

gi|73994354|ref|XP_848636.1| MEQRREGEPPQPPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|194674591|ref|XP_001788116.1| MERPEGEPPQPPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|8922675|ref|NP_060693.1| MERPEEGKSPPPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|27370050|ref|NP_766305.1| MELHGEPPPPPEPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|57164149|ref|NP_001009258.1| MEPHGEDEPPPPPEPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|118098395|ref|XP_415086.2| MERSEGECSRQQPPWGRLLRLGAEDEPHVLLRNRWETIGRRRGCDLSPFGNKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150
gi|153792019|ref|NP_001093485.1| MTNQDSD-----QAWGKLVKVDASPG-SEIVLINSECTVGRKKDCDLSPFANKLVSVDHCKIIVDEKSGQVSLDSTNGTIVINKLVVKKQTCPLQTDGVIYLVYRKNPEHNVAIYVESLNEKODITQDSFEANKENVFRVTKDTSG 150



gi|73994354|ref|XP_848636.1| AGGDDPP---VLPSSPTTQACFEPEPSTSTSDLFPNASTSSMEP--TSAGAPSSSSAPDAYISPKKEGSPVASDEIPIFPFALPDRERASFSLSLEPQDDELDLEPIRKKMKGGGDPDLTLQFLVADQ-CRDTHITLGNVSEAVKPP 300
gi|194674591|ref|XP_001788116.1| AGRGDDPPDQVLLSSPATQVCFEPEPSTSTSDLFPNASTSSMEP--TSAGRPPSSSSSRGRTDISPKKCGSPVASDEIPIFPFALPDRERASFSLSLEPQDDELDLEPIRKKMKGGGDPDLTLQFLVADQ-CRDTHITLGNVSEAVKPP 300
gi|8922675|ref|NP_060693.1| SS-----DP-----PILASQSIIVI--TCGSG-----GGGISPKKSGSPVASDEVSSFAALPDRKTAASFSLLEPQDDELDLEPIRKKMKGGGDPDLTLQFLVADQ-CRDTHITLGNVSEAVKPP 300
gi|27370050|ref|NP_766305.1| PGGGDDPP---VPLLSPMAQTCLREEPOPSTSTSDLLPASTSSIEPELTSAGAKHSSSSGPGNTSISPKGRSSLVANGELSSLSVPFQDKE-ASFSLLESKDHLELPKAKMKGGGELDTNLQLLVSGQ-RGNAQSSSEVDKDAVKKPP 300
gi|57164149|ref|NP_001009258.1| PGGGDDPP---VPLLSPMAQTCLREEPOPSTSTSDLLPASTSSIEPELTSAGAKHSSSSGPGNTSISPKKESLVANGELSSLSVPFQDKE-ASFSLLESKDHLELPKAKMKGGGELDTNLQLLVSGQ-RGNAQSSSEVDKDAVKKPP 300
gi|118098395|ref|XP_415086.2| PSCYEEPOPSTSTSNLNASSTSLIES---ASVEQDNPTSGKSYIK---YLLDVNAETSATISLSDKENAELGSRQTEEBEVLPEPAKMKGGGELDTNLQLLVSGQ-RGNAQSSSEVDKDAVKKPP 300
gi|153792019|ref|NP_001093485.1| PAP-----VEPVIIVKPLPQSHEDPQPSSTSSSLHFE---YNMPLSICSDVRSARKNPVSSSAVCKGDSISSGSPAQTRLKWTCWIDGEP--EEMQRKRKDRD-DPGFGSAHSDASA-DIPLRGASGKEKTEGATT 300



