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gi | 59859878 | ref | NP_001159.2 | -----MG--APTLPPA-----WQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEEHKKHSSGCAFLSVKRFEEELTGEFLKLDKERAKNKIAKETNNKKKEFEETAEKVRRRAIEG 137
gi | 114670699 | ref | XP_001156931.1 | -----MG--APTLPPA-----WQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEEHKKHSSGCAFLSVKRFEEELTGEFLKLDKERAKNKIAKETNNKKKEFEETAKKVRCATIEG 137
gi | 50979204 | ref | NP_001003348.1 | -----MG--ASSLPPA-----WQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEEHKKHSSGCAFLSVKRFEEELTGEFLKLDKERAKNKIAKETNNKKKEFEETAKKVRCATIEG 137
gi | 87196503 | ref | NP_001001855.2 | -----MG--AQSLPPA-----WQFLKDHRISTFKNWPFLGCACTPERMAAAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEEHKKHSSGCAFLSVKRFEEELTGEFLKLDKERAKNKIAKETNNKKKEFEETAKKVRCATIEG 137
gi | 6753090 | ref | NP_033819.1 | -----MG--APALPQI-----WQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEEHKKHSSGCAFLSVKRFEEELTGEFLKLDKERAKNKIAKETNNKKKEFEETAKTTRQSIIEG 137
gi | 59938766 | ref | NP_001012318.1 | -----MAAYAEMLPKE-----WLVVYLVSTRAAATFRNWPFLGCACTPERMAAAGFVHCPSENSPDVVQCFFCLKELEGWEPDDDDPLEEHKHSAGCAFAALQKPSNLTVEEFLKLDKRTKKNVKKKAIQKETDIEDVAKGVRHAIEG 139
gi | 35902992 | ref | NP_919378.1 | -----MD---LASDDQ-----TKMYFYENRLQTFVGVWPFEEGCVCTPENMAKAGFIHCPSENSPDIAQCFFCLKELEGWEPDDDDPEEHKHSAGCAFAALQKPSNLTVEEFLKLDKERTKKNVKKKAIQKETDIEDVAKGVRHAIEG 136
gi | 21355525 | ref | NP_650608.1 | -----MESPVVNEVAASLGGEKLEVFRKLNLEQHRVESYKSWPFEPETASCISIKMAEAGFYWIGTKRENDTATCFVCGKTLDGWEPEDDDPKKEHVKHAPQCEFAKLSCEPERNLTVSQFLEILGTVVKGSIEKTCFAFKSSVRENEKRLDEFTR 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 59859878 | ref | NP_001159.2 | LAAMD- 142
gi | 114670699 | ref | XP_001156931.1 | LAAMD- 142
gi | 50979204 | ref | NP_001003348.1 | LAAAE- 142
gi | 87196503 | ref | NP_001001855.2 | LAALE- 142
gi | 6753090 | ref | NP_033819.1 | LAA--- 140
gi | 59938766 | ref | NP_001012318.1 | MGF--- 142
gi | 35902992 | ref | NP_919378.1 | LAMGEE 142
gi | 21355525 | ref | NP_650608.1 | NQK--- 153
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