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gi |15237029|ref|NP_195274.1|  -MAAAAK-EILRRPVA-----AIIRLIVPAGGARPAAPVVPALGGYRLNLMFAFCDFNARTQKVKYDIPMAVITITAFKDNSEFEFVVKSPVSVWYIKKAAAGVDKGGSTRPGHL-----SVTTLEVRHVYEIAKVKQDPPFCQV 129
gi |115482420|ref|NP_001064803.1| -MATILKDAVARKPVL-----AIIRLIVPAGGARPAAPVVPALGGYRLNLMFAFCDFNARTQKVKAEIPMQVTLTAYKDSPEFEFVVKSPVSVWFLKKAAGIETASGRPGHT-----VVSLSLRHVYEIAKLKQSDPYCKH 130
gi |124803673|ref|XP_001347786.1|  -MSRITGR-----FNLIVLSGTAKPSASIGQILGGLGINMNTFFKFEFNDRTKCKTAKNVPIQVTLLEPLNDR---FYLRIPVTVVWFLRRCARVPMFSSMAKHN-----IVGSIITLAEVFFHIAKCKRMDPPILIN 116
gi |7705618|ref|NP_057134.1|    -MSKLGRAARGLRKPE-----VGGVIRAIVRAGLAMPGPPLGPVLGQGVGINQFCKEFNERTKDIKEGIPLPKILVKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARQTGKE-----VAGLVTLKHVYEIARIKAQDEAFAL 132
gi |55636509|ref|XP_522076.1|    -MSKLGRAARGLRKPE-----VGGVIRAIVRAGLAMPGPPLGPVLGQGVGINQFCKEFNERTKDIKEGIPLPKILVKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARQTGKE-----VAGLVTLKHVYEIARIKAQDEAFAL 132
gi |57099649|ref|XP_53221.1|     -MSKLNRAARALRKP-----AGGVIRTIIVRAGQAMTGPPLGPILGQGVGINQFCKEFNERTKDIKEGIPLPKIFVKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARQTGKE-----VAGLVTLKHVYEIAQVKAQDEAFAL 132
gi |62460560|ref|NP_001014932.1| -MSKLSRAATRALRKP-----AEGVIRTIIVRAGQAMPGPPLGPILGQGVGINQFCKEFNERTKDIKEGIPLPKIFVKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARNTGKE-----VAGLVTLKHVYEIARVKAQDEAFAL 132
gi |13384980|ref|NP_079829.1|    -MSKLSRAATRALRKP-----AGGVIRSIIVRAGQAIIPGPPLGPILGQGVGINQFCKEFNERTKDIKEGIPLPKIFIKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARHTGKE-----VAGLVSLKHVYEIACVKAQDEAFAM 132
gi |55742212|ref|NP_001006974.1| -MSKLSRVVRLTKKPE-----AGGVIRSIIVRAGQAIIPGPPLGPILGQGVGINQFCKEFNERTKDIKEGIPLPKIFIKPDRTEFEIKIGQPTVSYFLKAAAGIEKGARQTGKE-----VAGLVSLKHVYEIARVKAQDEAFAM 132
gi |50540178|ref|NP_001002556.1|    -MSKISKAARKAVKSD-----TGLLIRAIIVRSQAAAPGPPLGPILGQGVGINQFCKEFNERTKDIKEGIPLPVVKINVKPDRTEFEIKIGQPTVSYFLKAAAGIEKAGKGTGHE-----IAGMIVRVAVYEIARVKSQDECFKL 132
gi |17737961|ref|NP_524351.1|     -MSKAAGKLSLKKTVERVTHTSKLRITNIPAGMAAAGPPLGPMLGQRAINIAAFCKDFNAKTAEMKEGVPLPCRISVNSDRSVDLAIHHPATFFLKQAAAGIQRGTMTPGKE-----VAGMILKHLVYEIAIKIKQDPPNVL 136
gi |58383599|ref|XP_312637.2|     -MSKAAGRLKTMKTFDKINHTSKLRITNIPAGMAVAGPPLGPMLGQGINIAAFCKDFNERTKDIKEGIPLPKCRVAVTSDRAYELTITHPPATFLLKQAAAGIQRGAMSPGKE-----IAGKIRKHLVYEIAIKIKQDPPNVL 136
gi |17551818|ref|NP_498923.1|    MASKGAARVR--KKEIVKVVHGALLRTNIIKAGMASAAPPLGPQGLGQGLNVAANFCKEFNERKGFHFKQGVPLPTRITITVKPDRTEFEIKIGQPTVSYFLKAAAGIEKGRKASK-DE-----IVGKLVVKKHLYEIAIKIKSRDKALQH 134
gi |63241444|ref|NP_014214.1|    -MSQAANK-----VIVKLVIVGAGQAAPSPPVGPALGSGKGIKALDFCKEFNARISANYQGVVPLVITIKPDRTEFEEMKSPPGYLLKALKMKGHGQPNVCGMLGSAAPAKGPTRALGELSLKHVYEIAIKIKSDEHSL 135
