

gi |226498382| ref |NP_612385.2| -----MMADDEEEE-----VKPILOKLOELVDQLYFRDCYFETHSVEDAGRKQODVQKEMEKTLQOMEEVVGSGKAQVLMMLTGKALNVTDPYSPKAEELLSKAVKLEPELVE 150
gi |114651732| ref |XP_520664.2| -----MMADDEEEE-----VKPILOKLOELVDQLYFRDCYFETHSVEDAGRKQODVQKEMEKTLQOMEEVVGSGKAQVLMMLTGKALNVTDPYSPKAEELLSKAVKLEPELVE 150
gi |124358948| ref |NP_001074418.1| -----MMADDEEEE-----AKHVLQKLOGLVDRLYCFRDSYFETHSVEDAGRKQODVQEMEKTLQOMEEVVGSAQVEAQAALMLKGGKALNVTDPYSPKAEVLLSKAVKLEPELVE 150
gi |61557041| ref |NP_001013149.1| -----MMADDEEEE-----AKQVLQKLOELVDQLYCFRDSYFETHSVEDAGKQODVQEMEKTLQOMEEVVGSAQVEAQAALMLKGGKALNVTDPYSPKAEVLLSKAVKLEPELVE 150
gi |115495937| ref |NP_001068932.1| -----MMADDEEEE-----VKEVLQKLOELVDQLYFRDCYFETHSVDDAGRKQODVREEMEKTLQOMEEVVGSGNAQVLMMLTGKALNVTDPYSPKAEELLSKAVKLEPKLVE 150
gi |73978094| ref |XP_853663.1| MIFHLKLDQSVCPACGLPRGVVLLLEALLAPGREELWPRGRRGWDPAISFMIRGVRFPSWGRGODLVDQLYFRDCYFETHSVEDAGRKQODVREEMEKTLQOMEEVVGSGKAQVLMMLTGKALNVTDPYSPKAEELLSKAVKLEPKLVE 150
gi |62955285| ref |NP_001017654.1| -----MAEVDNDGQK-----ITDQDLQLVLELVDLYSFRGRYFETHSVEDAGRKQODVQEMAKTLRRLBEKADLTKHSAQFLLLRGRCLNVPFQAQAEELLSKAVKLEPELVE 150
gi |115436838| ref |NP_001043149.1| -----KPMSSRAGGAASASAPFP-----PRRTPLERADAABELYLRLDTFFPRDPVEKAALRALADDALAVLDSLPPRQRKTPQRAVVEFLRGIKLDVFPDYHKEAEDHLSKAVKLNPLSLVD 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi |226498382| ref |NP_612385.2| AWNLQGEVYWKKGDVAAAHTCFSGALTHCRNKVSLQNLMSVLRQLRDTDEDESHHVMDSVROAKLAVOMDVIDGRSWYILGNSVLSLYFSTGONPKIISQOALSAYAAQAEKVDKASSNPDLHLNRAATLHKYEEESYGEALEGFSRAAAL 300
gi |114651732| ref |XP_520664.2| AWNLQGEVYWKKGDVAAAHTCFSGALTHCRNKVSLQNLMSVLRQLRDTDEDESHHVMDSVROAKLAVOMDVIDGRSWYILGNSVLSLYFSTGONPKIISQOALSAYAAQAEKVDKASSNPDLHLNRAATLHKYEEESYGEALEGFSRAAAL 300
gi |124358948| ref |NP_001074418.1| AWNLQGEVYWKKGDVASAAHTCFSGALTHCRNKVSLQNLMSVLRQLQDTSGDEHSHRVMDSVROAKLAVOMDVIDGRSWYILGNAYLSLYFNTGONPKIISQOALSAYAAQAEKVDKASSNPDLHLNRAATLHKYEEESYGEALEGFSQAATL 300
gi |61557041| ref |NP_001013149.1| AWNLQGEVYWKKGDVAAAHTCFSGALTHCRNKVSLQNLMSVLRQLQDTSGDEHSHRVMDSVROAKLAVOMDVIDGRSWYILGNAYLSLYFNTGONPKIISQOALSAYAAQAEKVDKASSNPDLHLNRAATLHKYEEESYGEALEGFSQAATL 300
gi |115495937| ref |NP_001068932.1| AWNLQGEVYWKKGDVAAAHTCFSGALTHCRNKVSLQNLMSVLRQLRDTSGDEHSHRVMDSVROAKLAVOMDVIDGRSWYILGNAYLSLYFNTGONPKIISQOALSAYAAQAEKVDRTASSNPDLHLNRAATLHKYEEENYGEALEGFSRAAAL 300
gi |73978094| ref |XP_853663.1| AWNLQGEVYWKKGDIAAAHTCFSGALTHCRNKVSLQNLMSVLRQLRADTSGDEHSHRVMDSVROAKLAVOMDVIDGRSWYILGNAYLSLYFNTGONPKIISQOALSAYAAQAEKVDRTACSNPDHLNRAATLHKYEEENYGEALEGFSRAAAL 300
