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gi | 21312514 | ref | NP_081570.1 | -----MEEQQRARSHVTITTS-SSFAENFSTSSSFAYDREFLRLPPGLLIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAIVDASSVSPE-KEGHNFNFSW 150
gi | 38454248 | ref | NP_942049.1 | -----MEEQQRARSHVTITTS-SSFAENFSTSSSFAYDREFLRLPPGLLIIAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSACALYLSAAIVDASSVSPE-KEGHNFNFSW 150
gi | 32130536 | ref | NP_849199.2 | -----MEEPQRARSHVTITTA-SSFAENFSTSSSFAYDREFLRLPGFLIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVSPE-RDSHNFNFSW 150
gi | 114586231 | ref | XP_516349.2 | -----MEEPQRARSHVTITTA-SSFAENFSTSSSFAYDREFLRLPPGLLIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVSPE-RDSHNFNFSW 150
gi | 57103824 | ref | XP_542744.1 | -----MEEPQRARSHVTITTA-SSFAENFSTSSSFAYDREFLRLPPGLLIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVSPE-RDSHNFNFSW 150
gi | 114052244 | ref | NP_001039823.1 | -----MEEPQRARSHVTITTA-SSFAENFSTSSSFAYDREFLRLPPGLLIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVSPE-RDSHNFNFSW 150
gi | 118086083 | ref | XP_418764.2 | MEEPPPLEQPPRPRSHVTITTS-SSFTANLSASSSTLAYDREFLRLPPGLLIVAEIVLGLLVWTLIAGTEYFLVPAFGWVMFVAVFYWVLTVFVFLIIVITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVKE-LDSHNFNFSW 150
gi | 123707695 | ref | NP_001074114.1 | ---MEVDSSESRIDSSADRTSRSSNLESLGLTHKLAYDGNFIRASGVLMVGEIVFGLFVWTLIGGTEYLHVPALRWVMFVSVFYWVLTVILFLLYLIHLHIRTWIPWNI LGMCFHGSATVLYLSAAVMCTLSLNVA NRGRYFICW 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 21312514 | ref | NP_081570.1 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 38454248 | ref | NP_942049.1 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 32130536 | ref | NP_849199.2 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 114586231 | ref | XP_516349.2 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 57103824 | ref | XP_542744.1 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 114052244 | ref | NP_001039823.1 | AASSFFAFLVTCYAGNTYFSFIAWRSRTIAC- 182
gi | 118086083 | ref | XP_418764.2 | AASSFFAFLVTCYAGNTYFSFIWQSRITLQ- 182
gi | 123707695 | ref | NP_001074114.1 | VASTIFASLALCLYAGNTAVNFKSWRSKSED- 182
.....160.....170.....180..

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