLAAILALLSLPTICSAVPLHGAVTQGHPSMDLAQOYLEKYINFRKNEKQIFKRRKDSPPVVKKIEMOKFLGLEMTGKLDSENTMELMHKPRCGVDPVGGFSTFPQSPKWRKSHITRIVNYPDLPRQSVDSAIEKALKVWEEVPLT 150
gi|19424154|ref|NP_598198.1|  --MEPLAAILVLLCFPICSAVPLHGAVRQDHSIMDLAQOYLEKYINFRKNEKQIFKRRKDSPPVVKKIEMOKFLGLEMTGKLDSENTVEMMHKPRCGVDPVGGFSTFPQSPKWRKNHISYRIVNYTLDLPRESVDSAIEKALKVWEEVPLT 150
gi|94536884|ref|NP_001035381.1|  MAHWPAALILVVSLLTLCNGAPTITPSTED--RELAEAAYLSQFYRDSKAAKT-LGRMFVSNLENELEKAMQSFVGLVETGQLDSNTLKIIMKLPKRCVITDVARFGHFEGKPRWQSVVYTRITETTTQLSREVDSTIAKAFQLNSDVIIPVD 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|4505205|ref|NP_002416.1|  FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHDDDEKWTEDASGTLNLFVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSE 300
gi|114640098|ref|XP_001153881.1|  FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHDDDEKWTEDASGTLNLFVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSE 300
gi|9506899|ref|NP_062344.1|  FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHDDDEKWTEDASGTLNLFVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSE 300
gi|19424154|ref|NP_598198.1|  FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHDDDEKWTEDASGTLNLFVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSE 300
gi|94536884|ref|NP_001035381.1|  FKQIFSGTADIMILFKGGDHDGDFYFDGPNGLAHANSPPGEGGDTFHDDDEKWTEDASGTLNLFVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSE 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|4505205|ref|NP_002416.1|  DAISTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITIRKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 450
gi|114640098|ref|XP_001153881.1|  DAISTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITIRKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 450
gi|9506899|ref|NP_062344.1|  DAVSTLRGEVLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITIRKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 450
gi|19424154|ref|NP_598198.1|  DAVSTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITIRKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 450
gi|94536884|ref|NP_001035381.1|  DAASTRIRGELYFFKDRYWKQYYSGLTLEIKITWPSIDS-VDAAYEFQDKGQINFLFKGQFVAWVKGNTILSGYKPISTYGFSSVNNKIDAAVSVKSTRILFFVGSKYWVFNDRIKMDRGEFKSIADFPGIGSKVDAAFENYGY 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|4505205|ref|NP_002416.1|  FVFFSGSSQFEEDPNARMVTHILKSNWSLHC- 482
gi|114640098|ref|XP_001153881.1|  FVFFSGSSQFEEDPNARMVTHILKSNWSLHC- 482
gi|9506899|ref|NP_062344.1|  FVFFSGSSQFEEDPNARTVTHILKSNWSLHC- 482
gi|19424154|ref|NP_598198.1|  FVFFSGSSQFEEDPNARTVTHILKSNWSLHC- 482
gi|94536884|ref|NP_001035381.1|  LVFSDGARDEYIFASRRVNRVLLNNGWLDCC- 482
.....460.....470.....480..

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