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gi | 4503123 | ref | NP_001892.1 | MTAASMGFVRFVAVVLLALCSRPAVGN-CSGPCRCPDEPAAPRCAGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 149
gi | 114609332 | ref | XP_518744.2 | MTAASVGPVRFVAVVLLALCSRPAVGN-CSGPCRGSDEPAAPRCAGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 149
gi | 27806677 | ref | NP_776455.1 | MSATGLGPVRCFAVLLALCSRPAASSDCCSAPCCCPAGAPAPRCAGVSLVLDGCGCC-VCAKQLSELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 149
gi | 6753878 | ref | NP_034347.1 | MLASVAGPISLALVLLA-LCTRPAATGDD-CSAQCQCAAEAAAPRCAGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFVFGGSVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 148
gi | 11560085 | ref | NP_071602.1 | MLASVAGPISLALVLLA-LCTRPAATGDD-CSAQCQCAAEAAAPRCAGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFVFGGSVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 147
gi | 45383590 | ref | NP_989605.1 | ----MSPASLAVALLLALLGPEVRGDE-CSGQCQCGSGPGPSCPAGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFVFGGSVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 144
gi | 62632756 | ref | NP_001015041.1 | ---MFGMTQSVIALLLFTLRWAVAGE-CSGQCCHCPEVP-PQCSPGVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRRIKIGVCTAKDGAPCFVFGGSVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLFSPDCP 145
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 4503123 | ref | NP_001892.1 | FPRRVKLPGKCCCEEWVCDEPKDQAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNASCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 299
gi | 114609332 | ref | XP_518744.2 | FPRRVKLPGKCCCEEWVCDEPKDQAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNASCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 299
gi | 27806677 | ref | NP_776455.1 | FPRRVKLPGKCCCEEWVSRDEKEHTAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNASCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 299
gi | 6753878 | ref | NP_034347.1 | FPRRVKLPGKCCCEEWVCDEPKDQAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNTFCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 298
gi | 11560085 | ref | NP_071602.1 | FPRRVKLPGKCCCEEWVCDEPKDQAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNTFCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 297
gi | 45383590 | ref | NP_989605.1 | YPRRVKLPGKCCCEEWVCDEAKQETAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGMGISTRVTNDNTFCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTA 294
gi | 62632756 | ref | NP_001015041.1 | MPRRVKLPGKCCCEEWVCSPRQNTAVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTSEWASCKTCGLGISTRVTNDNRCRLEKQSRICMVRPCEADLEENIKKGGKCIKIRPKISKPIKFKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTA 295
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 4503123 | ref | NP_001892.1 | TLVVEFKCPDGEVMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 349
gi | 114609332 | ref | XP_518744.2 | TLVVEFKCPDGEVMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 349
gi | 27806677 | ref | NP_776455.1 | TLVVEFKCPDGEVMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 349
gi | 6753878 | ref | NP_034347.1 | TLVVEFKCPDGEIMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 348
gi | 11560085 | ref | NP_071602.1 | TLVVEFKCPDGEIMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 347
gi | 45383590 | ref | NP_989605.1 | TLVVEFKCPDGEIMKKNMMFIKTCACHYCPGDNDIFESLYYRKMVGDMA 344
gi | 62632756 | ref | NP_001015041.1 | TLVMEFKCPDGEVMKKNMMFIKTCACHYCPGENDIFESMYKKMVGDMA 345
.....310.....320.....330.....340.....350

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