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gi | 4505205 | ref | NP_002416.1 | --MMHLAFLVLLCLPVCSAVPLSGAAKEEDSNKDLAQOYLEKYINLEKDVKQ-FRRKDSNLIVKKIQGMOKFLGLEVTGKLDTDLEVMRKPRCGVDPVGHFSSFPQMPKWRKTHLYRIVNYPDLPRDAVDSAIEKALKVWEEVPLT 147
gi | 114640098 | ref | XP_001153881.1 | --MMHLAFLVLLCLPVCSAVPLSGAAKEEDSNRDLAQOYLEKYINLEKDVKQ-FRRKDSNLIVKKIQGMOKFLGLEVTGKLDTDLEVMRKPRCGVDPVGHFSSFPQMPKWRKTHLYRIVNHTPDLPRDAVDSAIEKALKVWEEVPLT 147
gi | 9506899 | ref | NP_062344.1 | --MEPLAAILLALLSLPICSAVPLHGAVTQGHPSMDLAQQOYLEKYINFRKNEKQIFKRRKDSPPVVKKIEMOKFLGLEMTGKLDSENTMELMHKPRCGVDPVGGFSTFPQSPKWRKSHITTYRIVNYTPDLPRQSVDSAIEKALKVWEEVPLT 148
gi | 19424154 | ref | NP_598198.1 | --MEPLAAILLALLSLPICSAVPLHGAVTQGHPSMDLAQQOYLEKYINFRKNEKQIFKRRKDSPPVVKKIEMOKFLGLEMTGKLDSENTMELMHKPRCGVDPVGGFSTFPQSPKWRKSHITTYRIVNYTPDLPRQSVDSAIEKALKVWEEVPLT 148
gi | 94536884 | ref | NP_001035381.1 | MAHWPAALILVVSLLTLCNGAPITTPSTED--RELAEAAYLSQFYRDSKAAKT-LGRMFVSNLENELEKAMQSFVGLVETGQLDSNTLKIIMKLPKRCVITDVARFGHFEGKPRWQSVVYTRITTEYTTQLSREVDSTIAKAFQLNSDVIIPVD 149
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 | FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHFDDEKWTEDASGQNLFLVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSF 295
gi | 114640098 | ref | XP_001153881.1 | FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHFDDEKWTEDASGQNLFLVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSF 295
gi | 9506899 | ref | NP_062344.1 | FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHFDDEKWTEDASGQNLFLVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSF 295
gi | 19424154 | ref | NP_598198.1 | FSRLYEGEADIMISFAVKEHGDFYSFDGPGHSLAHAYPPGPGLYGDIFHFDDEKWTEDASGQNLFLVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSF 295
gi | 94536884 | ref | NP_001035381.1 | FKQIFSGTADIMILFKGGDHDGDFYFDGPNGLAHANSPPGEGGDTHFDDEKWTEDASGQNLFLVAAHELGHSLGLFHSANTEALMYPLVNSFTELAQFRLSQDDVNGIQSLYGPPAST--EPLVPTKSVPSGSEMPAKCDPALSF 295
.....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 | DAISTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITRKKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 445
gi | 114640098 | ref | XP_001153881.1 | DAISTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITRKKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 445
gi | 9506899 | ref | NP_062344.1 | DAVSTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITRKKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 445
gi | 19424154 | ref | NP_598198.1 | DAVSTLRGEYLFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITRKKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 445
gi | 94536884 | ref | NP_001035381.1 | DAASTRIRGELYFFKDRYFWRSSHWNPEPEFHLLISAFWPSLPSYLDAAEYVNSRDTVFIFKGNFVAIRGNEVQAGYPRGIHTLGFPPITRKKIDAAVSDKEKKKTYFFAEDKYWRFDENSGSMEQGFPRLIADDFPGVEPKVDAVLQAFGF 445
.....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 | FVFFSGSSQFEFDPNARMVTHILKSNWLLHC- 476
gi | 114640098 | ref | XP_001153881.1 | FVFFSGSSQFEFDPNARMVTHILKSNWLLHC- 476
gi | 9506899 | ref | NP_062344.1 | FVFFSGSSQFEFDPNARTVTHILKSNWLLC- 476
gi | 19424154 | ref | NP_598198.1 | FVFFSGSSQFEFDPNARTVTHILKSNWLLC- 476
gi | 94536884 | ref | NP_001035381.1 | LVFSDGARDEYIFASRRVNRVLLNNGWLLDC- 475
.....460.....470.....480..

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