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gi |112181164|ref|NP_082312.3| MWNRR--GRLRLTFAGVEELRRRRREREAAALRKARREOOLVSKRLLREDAPF--EVGGQSAAVLLG--EAEVQOFLRLAQRGTDEKEREKALVSLRRGLOHPDFOOTFIRLEGSMTLVGLLTSNRALLQLEAARCLHELHSHSEOSA 142
gi |109506452|ref|XP_214574.4| MWGRR--GRLRLTFACVVELRRRRREREAAALRKARREOOLVSKRLLREDAPF--ETGGQSAAVLLG--EAEVQOFLRLAQRGTDEKEREKALVSLRRGLOHPDFOOTFIRLEGSMTLVGLLTSNRALLQLEAARCLHELHSHSEOSA 142
gi |94536840|ref|NP_060972.3| MWSRR--GRLRLPVCVVEELRRRRREREAAALRKARREOOLVSKRLLRNDAPF--EAGEGCVAAAILG--ETEVQOFLRQAQRGTDEKEREGALVSLRRGLOHPDFOOTFIRLEGSMTLVGLLTSNQALLQLEAARCLHELHSHSEOST 142
gi |114602170|ref|XP_001140277.1| MWSRR--GRLRLPVCVVEELRRRRREREAAALRKARREOOLVSKRLLRNDAPF--EAGEGCVAAAILG--ETEVQOFLRQAQRGTDEKEREGALVSLRRGLOHPDFOOTFIRLEGSMTLVGLLTSNQALLQLEAARCLHELHSHSEOST 142
gi |73949332|ref|XP_544291.2| -----MVLG--EABIQOFLGLAQRGTDEKEREKALVSLRRGLOHPDFOOAFILLEGSMRTLVGLLTSNQALLQLEAARCLHELHSHSEOSA 83
gi |194668959|ref|XP_001790629.1| MWSGR--RGLLRSAGCGVEELRCRRREREAAALRKARREOOLVSKRLLRDEAPF--EAEGGCVVVLG--EAEIQEFLRLAQRGTDEKERERALVSLRRGLOHPDFOOTFIRLEGSIRTLVGLLTSNQALLQLEAARCLHELHSHSEOSA 142
gi |118097168|ref|XP_414468.2| MSRRK--HLGFG-----ETSAEPRTEPRLLEQSRLLRDEAERWHDRAADAAEAVLPEVLGGVSELLRGVQRGSEDRR--WLRCLRRALQSKETQOEFVRLDGAVRTLVGLLFTCSLPDVOLEAARCLHELHSHSDAA 133
gi |147907202|ref|NP_001083006.1| MWRLKTHHKASASASLEEFKRRKREFKALRQARKDQOLVSKRLLQNDVVEE--EKEEESMECFTEFLSEVQKEMIRGVQMGGEKAAR--LALRRKALRNFENLQAFIKSENMMHMLIGQLSAHNAQCQLEAARCLHELHSHSHP 147
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |112181164|ref|NP_082312.3| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRKQLLPQGIVPFAFAACIQSP--HVAVLEALGYALSQLLQAKEAPEKIIP-----SILDSSLPQQLMLWLMQPGPKNLGVAMEFAWCLHYIICSOVNNAVLLTHGALPT 284
gi |109506452|ref|XP_214574.4| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRKQLLPQGIVPFAFAACIQSP--HVAVLEALGYALSQLLQAKEAPEKIIP-----SILDSSLPQQLMLRMLMGPGPKNLGVAMEFAWCLHYIICSOVNNAVLLTHGALPT 284
gi |94536840|ref|NP_060972.3| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRRQLLPQGIVPAALAAACIQSP--HVAVLEALGYALSQLLQAKEAPEKIIP-----SILASTLPOHMLQMLQPGPKNLPGVAVEFAWCLHYIICSOVSNPLLIHGHALST 284
gi |114602170|ref|XP_001140277.1| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRRQLLPQGIVPAALAAACIQSP--HVAVLEALGYALSQLLQAKEAPEKIIPASASSSILASTLPOHMLQMLQPGPKNLPGVAVEFAWCLHYIICSOVSNPLLIHGHALST 290
gi |73949332|ref|XP_544291.2| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRRQLLPQGIVPSLAACIQSP--HLTVLEALGYALSQLLQAKEAPEKIIP-----SVLGSTLPOHMLQMLQPGPKNLPGVAVEFAWCLHYIICSOVNNALLIHHGCLST 225
gi |194668959|ref|XP_001790629.1| VAEACLPAATSYLLTYLSSHSSDFIELCLYTLGNLIVSEAVRRQLLPQGIVPAALAAACIQSP--HLTVLEALGYALSQLLQAKEAPEKIIP-----LVLGSTLPOHMLQMLQPGPKNLPGVAVEFAWCLHYIICSOVNNALLIQQALPT 284
gi |118097168|ref|XP_414468.2| VAEACVPVTSYLLTYLSSHSTIEMELCLYTLGNLVSEVVRKQLLPQGIIPVLASCIQSP--HEAVLEGLGYVLSQLLQAKEAPEKIIP-----LVLDVLPQHMLRLVCSGLKFGGAAVEFAWCLHYIICSHANVELMELGAVPA 275
