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gi | 35902992 | ref | NP_919378.1 | ----MD---L-ASDD-----KMYFYENRLEQTFVGVGPPFEEGCVCTPENMAKAGFIHTPSSENSPDIAOCFFCLKELEGWEPEDDPEKHEKHAHSPSCDFILLKKTVDLSLTVEEFLKQKERQKFIKKSCGHAIKDFEDAVKLRNQIIG 136
gi | 292619632 | ref | XP_002664042.1 | ----MD---LASDD-----KMYFYENRLEQTFVGVGPPFEEGCVCTPENMAKAGFIHTPSSENSPDIAOCFFCLKELEGWEPEDDPEKHEKHAHSPSCDFILLKKTVDLSLTVEEFLKQKERQKFIKKSCGHAIKDFEDAVKLRNQIIG 136
gi | 292619640 | ref | XP_002664046.1 | ----MD---LASDD-----KMYFYENRLEQTFVGVGPPFEEGCVCTPENMAKAGFIHTPSSENSPDIAOCFFCLKELEGWEPEDDPE----- 73
gi | 59859878 | ref | NP_001159.2 | ----MG--APTLPFA-----WQPFKLDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLACFFCFKLELGWEPDDDDPIEHHKHSAGCAFLEVKKQFEELTLGEFLKLDREKAKKIAKETNNKKKQEFEEIAEKVRRAIEG 137
gi | 114670699 | ref | XP_001156931.1 | ----MG--APTLPFA-----WQPFKLDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLACFFCFKLELGWEPDDDDPIEHHKHSAGCAFLEVKKQFEELTLGEFLKLDREKAKKIAKETNNKKKQEFEEIAEKVRRAIEG 137
gi | 50979204 | ref | NP_001003348.1 | ----MG--ASSLPFA-----WOLYLKDHVRVSTFKNWPFLEGCACTPDRMAEAGFIHCPTENEPDLACFFCFKLELGWEPDDDDPIEHHKHSAGCAFLEVKKQFEELTLSEFLKLDKERAKKIAKETNNKQKQEFEEIAKKVRCATIEG 137
gi | 87196503 | ref | NP_001001855.2 | ----MG--AQSLPFA-----WOLYLKDHVRVSTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLACFFCFKLELGWEPDDDDPIEHHKHSAGCAFLEVKKQFEELTLSEFLKLDKERAKKIAKETNNKQKQEFEEIAKKVRCATIEG 137
gi | 6753090 | ref | NP_033819.1 | ----MG--APALPQI-----WOLYLKKNYRIATFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLACFFCFKLELGWEPDDDDPIEHHKHSAGCAFLEVKKQFEELTVSEFLKLDREKAKKIAKETNNKQKQEFEEIAKTTRQSIIEG 137
gi | 59938766 | ref | NP_001012318.1 | ----MAAVAEMLPKK-----WLVLVLSVTRAAIFRNWPFTEGCACTPERMAAAGFVHCPSSENSPDVVQCFCLKELEGWEPDDDDPIEHHKHSAGCAFAALQKDPENLTQVEEFLKLDKRRTKNVIKKAKISQKETDIEDVAKGVRRHAIEG 139
gi | 21355525 | ref | NP_650608.1 | MESPVVNEVAASLGGEKLEVFRRKLNLLLEQHRVESYKSWPFPEPTASCSISKMAEAGFYWTGIKRENDTATCFVCGKTLTDGWEPEDDPAWKEHVKKHAPQCEFAKLSCEPRLNLVSDLEILGTVVKGSIEKTCFAFKSSFVRENEKRLDEFTR 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 35902992 | ref | NP_919378.1 | TAMGEE 142
gi | 292619632 | ref | XP_002664042.1 | TAMGEE 142
gi | 292619640 | ref | XP_002664046.1 | ----- 73
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 | LAAAL- 142
gi | 6753090 | ref | NP_033819.1 | LAA--- 140
gi | 59938766 | ref | NP_001012318.1 | MGP--- 142
gi | 21355525 | ref | NP_650608.1 | NQK--- 153
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