gi|73994354|ref|XP_848636.1| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|194674591|ref|XP_001788116.1| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|8922675|ref|NP_060693.1| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|27370050|ref|NP_766305.1| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|57164149|ref|NP_001009258.1| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|118098395|ref|XP_415086.2| KMEELTLCIICODLLHDCVSLQPCMHTFCAACYSGWMMERSLWCPICRCPVERICKNHILNLLVEAYLLOHPDKRSSEEDVRSMAARNKIITQDMLQPKVRRFSDEEGSSEDLELSDVDESSESDVSPVIVCRQCPYRRQGGQALPCPG 450
gi|153792019|ref|NP_001093485.1| KMEELTLCIICODLLDCISVQPCMHTFCAACYSGWMMERSLWCPICRCPVERIRKNHILNLLVEAYLLOHPDKRTEEDLRSMDARNKIITQDMLQPKVRRFSDEEASSDYLFELSDNDSDTSDMSQPMYCRQCPYRRQGGQALPCPG 450



gi|73994354|ref|XP_848636.1| PNSEPGVPOAAG-DAPSTSTSVKTAADYVICALQGSHAICTCCFOPMPDRRAEREQDPRIAPOOCVAVCLQPFCHLYWGCARTGCLGCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|194674591|ref|XP_001788116.1| PGSEPGAPQVPG-DAPSTASV-TAAQDYVICALQGSHAICTCCFOPMPDRRAERERDRIAPOOCAICLQPFCHLYWGCARTGCLGCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|8922675|ref|NP_060693.1| PEGEPGAPQALG-DAPPTSVSLITAVQDYVICALQGSHAICTCCFOPMPDRRAEREQDPRIAPOOCVAVCLQPFCHLYWGCARTGCGYCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|27370050|ref|NP_766305.1| PSELGALALGGEAPSTASLTPAD-YTCCPLQGSHAICTCCFOPMPDRRAEREQDPRIAPOOCVAVCLQPFCHLYWGCARTGCGYCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|57164149|ref|NP_001009258.1| PSELGALALGGEAPSTASLTPAD-YTCCPLQGSHAICTCCFOPMPDRRAEREQDPRIAPOOCVAVCLQPFCHLYWGCARTGCGYCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|118098395|ref|XP_415086.2| QETEAGGMOALG-DAPSTANFPAAVQEVVCPAQGSHVICTCCFOPMPDRRAEREQDPRIAPOOCVAVCLQPFCHLYWGCARTGCGYCLAPFCELNLGDKCLDGVLSNHHVESDVLKNYLAIRGLTWKNMLESLSVALQRGAFLLSDYRIT 600
gi|153792019|ref|NP_001093485.1| SAQSESLAKTAGDQPSFSSDSTIAAPQEFRCPPQASHLICCCLOPMPDRRFEHLF-PQVSPQHCLVQKPFCHVYWGCPRIQCHGCLARFSELNLNDKCLDGVFNQVSEVLYLSCRGMSEWRHLLQDSLQALQGLYHLSDYRIT 600



gi|73994354|ref|XP_848636.1| GNTVLCYCCGLRSFRELTYQYRNI PASLPPAVTSRPDCYWGRNCRTOVKAHAM----- 669
gi|194674591|ref|XP_001788116.1| GNTVLCYCCGLRSFRELTYQYRNI PASLPPAAVTSRPDCYWGRNCRTOVKAHAMKFNHICEQTRFKN 669
gi|8922675|ref|NP_060693.1| GDTVLCYCCGLRSFRELTYQYRNI PASLPPAVTSRPDCYWGRNCRTOVKAHAMKFNHICEQTRFKN 669
gi|27370050|ref|NP_766305.1| GNTVLCYCCGLRSFRELTYQYRNI PASLPPVTVTSRPDCYWGRNCRTOVKAHAMKFNHICEQTRFKN 669
gi|57164149|ref|NP_001009258.1| GNTVLCYCCGLRSFRELTYQYRNI PASLPPVTVTSRPDCYWGRNCRTOVKAHAMKFNHICEQTRFKN 669
gi|118098395|ref|XP_415086.2| GNTVLCYCCGLRSFRELAYQYRNI PAVLPPVTVTSRPDCYWGRNCRTOVKAHAM----- 669
gi|153792019|ref|NP_001093485.1| ANSFLCYCCGLRTFRELAYKYRERIPPSLPPDAVTVNRPDCYWGRNCRTOVKAHAMKFNHICEQTRFKN 669