gi |147907202|ref|NP_001083006.1| VSAACVPAAGPYLLTYLSQSTQLTEVCLYTLGNLCPDAAVREKLLAQGIIVSALANCIINQRYNLAVVEAFGFLLSQLLQAKDATEKIIP-----AVMASGIVPHLISALTPDPEFGFGPAIECSWCLHYIIVS--SLDNLMLIAHGALSH 291
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |112181164|ref|NP_082312.3| LALLLLDLAGVQRMD--DVGLELLACPVLRCLSNLLTEVPAEVMGQOMELRDERLVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLLSLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLSCLNLTLA 433
gi |109506452|ref|XP_214574.4| LVLLLVLDLAGAVQRMD--DVGLELLACPVVRCLSNLLTEVPAEAMGQOMELRDERLVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLLSLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLSCLNLTLA 433
gi |94536840|ref|NP_060972.3| LGLLLDLAGAVQRTE--DAGLELLACPVLRCLSNLLTEAAVETVGGOMLDRDERRVVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLLSLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPALLHTLA 433
gi |114602170|ref|XP_001140277.1| LGLLLDLAGAVQRTE--DAGLELLACPVLRCLSNLLTEAAVETVGGOMLDRDERRVVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLLSLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPALLHTLA 439
gi |73949332|ref|XP_544291.2| LGLLLDMAGAVQRTE--DARMELLAAPVLRCLSNLLTEAAVEVGGPNOLDERVVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLISLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPCLIGTTLA 374
gi |194668959|ref|XP_001790629.1| LGLLLDLAAVQRTE--DAGLELLVCPVLRCLSNLLTEAAAEVGGPNOLDERVVAALFIFLQFFLQKQAPALLPEGLWLLNLTANSPTFCTSLISLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPALLHTLA 433
gi |118097168|ref|XP_414468.2| LLSLLCDIAFEISQSD--SEGLELLIAPVLRCLGNLL-----AEETGHEVQPODERLLVALFVVMQCYLQHPFPIIPESLWLNLTANSPTFCTSLISLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPALLHTLA 420
gi |147907202|ref|NP_001083006.1| CSAVLLIAGGAVAKGNPQDGLLELLIWPVLRCLGNLL-----ASGGVPVPEPTRLAALCVFACIYVHLHPALRESLWTLNLTANSPTFCTSLISLDLIEPLLOLPLSNVAVCMMLVLTIVLGNVVEKGPAYCORLWPGPLLPALLHTLA 435
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |112181164|ref|NP_082312.3| LSDTEVVGOSLELLQLLFLHCPAAARAFLOOSGLQALEKLEETQLQERIHALQOIAATHG----- 494
gi |109506452|ref|XP_214574.4| LSDTDVVGOSLELLQLLFLYCPAAAHAFLOOSGLQALEKHQEEQLDHRHAIHALROTAALG----- 494
gi |94536840|ref|NP_060972.3| FSDTEVVGOSLELLHLLFLYCPAAVAVFLOOSGLQALERRHQEEAQLQDRVYALQOATALG----- 493
gi |114602170|ref|XP_001140277.1| FSDTEVVGOSLELLHLLFLYCPAAVAVFLOOSGLQALERRHQEEAQLQDRVYALQOATALG----- 499
gi |73949332|ref|XP_544291.2| FSDTEVVGOSLELLQLLFLYCPETAFAFLOOSGLQVLERHQEEAQLQDRVHALOKTALHR----- 434
gi |194668959|ref|XP_001790629.1| LSDTEVVGOSLELLQLLFLYCPGAAAFLOOSGLQALORHEEVAQLQDRVHALQOATALG----- 493
gi |118097168|ref|XP_414468.2| VDDPEVVGOSLELLHLLFLHWPQVAVDFVROGGHQLTLEQHSSTPELQERVRALDMALQPDASVFSPPSAASSTFSQMM----- 500
gi |147907202|ref|NP_001083006.1| MADPEVVTLSLEVLMLVSNPQGVVEEFLRLNGIPLLEAIIYNNEGQRVRAAYILDHHPSEFSEVSEL----- 504
.....460.....470.....480.....490.....500.....510.....520.....530

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