gi |45185086|ref|NP_982803.1|    -MSQRAKE-----ILVKLIVGAGQAAPSPPVGPALGSGKGIKAMDFCKEFNARISASTPGVPIPVLTITIKPDRSFTFEMKSPPGYLLLRALNQEKHGKPNII-----KKPEGILGELSLKHVYEIAIKIKADGRHTY 126
gi |50306925|ref|XP_453438.1|    -MSKVLKN-----VIVKLVIVGAGQAAPSPPVGPALGSGKGIKALDFCKEFNARISANFQGTPIPVLINIKPDRTEFEEMKSPPGYLLLRALKSLKLEKGGHQPNI-----NFDNVGELSLKHVYEIAIKIKTDGRHAA 126
gi |39976005|ref|XP_369393.1|    -MSK-ARAAAG-----GADQIVKLVIVGAGQAAPSPPVGPALGSGKGVKSMDFCKEFNARISAHITGTPVPRVTVRPRDIFSFDIRTPQTSWLLLNAAADAPMGRKGRKG-----GLAGKEIVGTVSLKHVYEIAIKIKQTEMRLSG 134
gi |32406152|ref|XP_323689.1|    -MSKAAKGAG-----GVEQVVKLVIVGAGQAAPSPPVGPALGSGKGIKAMDFCKEFNARISAHINTGTPMPVTVRPRDIFSFDFVTRPHTSWLLLNAAEAPIGKGGKRG-----ASNPGKEVVGTVSLKHVYEIAIKIKSELRLSG 135
gi |19115007|ref|NP_594095.1|    -MASIRTT-----IILKLVIVPAGKAITPPIIPALGARGLSIDFCKEFNARISAGWMPNIPVCKITVTPQRTFTFTTHPPQTSWLLISKTLDELKGGSSPLHD-----IKQLSLKHVYEIAIKIKSTDPSLQ 121
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |15237029|ref|NP_195274.1|  --MPLESICKSIIGTANSMGIKIVQ--DLE----- 155
gi |115482420|ref|NP_001064803.1| --MSLEALCKSIIGTANSMGIEIVK--DL----- 155
gi |124803673|ref|XP_001347786.1| --LSLKSICKYIIGTANSMGIRVCK--ELNDEKKKYFVDVNLKDNKIDIRRNKQOKRSKK-- 175
gi |7705618|ref|NP_057134.1|    QDVPLSSVVRSIIGSARSLGIRVVK--DLSEELAFAFKERAFFLAAQKEADLAAQEAFAAK-- 192
gi |55636509|ref|XP_522076.1|    QDVPLSSVVRSIIGSARSLGIRVVK--DLSEELAFAFKERAFFLAAQKEADLAAQEAFAAK-- 192
gi |57099649|ref|XP_53221.1|    QDVPLSSVVRSIIGSARSLGIRVVK--DLSEELAFAFKERAFFLAAQKEADLAAQEAFAAK-- 192
gi |62460560|ref|NP_001014932.1| QDVPLSSVVRSIIGSARSLGIRVVK--DLSEELAFAFKERAFFLAAQKEADLAAQEAFAAK-- 192
gi |13384980|ref|NP_079829.1|    QDVPLSSVVRSIIGSARSLGIRVVK--DLSEELAFAFKERAFFLAAQKEADLAAQEAFAAK-- 192
gi |55742212|ref|NP_001006974.1| QDVPLSSIVRSIIGSARSLGIRVVK--DLSEELAFAFKERAVFLAAQKRRIRWQLRQKLPKSDPPLLHSEVRD 203
gi |50540178|ref|NP_001002556.1| RDTTMCNVVKSIIIGSARSLGIQVNV--DLSPEEYGEFLREREVILKAQAEAAAAEAAAAAAAVKKK-- 196
gi |17737961|ref|NP_524351.1|    --LTMQCMCEMLIISTARTCGIKVVR--EIDPAAYGEFLEERKLIVQORRELQEKREAKMLRTG----- 196
gi |58383599|ref|XP_312637.2|    --LTLHEMCKALVGQVARTCGIEIVN--ELDPAEYKDFLEORRQVVEDQRKELQEKREARMLRVG----- 196
gi |17551818|ref|NP_498923.1|    --VLEQLCRMLIKICRTLIDVQYDLDLDEVLKKEFLVARKEKVDALKDLADKKAAMLRIT-- 195
gi |63241444|ref|NP_014214.1|    --LEMEGIVKSIIVGVAKSMGIKIVP----- 158
gi |45185086|ref|NP_982803.1|    --LDMENIVKSIIVGVAKSMGIAVVP----- 149
gi |50306925|ref|XP_453438.1|    --LELEGIVKSIIVGVAKSMGIKIVP----- 149
gi |39976005|ref|XP_369393.1|    --HSLLEGLCKSIITYCKSIIVGVEVVP----- 157
gi |32406152|ref|XP_323689.1|    --LPLEGLCRAVITYQARSIGINVIP----- 158
gi |19115007|ref|NP_594095.1|    --IELLSLCKSVIGTAKSMGVKIVP----- 144
.....160.....170.....180.....190.....200.....210.....220..

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