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gi | 6753748 | ref | NP_034258.1 | -----MLVLLAGLFVVHIAIIMLFVSTIANVVMV--ADYANASVGLWKNCTGGNCDGSLSYGNEDAIAKAVQAFMILSIIFSIIISLVVVFVOLFIMEKGNRFFLSSGSMMLVCWL 107
gi | 6978807 | ref | NP_036975.1 | -----MLVLLAGLFVVHIAIIMLFVSTIANVVMV--ADGIDSSIGLWKNCTSGSCDGSLSYGNDDAIAKAVQAFMILSIIFSIIISLVVVFVOLFIMEKGNRFFLSSGSMMLVCWL 107
gi | 4503559 | ref | NP_001414.1 | -----MLVLLAGIFVVHIAIVIMLFVSTIANVWLV--SNTVDASVGLWKNCTNISCSDSLAYSADALKTVQAFMILSIIFCVIALLVVVFOLFIMEKGNRFFLSSGATTLVCWL 107
gi | 114643707 | ref | XP_001156226.1 | -----MLVLLAGIFVVHIAIVIMLFVSTIANVWLV--SNTADASVGLWKNCTNVSCDSLAYSADALKTVQAFMILSIIFCVIALLVVVFOLFIMEKGNRFFLSSGATTLVCWL 107
gi | 119921838 | ref | XP_001251794.1 | -----MLVLLASIFVVHIAIVIMLFVSTIANVVMV--SDDLGTGSVGLWKNCTSGGCGDNLASYAGEDALKAVQAFMILSIIFSIVISLVVVFVOLFIMEKGNRFFLSSGATMLVCWL 107
gi | 119925978 | ref | XP_599688.3 | -----MLVLLASIFVVHIAIVIMLFVSTIANVVMV--SDDLGTGSVGLWKNCTSGGCGDNLASYAGEDALKAVQAFMILSIIFSIVISLVVVFVOLFIMEKGNRFFLSSGATMLVCWL 107
gi | 73997614 | ref | XP_543803.2 | -----MSKKEELRRRILREADAWARLGSSELGKDNNSHCSLRHQKAKMLVLLAGIFVVHIAIVIMLFVSTIANVVMV--SDFTKASVGLWKNCTSDGDDVLSYASADALKAVQAFMILSIIFSIVISLVVVFVOLFIMEKGNRFFLSSGATMLVCWL 148
gi | 50728614 | ref | XP_416203.1 | -----MLVLLAGIFVVHIAIVIMLFVSTIANVVMVGRSLSLGNVHWGLWMYNNTCEPLILSGDNEPSLKAAQAFMILSIIFSIVIALVTFIVOLFIMEKGNRFFLSSGATMLVCWL 109
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 6753748 | ref | NP_034258.1 | CILVGVSIYTHHYAHSE---GNFNSSSHQGYCFILTWICFCFSFIIGILYMLVLRKK 160
gi | 6978807 | ref | NP_036975.1 | CILIGVSIYTHHYAHSE---GNFFPSSHQGYCFILTWICFCFSFIIGILYMLVLRKK 160
gi | 4503559 | ref | NP_001414.1 | CILVGVSIYTHSHYANRD---GTQY---HHGYSYILGWICFCFSFIIGVLYLVLRKK 157
gi | 114643707 | ref | XP_001156226.1 | CILVGVSIYTHSRVANRD---GTQY---HHGYSYILGWICFCFSFIIGVLYLVLRKK 157
gi | 119921838 | ref | XP_001251794.1 | CVMVGASIVTHHYANGS---INNYEPSSHGYSFILTWICFCFSFIIGILYLVLRKK 160
gi | 119925978 | ref | XP_599688.3 | CVMVGASIVTHHYANGS---INNYEPSSHGYSFILTWICFCFSFIIGILYLVLRKK 160
gi | 73997614 | ref | XP_543803.2 | CIMVGVSIYTHHYANGS---GTQYQSSHGYSFILTWICFCFSFIIGVLYLVLRKK 201
gi | 50728614 | ref | XP_416203.1 | CILIGVSIYTHARFTDSQSVSQITLISHHGYSFILAWICFCFSFIIGILYLVLRKK 165
.....160.....170.....180.....190.....200.....

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