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gi | 21356279 | ref | NP_651959.1 | IFPEILRTMADNERPFVVFALSNPTSKAECTAEADAYKHTDARVIFSSGSPFPVQIG-DKTFYPGGNNAYIFPGVGLGVICTGHHHIPDEMFLIAAQVELANFVEPSDIERGSLYPPLSLIRNVSMNIAVGVKCAYDRGLASTYPEPQ 750
gi | 158291541 | ref | XP_313043.4 | AFTPEILQAMGQFNERPIIFALSNPTSKAECTAQAYDNTEGRCIFASGSPFPVQYG-GKTFITGOGNNAYIFPGVALGVIVTGHHIPEDMFLIAAQVVADHVSEADLEKGSLYPPLSLAIKECSMDIAVGVNYAYQKGLASTYPEPQ 750
gi | 4505143 | ref | NP_002386.1 | AFSEQILKDMAAFNERPIIFALSNPTSKAECSABQCYKITKGRAIFASGSPFPVTLNGOTLYPGGNNSYVFPPGVALGVVACGLRQITDNIFLTTAEVIAQQVSDKHLEEGRLYPPLNTIRDVSLKAEKIVKDAYQKTAIVPEPQ 750
gi | 114608383 | ref | XP_518610.2 | AFSEQILKDMAAFNERPIIFALSNPTSKAECSABQCYKITKGRAIFASGSPFPVTLNGOTLYPGGNNSYVFPPGVALGVVACGLRQITDNIFLTTAEVIAQQVSDKHLEEGRLYPPLNTIRDVSLKAEKIVKDAYQKTAIVPEPQ 750
gi | 6678912 | ref | NP_032641.1 | AFTEQILKDMAAFNERPIIFALSSPTSKAECSADECYKVTKGRAIFASGSPFPVTLDGRTLFPPGGNNSYVFPPGVALGVVACGLRHIDDKVFLTTREVISQQVSDKHLQEGRLYPPLNTIRGVSLKAIVKIVQDAYQKKEMAIVYPEPQ 750
gi | 7106353 | ref | NP_036732.1 | AFTEQILKDMAAFNERPIIFALSNPTSKAECSABECYKVTKGRAIFASGSPFPVTLDGRTLFPPGGNNSYVFPPGVALGVVACGLRHINDSVFLTTAEVISQQVSDKHLEEGRLYPPLNTIRDVSLKAIVKIVQDAYQKKEMAIVYPEPQ 750
gi | 73973868 | ref | XP_532217.2 | AFSEQILKDMAAFNERPIIFALSNPTSKAECTAEQCYKLTKGRAIFASGSPFPVTLNGRTLFPPGGNNSYVFPPGVALGVVACGLRHITDNIFLTTAEVIAQQVSDKHLEEGRLYPPLNTIRDVSLKAIAKIVQDAYQKTAIVPEPQ 750
gi | 194670273 | ref | XP_613987.4 | AFSEQILKDMAAFNERPIIFALSNPTSKAECTAEQCYKLTKGRAIFASGSPFPVTLSPGKTLYPPGGNNSYVFPPGVALGVVACGLRHITDKIFLTTAEVIAQQVSDKHLEEGRLYPPLNTIRDVSLKAEKIVKDAYQKTAIVPEPQ 750
gi | 45383538 | ref | NP_989634.1 | APTKIIQDRAAFKNPIIFALSNPTSKAECTAEQCYKYTEGRGIFASGSPFPVTLNGKTLYPPGGNNSYVFPPGVALGVICCGLKHIGEDVFLTTAEVIAQQVSEENLQEGRLYPPLVTIQVSLKAIVRIAEAEYRNNTATYPOPE 750
gi | 15225262 | ref | NP_179580.1 | SFTKEVIEAMSSINERPLIMALSNPTSQSECTABEAYTWSKGRAIFASGSPFPVVEY-GKVFVSTQANNAYIFPGFGLGVISGAIRVHDDMLAAEALAGQVSKENYEKGMIVPSFSIRKISAQIAANVATKAYELGLAGRLPRPK 750
gi | 115439879 | ref | NP_001044219.1 | SFTKEVIEAMSSINERPILLALSNPTSQSECTABEQAYSWSKRAIFGSSPFPVKYN-DKLFVPAQANNAYIFPGFGLGVISGAIRVKDEMLAAEGLADVTPEVDKGLINPFSCIRKISANIAARVAAKAVDLGLASHLPRPPK 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi | 21356279 | ref | NP_651959.1 | DKRWLENQLNFNYESMPPASWVWRPM-YIKTREESPLIAAK----- 802
gi | 158291541 | ref | XP_313043.4 | DKKSYIESHLNYNYQSAMPVWPWKQHESSKTREINPTLQAA----- 802
gi | 4505143 | ref | NP_002386.1 | NKEAFVRSQMYSTDYDQILPDCYSWPEEVVOK---IQTKVDQ----- 802
gi | 114608383 | ref | XP_518610.2 | NKEAFVRSQMYSTDYDQILPDCYSWPEEVVOK---IQTKVDQ----- 802
gi | 6678912 | ref | NP_032641.1 | NKEEFVRSQMYSTNYDQILPDCYWPAEVOK-----IQTKVNQ----- 802
gi | 7106353 | ref | NP_036732.1 | NKEEFVRSQMYSTNYDQILPDCYSWPEEVPENTDSQSVTQLEFLALLIRS 802
gi | 73973868 | ref | XP_532217.2 | NKEAFVRSQMYSTDYDQILPDCYSWPEEAOK---IQTKLDQ----- 802
gi | 194670273 | ref | XP_613987.4 | NKEAFVRSQMYSTDYDQILPDCYWPKEAAOK---IQTKLDQ----- 802
gi | 45383538 | ref | NP_989634.1 | DLKAFIRSMYSTDYNSFVADSYTPEDAMK----VKL----- 802
gi | 15225262 | ref | NP_179580.1 | DIVKCAESSMYSPTYRLYR-----VKL----- 802
gi | 115439879 | ref | NP_001044219.1 | DLVKCAESSMYSPTYRSYR-----VKL----- 802
.....760.....770.....780.....790.....800..

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