

gi|6755881|ref|NP\_035770.1| MAMEESQSDISLELPLSQETFSGLWKLKLLPPEDILP----SPHCMDDLL--PDVVEEFGEP--SEALRQVSGAPAAQDPVTEPGPVAPAPAPWPLSSSFVPSQKTYQGNVGFHLGFLQSGTAKSVMTYSPPLNKLFCOLVKTCPVG 141  
 gi|13591878|ref|NP\_112251.1| ---MEDSQSDMSIELPLSQETFSCLWKLKLLPPDDILPTTATGSPNSMEDLFL--PDVAELLEGP---EALQVS-AAPAAQEPGTEAPAPVAPASAPWPLSSSVPSQKTYQGNVGFHLGFLQSGTAKSVMTYSPPLNKLFCOLAKTCPVG 142  
 gi|187830777|ref|NP\_001119584.1| ---MEEPQSDPSVEPPLSQETFSDLWKLKLLPENNVLSL--LPSQAMDDLMSDDIEQWFTEDPGDEAPRMPPEAAPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGNVGFHLGFLHSGTAKSVTCYSPALNKMFCOLAKTCPVG 144  
 gi|114666241|ref|XP\_511957.2| ---MEEPQSDPSVEPPLSQETFSDLWKLKLLPENNVLSL--LPSQAMDDLMSDDIEQWFTEDPGDEAPRMPPEAAPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGNVGFHLGFLHSGTAKSVTCYSPALNKMFCOLAKTCPVG 144  
 gi|50978974|ref|NP\_001003210.1| ---MEESQSELNIDPPLSQETFSSELWNLKLLPENNVLSL--ELCPAVDELLE--PESVNVNLDLDD--SDDAPRMPAASAPTAPG-----PAPSWPLSSSVPSQKTYQGNVGFHLGFLHSGTAKSVTCYSPALNKLFCOLAKTCPVG 131  
 gi|28849929|ref|NP\_776626.1| ---MEESQAEINVEPPLSQETFSDLWNLKLLPENNVLSL--ELSAVDLDDLP--TIDVATWLDLC--PNEAPQMPPEPSAPAAFP--PATPAPATSWPLSSSFVPSQKTYQGNVGFHLGFLQSGTAKSVTCYSPALNKLFCOLAKTCPVG 136  
 gi|18859503|ref|NP\_571402.1| ---MAQND-----SQE-FAELW---EKLLIQP--PGGSCWDIIN--DEELPGSS---FDPNFFNVLEEQPQ-----PSTLPPTSTIVPETSIVPGDGHGFLRFQSGTAKSVTCYSPDLNKLFCOLAKTCPVG 112



