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gi | 4757876 | ref | NP_004326.1 | -----MASISYDYCRVPME-----DGDKR-----CKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQBELTEAKGFQDVEAQAATCNHTVMALMASLDAEKAQGOKKVEELGEEITTLNHLKLDAS 131
gi | 114676019 | ref | XP_512491.2 | -----MASTLYDYCRVPMDDIWKDGDGR-----CKLLLGIGILMLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQBELTEAKGFQDVEAQAATCNHTVMALMASLDAEKAQGOKKVEELGEEITTLNHLKLDAS 136
gi | 119894562 | ref | XP_876152.2 | MHYRVPVTDTEEDISELVMP-----IDKKT-----LDRKLLPLGVGVLVAVGLLVPMIYFAVIANSKACVDGLQAKKECEVNVQHVQROLTQAEFSSHKKEAQAATCNHTVMTLRESLKKKQAAQ-----VAEFOGKILKLNQNLKDAL 136
gi | 76620944 | ref | XP_584000.2 | -----MDTEEDMSEFLMP-----IDKEDSESEALCGRKLPWLGLLLLVAVGLLVPMIYFAVIANSKACVDGLQAKKECEVNVQHVQROLNQAQELLHKKEAQAATCKQAVVTLRDSLKKKQAAQ-----VEELQELASLNQQLDAL 135
gi | 37674242 | ref | NP_932763.1 | -----MAPSFVHYLFPVPMDEMGKQGWGS-----HRQWLGAAILVVLFGVTLVILTIYFAVTANSVACRDGLRAQAECRNTHLLQRLTRTODSLLQAEITQANS CNLTVVTLQESLKKKVS-----ALFQARIKELENEVTKLN 132
gi | 37693510 | ref | NP_937767.1 | -----MAPSFVHYLFPVAMDERWEKQWGI-----RRWWLVAAAILVVLIGVVLVCLIVFANAASSEACKNGLRLQDECRNTHLLKHQLTRAQDSLLOTEMQANS CNQTVMDLRDSLKKKVS-----TQEQARIKELENKTERLN 132
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 4757876 | ref | NP_004326.1 | AEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIVLLGLSALLQ 180
gi | 114676019 | ref | XP_512491.2 | AEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIVLLGLSALLQ 185
gi | 119894562 | ref | XP_876152.2 | AEVERLRRCSETCSEK-----NNASSCSSFLFVVIIVLVINALLT 175
gi | 76620944 | ref | XP_584000.2 | TK-E--RRKSEASAE-----DNSS-VWFFMLLMCTFIICKCLKK 170
gi | 37674242 | ref | NP_932763.1 | QELENLRITKETSSTVOVN-----SGSSMVVSSLLVLKVSFLFLF-- 172
gi | 37693510 | ref | NP_937767.1 | QELENLRITKEISTVOVN-----SGSSVVVSSLLVLVAVLFLHF-- 172
.....160.....170.....180.....190.....

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