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gi|4505865|ref|NP_002650.1| MGHPPLLP LL-LLLHCVPA SWGLRCMOCKTNGDCRVEECALGODLCRTTIVRLWEEGEELELVKESCTHSEKTNRTLSYRTGLKITSLEVVVCGLDLDCNOGNSG-RAVTYS--RSRYLEICISCGSSDMS CERGRHOSLQCRSPPEOCLD 150
gi|57113947|ref|NP_001009031.1| MGHPPLLP LL-LLLHCVPA SWGLRCMOCKTNGDCRVEECALGODLCRTTIVRMWEEGEELELVKESCTHSEKTNRTLSYRTGLKITSLEVVVCGLDLDCNOGNSG-RAVTYS--RSRYLEICISCGSSNMS CERGRHOSLQCRNPPEOCLD 150
gi|73948230|ref|XP_533652.2| MGHPPLLP LLG LLLHCVPVSWSLQCM LCGTTGKQVVEECTPGQDLCRTTIVRMWEEGEELELVKESCTHSEKTNRTLSYRTGLKITSLEVVVCGLDLDCNOGNSG-RAVTYS--RSRYLEICISCGSSDLS CERGLDQSLQCRSPTEOCVE 150
gi|27806067|ref|NP_776848.1| MGQPLLLLLL---VVTYIPGSWGLRCLQCENNTSCSVEECTPGQDLCRTTIVLSVWEEGEMNVMVVRKGC THPKTNRSMSYRAADIIITLSETVCRSDLCNKPNPG-RDATVS--RNRYLECASCSITDLS CERGWDTMQLKSRDQCVD 150
gi|7242179|ref|NP_035243.1| MGLPRRLLLLLL LLAHCVPA SWGLRCMOCKESNQCSEVVEECALGODLCRTTIVLRWQDRELEVVTTRGCAHSEKTNRTLSYRMGSMIISLETVCAINLNRPRPGARGRAF--GGRYLECASCTELDQ CERGREOSLQCRYPTFHGIE 150

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gi|4505865|ref|NP_002650.1| VVTHWIQEGEEGRPKDDRHLRGCYLPCCPGSNGFHNNDIFHFLKCCNTTKCNEGPILLELENLPQNGRCYSCCKGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMN-HIDVSCCTKSGCNE 300
gi|57113947|ref|NP_001009031.1| VVTHWIQEGEEGRPKDDRHLRGCYLPCCPGSNGFHNNDIFHFLKCCNTTKCNEGPILLELENLPQNGRCYSCCKGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMN-HIDVSCCTKSGCNE 300
gi|73948230|ref|XP_533652.2| VVTHR---GLDSPRDEHHTRGCCNLPGCCPGTGFHNNDIFHFLKCCNTTKCNEGPVLELONLPLNGLQCFGCEGNSHTGCSSEETSLIACRGPMMQCLDATGTNGLGNPSYTVRGCAIPSWCQSLHVAEAFDIT-HVNVSCCTKSGCNE 300
gi|27806067|ref|NP_776848.1| VIITHR---SLKENPGRDEHHTRGCCNLPGCCPGTGFHNNDIFHFLKCCNTTKCNEGPVLELONLPLNGLQCFGCEGNSHTGCSSEETFLIDCRGPMNQCLEATGTRGLRNPSYTVRGCAIPSWCQSLHVAEAFDIT-HVNVSCCTKSGCNE 300
gi|7242179|ref|NP_035243.1| VVTLQ---STERSLKDEYTRGCGSLPGCCPGTAGFHSNQTDFHFLKCCNTTKCNGGVPVLDLQSFPPNFGQCYSCCGNNTLGCSEEAASLINCGRGPMNQCLVATGLDVLGNRSYTVRGCAIPSWCQSHVADSPFTHLNVSVSCCHGSGCNE 300

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gi|4505865|ref|NP_002650.1| PDLDVQYRSGAAPQPGPAHLSLITLLMTARLWGGTLLWT 340
gi|57113947|ref|NP_001009031.1| PDLDVQYRSGAAPQPGPAHLSLITLLMTARLWGGTLLWT 340
gi|73948230|ref|XP_533652.2| PILDHQPRIQSAPRPGPAHLSLITVLLLTARLWGGTLLWT 340
gi|27806067|ref|NP_776848.1| PARDDQPKGGAPKTPPAHLSLITVLLLTARLWGA LLLCT 340
gi|7242179|ref|NP_035243.1| PT-----GGAPRPGPAQLSLIASLLLTGLWNG-VLLWT 340

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