gi|6755881|ref|NP\_035770.1| LWSA LPPAGSRVRAMAIYKKSQHMTVEVRRCPHHERCSDG-DGLAPPOHLIRVEGNLYPEYLEDROFRHSVVVVPYEPPEAGSEYTIHYKVMCNSSCMGGMNRRLILITILEDSSGNLLGRDSFEVVRVCACPGDRDRTEENFRKKE 290  
 gi|13591878|ref|NP\_112251.1| LWVTS LPPPGTRVRAMAIYKKSQHMTVEVRRCPHHERCSDG-DGLAPPOHLIRVEGNLYPEYLEDROFRHSVVVVPYEPPEVGSDYTTIHYKVMCNSSCMGGMNRRLILITILEDSSGNLLGRDSFEVVRVCACPGDRDRTEENFRKKE 291  
 gi|187830777|ref|NP\_001119584.1| LWVDS LPPPGTRVRAMAIYKKSQHMTVEVRRCPHHERCSDS-DGLAPPOHLIRVEGNLYPEYLEDROFRHSVVVVPYEPPEVGSDCYTIHYNYMKNSSCMGGMNRRLILITILEDSSGNLLGRNSFEVVRVCACPGDRDRTEENLRKKK 293  
 gi|114666241|ref|XP\_511957.2| LWVDS LPPPGTRVRAMAIYKKSQHMTVEVRRCPHHERCSDS-DGLAPPOHLIRVEGNLYPEYLEDROFRHSVVVVPYEPPEVGSDCYTIHYNYMKNSSCMGGMNRRLILITILEDSSGNLLGRNSFEVVRVCACPGDRDRTEENLRKKK 293  
 gi|50978974|ref|NP\_001003210.1| LWVS LPPPNLCVRAMAIYKKSQHMTEVRRCPHHERCSDSDGLAPPOHLIRVEGNLYRAKYLDDRNFRHSVVVVPYEPPEVGSDYTTIHYNYMKNSSCMGGMNRRLILITILEDSSGNVLRNSFEVVRVCACPGDRDRTEENFRKKG 281  
 gi|28849929|ref|NP\_776626.1| LWVDS LPPPGTRVRAMAIYKKSQHMTVEVRRCPHHERCSDSDGLAPPOHLIRVEGNLYRAKYLDDRNFRHSVVVVPYEPPEVGSDCYTIHYNYMKNSSCMGGMNRRLILITILEDSSGNVLRNSFEVVRVCACPGDRDRTEENLRKKK 286  
 gi|18859503|ref|NP\_571402.1| MVVDVAPPQGSVVRATAIYKKSQHMTEVRRCPHHERCPDG-DNLAPAGHLIRVEGNLYRAKYLDDRNFRHSVVVVPYEPPEVGSDCYTIHYNYMKNSSCMGGMNRRLILITILEDSSGNVLRNSFEVVRVCACPGDRDRTEENFRKKG 261



gi|6755881|ref|NP\_035770.1| VLCPELPPGS-AKR-----ALPTCTSSA--PQKQKP--LDGEYFLLKIRGRERFEMFRELNEALELKDAAHATEESGDSRAHSSYLKTKKGQSTS---RHKKLMVKKVG-PDSD 390  
 gi|13591878|ref|NP\_112251.1| EHCPELPPGS-AKR-----ALPTS TSSA--PQKQKP--LDGEYFLLKIRGRERFEMFRELNEALELKDARAEEESGDSRAHSSYLKTKKGQSTS---RHKKLMVKKVG-PDSD 391  
 gi|187830777|ref|NP\_001119584.1| EPHHELPPGS-TKR-----ALPNTTSSS--PQKQKP--LDGEYFLLQIRGRERFEMFRELNEALELKDQAQKKEPQGSRAHSSHLKSKKGQSTS---RHKKLMFKTEG-PDSD 393  
 gi|114666241|ref|XP\_511957.2| EPHHELPPGS-TKRDSLSPFLASFLALPNTTSSS--PQKQKP--LDGEYFLLQIRGRERFEMFRELNEALELKDQAQKKEPQGSRAHSSHLKSKKGQSTS---RHKKLMFKTEG-PDSD 405  
 gi|50978974|ref|NP\_001003210.1| EPCPEPPPSS-TKR-----ALPPTS TSSA--PQKQKP--LDGEYFLLQIRGRERFEMFRELNEALELKDQAQKKEPQGSRAHSSHLKSKKGQSTS---RHKKLMFKREG-LDSD 381  
 gi|28849929|ref|NP\_776626.1| QSCPEPPPSS-TKR-----ALPTNTSSS--PQKQKP--LDGEYFLLQIRGRERFEMFRELNEALELKDALDGREPGESEHSSHLKSKKRFPSS---CHKPMLKREG-PDSD 386  
 gi|18859503|ref|NP\_571402.1| ETKTKMAKTTGTKR-----SLVKESSSATLRPEGSKKAKGSSDEEIFFLQVGRGRERYEILKKNLNSLELSDVVPASDAEKYRQKFMKKNKKNRESEPKQGGKLMVKDEGRSDSD 373

