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gi | 6680387 | ref | NP_032370.1 | MTWDGLPTQPLLMMLLFAAGSSSALAGCPGCGPMOTGCRGGCV EEDAGSPADGCTEAGGCLRREGQPCGVYSPKCAPGLQCPRENEETPLRALLIGGRCQRARGP--SEETTKESKPGGASRRSDTNHRDRQKNPRTSAAPI- 150
gi | 6981090 | ref | NP_037236.1 | MTWDGLPTQPLLMMLLFAAGSSSALAGCPGCGPVG-----EEDAGSPADGCAETGGCFRRREGQPCGVYIPKCAPGLQCPRENEETPLRALLIGGRCQRARGP--SEETTKESKPHGGASRRPD---RDROKNPRTSAAPI- 150
gi | 11321593 | ref | NP_002169.1 | MTPHRLLP-LLLLLALLLAASPGGALARCPGCGQGVQAGCPGGCV EEDGGSPAEGCAEAGCLRRREGQECGVYTPNCPAGLQCHPPKDEAPLRALLLGRGRCLPARAPAVABENPKESKPOAGTARPODVNRRDQORNPGTSTTPS- 150
gi | 114644526 | ref | XP_509089.2 | MTPHRLLP-LLLLLALLLAASPGGALARCPGCGQGVQAGCPGGCV EEDGGSPAEGCAEAGCLRRREGQECGVYTPNCPAGLQCHPPKDEAPLRALLLGRGRCLPARAPAVABENPKESKPOAGTARPODVNRRDQORNPGTSTTPS- 150
gi | 110626119 | ref | NP_001035585.1 | MTPHRLLP-LLLLLALLAARPGGALARCPGCGQGVQAGCPGGCA EEDGGSPAEGCAEAGCLRRREGQECGVYTPNCPAGLQCPPEKEDLPLRALLQGRGRCLPARAPAVABENPKESKPOAGTARSDVNRRDQORNPGTSTTPS- 150
gi | 73996267 | ref | XP_849343.1 | MTPHRLLP-LLLLLALLAARSGAALARCPGCGQGAQAGCPGACVQ EEDGGSPAEGCAEAGCLRRREGQECGVYTPNCPAGLQCPPEKEDLPLRALLLGRGRCLRRARGPAPARENPKESKPOAGTTRPODVNRRDQORNPGASTTTS- 150
gi | 238637259 | ref | NP_001154874.1 | MSFLSNLTAVVLLLVHCGSWCLAGRLGPHKNCPTCKDGHF-----SGAGRASRDPAAGASTVLAALGEPGCVYTLSCARGLRCPPEPREHSPQLALLQGRGFCAK-----HSRTSPNERPRP- 150
gi | 238637253 | ref | NP_001154873.1 | MSFLSNLTAVVLLLVHCGSWCLAGRLGPHKNCPTCKDGHF-----SGELKSHR--SGDEMTSMLALDEPCGVYTLPCALGLRCIPPTGEOPLQALLQGRGACR-----NSKNTIIDIPFP- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 6680387 | ref | NP_032370.1 | RPNP--VQDSEMGPCRRHLDVSLQQLQTEVFRGGARGLYVPCDLRGFYRKKQCRSSQGNRRGPCWCVDPMGQPLPVSPDG-QGSSQCSARSSG 244
gi | 6981090 | ref | NP_037236.1 | RPNP--VQDSEMGPCRRHLDVSLQQLQTEVFRGGANGLYVPCDLRGFYRKKQCRSSQGNRRGPCWCVDPMGQPLPVSPDG-QGSSQCSARSSG 244
gi | 11321593 | ref | NP_002169.1 | QPNSAGVQDTEMGPCRRHLDVSLQQLQTEVYRG-AQTLVYVPCDHRGFYRKRQCRSSQGRRGPCWCVDRMGKSLPGSPDG-NGSSSCPTGSSG 244
gi | 114644526 | ref | XP_509089.2 | QPNSAGVQDTEMGPCRRHLDVSLQQLQTEVYRG-AQTLVYVPCDHRGFYRKRQCRSSQGRRGPCWCVDRMGKSLPGSPDG-NGSSSCPTGSSG 244
gi | 110626119 | ref | NP_001035585.1 | RSNSSGGVQDTEMGPCRRHLDVSLQQLQTEVYRG-AHTLVYVPCDQRGFYRKRQCRSSQGRRGPCWCVERMGOPLPGSSGGDSSLCPGSSG 244
gi | 73996267 | ref | XP_849343.1 | RPNPGGVQDAEMGPCRRHLDVSLQQLQTEVYRG-VHTLVYVPCDHKGFYRKRQCRSSQGRRGPCWCVDRMGQPLSGSPDG-DGSSSCPTGSSG 244
gi | 238637259 | ref | NP_001154874.1 | GPHPSHSGEMEKAPCRKLLNSVLRGLELTFIS-DRDIYIPNCDTRGFYRKRQCRSSKGMQRGHCWCVDELGNTVPSRAGE-DGILPCDGE--- 244
gi | 238637253 | ref | NP_001154873.1 | DWEPSTENNEKGPCKLLNSVLSIELTVIHS-VQDIYIPNCDKQGSFRRKQCRSSRGMQRGHCWCVDEKSKISSRRRS-DGSIISCSA--- 244
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....

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