

gi|30840984|ref|NP_081072.1| MRARAR---GGLERFCSAGKGRGLRALRPFHVGDLLFSCPAYACVLTVGERGHHCCECFARKEGLSKGCRCKQAFYCDVECKEDWPLHKLECSMVVLFGENWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKKD 147
gi|34881150|ref|XP_213972.2| MRARAR---GGLERFCSAGKGRGLRALRPFHVGDLLFSCPAYACVLTVGERGHHCCECFARKEGLSKGCRCKQAFYCDVECKEDWPLHKLECSMVVLFGENWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKKD 147
gi|73960928|ref|XP_537149.2| MRAAGD---GGLERFCSPGKSRGLRALQPFHVGDLLFC-DYMYILEYQLPGVHLFPLFLRKEGLSKGCRCKQAFYCNVECKEDWPMHKLCSMPVVFGENWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKKD 146
gi|115496736|ref|NP_001069832.1| MRAEGD---GGLERFCSPGKGRGLRALQPFHVGDLLFSCPAYAVLTVSERGNHCFCFARKEGLSKGCRCKQAFYCNVECKEDWPMHKLCSMPVVFGENWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKRD 147
gi|188035871|ref|NP_064582.2| MRAEGL---GGLERFCSPGKGRGLRALQPFHVGDLLFSCPAYAVLTVNERGNHCYCFTRKEGLSKGCRCKQAFYCNVECKEDWPMHKLCSMPVVFGENWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKKD 147
gi|50740296|ref|XP_419420.1| MRSEAVPQPGGLERFASPGKGRGLRALRRYAVGELLFSCPAYTAVLTVSERGSHCDGCFARKEGLSKGCRCKQAFYCNVECKEDWPMHKLCAAMCAFQGNWNPSETVRLTARILAKOKIHPERTPSEKLLAVREFESHLDKLDNEKRE 150
gi|61806679|ref|NP_001013568.1| MKKEGI---EGTERFLSPGKGRGLKAIKHFVGDLVFACPAYAVLTVNERGGRCCEFTRKEGLSKGCKQAFYCNVECKEDWPMHKLCSAMCAYGENWCPSETVRLVARIILKQKHQTERPSEKLLAVREFESHLDKLDNEKNE 147



gi|30840984|ref|NP_081072.1| LIQSDIAALHQFYSKYLEFPDHSILVVLFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGDEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLSDPPQAEAIRDMVR 296
gi|34881150|ref|XP_213972.2| LIQSDIAALHQFYSKHLEFPDHSILVVLFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGDEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLSDPPQAEAIRDMVR 296
gi|73960928|ref|XP_537149.2| LIQSDIAALHHFYSKHLEFPDSESLVVLFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGEEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLSDPPKAEITIRDMVR 295
gi|115496736|ref|NP_001069832.1| LIQSDIAALHHFYSKHLEFPDNDLVLVFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGEEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLNDPPKAEITIRDMVR 296
gi|188035871|ref|NP_064582.2| LIQSDIAALHHFYSKHLEFPDNDLVLVFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGEEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLSDPPKAEAIRDMVR 296
gi|50740296|ref|XP_419420.1| LIQSDIAALHHFYSKHMEYPDNAALVVLFAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCCPNVIVTYKGTAEVRAVQEIHPGEEVFTSYIDLLNPTEDRNDRLRDSYFFTCCECRECTTKDKDKAKVEIR-KLNDPPSABAVRDMIK 299
gi|61806679|ref|NP_001013568.1| MNDIDIAALHHFYSRHLDFPDNAALTELIAQVNCNGFTIEDEELSHLGSALFPDVALMNHSCSPNVIVTYKGTAEVRAVQEIHPGEEVFTSYIDLLNPTEDRIRLKDYSYFFNCDCRECTKSKDKAKMEIRKLSLIPPEEIEIKQOMVI 297



gi|30840984|ref|NP_081072.1| YARNVIEEFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMGLNKAAGEKALKKATAIMEVAHGKDHPISEIKQETESH- 433
gi|34881150|ref|XP_213972.2| YARNVIEEFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMGLNKAAGEKALKKATAIMEVAHGKDHPISEIKQETESH- 433
gi|73960928|ref|XP_537149.2| YARNVIEEFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMGLNKAAGEKALKKATAIMEVAHGKDHPISEIKQETESH- 432
gi|115496736|ref|NP_001069832.1| YARNVIEEFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMGLNKAAGERALKKATAIMEVAHGKDHPISEIKQETESH- 433
gi|188035871|ref|NP_064582.2| YARNVIEEFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMGLNKAAGEKALKKATAIMEVAHGKDHPISEIKQETESH- 433
gi|50740296|ref|XP_419420.1| YARNVIEEFRRAKHYKSPSELLEICELSLDKMGAVFEDSNVYMLHMMYQAMGVCLYMDWEGALRYGQKIIKPKYKHYPLYSLNVASMWLKLGRLYMALENRPAGDKALKKATAIMEVAHGKDHPISEIKKLEEDH- 436
gi|61806679|ref|NP_001013568.1| YARNVIEEFRRAKHYKTPSELLEICELSMKMGALFAETNVYMLHMMYQAMGVCLYMDWDGAMKYGEKIIHPYSVHYPPYSLNVASMWLKLGRLYLGLKRTQGVKALKKALAIMDIAHGKDHPISEIKKEMEEQ- 435