gi |62955285| ref |NP_001017654.1| GWNLTGECQYWKKGDLTAAKTCFSGALQSKNKVSLRSLMSVLRQLPEGDAQSQSKRILLESVDLARHAVOLDVDTGTSWYILGNAYLSMFFTSGONPKIISQOALSAYAAQAEKIDKASSNPDLHFNRAATLFOYEMFSSALGGYSRAAAL 300
gi |115436838| ref |NP_001043149.1| AWLCLGNCIWKKGDLDSAMNCFSLALSKGADKIKLQSLMLERSMAQG--SEGQAQLVEESIKHAKAVMLDIRDGNSSWNLGNAYLTSFFVSGSWDHMKLHHSVKAYQNAEKDETCKCNPDLYNCAIADKYLKNFERALRGFEAAALK 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi |226498382| ref |NP_612385.2| DPAPPEPRQREQQLLEFLDRLLTSLLESKQKVKTKKLOQSMGLSLRPAHLGPCSDGHYQASAGQKVLLELKLPLSTLQPGVNSGAVILGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |114651732| ref |XP_520664.2| DPAPPEPRQREQQLLEFLDRLLTSLLESKQKVKTKKLOQSMGLSLRPAHLGPCSDGHYQASAGQKVLLELKLPLSTLQPGVNSGAVILGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |124358948| ref |NP_001074418.1| DPVWPEPQREQQLLEFLSRLTSLLESKQKTKPKKLOQSMGLSLRPAHLGPCDGRYQASAGQKVLLELKLPLSTLQPGVNSGAVVVGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |61557041| ref |NP_001013149.1| DPAPPEPQREQQLLEFLSRLTSLLESKQKTKPKKLOQSMGLSLRPAHLGPCDGRYQASAGQKVLLELKLPLSTLQPGVNSGAVVVGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |115495937| ref |NP_001068932.1| DPAPPEPQREQQLLEFLSRLTSLLESKQKTKPKKLOQSMGLSLRPAHLGPCDGRYQASAGQKVLLELKLPLSTLQPGVNSGAVVVGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |73978094| ref |XP_853663.1| DPVWPEPQREQQLLEFLSRLTSLLESKQKTKPKKLOQSMGLSLRPAHLGPCDGRYQASAGQKVLLELKLPLSTLQPGVNSGAVVVGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |62955285| ref |NP_001017654.1| DPAPPEPQREQQLLEFLSRLTSLLESKQKTKPKKLOQSMGLSLRPAHLGPCDGRYQASAGQKVLLELKLPLSTLQPGVNSGAVVVGKVVFSLTTEEKVFFTFGLVDSDDGPCYAVMVYNNVQSWGVLIGDSVAIPEPNLRLHRIQHRGKDY 450
gi |115436838| ref |NP_001043149.1| DPGLGADTEVQKILISLDDKLDQAMK--GQLRSKRLASVSSLSSEVNIKSS-----HKKATIGILSEGLNKTVAVLGKVVILLIRHDNIAFMYLNCDLDSQSVFILLSVYGLRN-EAIKEGDRVALLDPYRILLDISWKEQRY 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi |226498382| ref |NP_612385.2| SFSSVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |114651732| ref |XP_520664.2| SFSSVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |124358948| ref |NP_001074418.1| SFSSVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |61557041| ref |NP_001013149.1| SFSSVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |115495937| ref |NP_001068932.1| SFSSVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |73978094| ref |XP_853663.1| SFASVRVETPLLLLVNGKPGSSSSQAVAVASRPQCE 487
gi |62955285| ref |NP_001017654.1| DFRSIRVDFPILLLVNGKRVMKSSQSAAFVYKPKQSE 487
gi |115436838| ref |NP_001043149.1| QFKSIRVDFPEQLLVNEKAPPPHHVVRASIHANRKP- 487
.....460.....470.....480.....

