

gi | 291575192 | ref | NP_001167567.1 | MADGPRCKRRK-----QANPRRNN-----VTNYNTVVEVETNSDSDDEDDKLVHVEE--SVTDAADCEG--VPEDDLPDQTVLPGRRSSEREGNAKNCWEDDGTGKEGQEIL 95
gi | 73948810 | ref | XP_849865.1 | MADGPRCKRRK-----QANPRRNN-----VTNYNTVVEVETNSDSDDEDDKLVHVEE--SITDAADCEGGVPEDDLPDQTVLPG--SSEREGNAKNCWEDDAGKEGQEIL 95
gi | 76670887 | ref | XP_615192.2 | MAVGNKYFKQKEITCRGVCVNSIAREGLSEEVKLNRAGRATQVERHDCRLLGQCLWSARSRREGRGDVWEVAVNYNTVVEVETNSDSDDEDDKLVHVEE--SITDAADCEGGVPDDLPDQTVLPG--SAREGSAKNCWEDDAGKEGQEIL 148
gi | 6756073 | ref | NP_035676.1 | MADGPRCKRRK-----QANPRRNN-----VTNYNTVVEANSDDDEDDKLVHVEE--SITDAADCEGGMPDDELPAQTVLPG--GDRGGGAKNCWEDDQNVK-- 88
gi | 62899016 | ref | NP_037296.1 | -----MWTYITMEYSAIKN--DFMKFVG-----KWLKLESIILISE--LFGSK--DIHVK 45
gi | 45384096 | ref | NP_990462.1 | MADGPRCKRRK-----QANPRRNN-----VTNYNVIEANSDDDEDDKLVHVEE--SITDAADQASVPEDDLPDQTVLPG--NSEREGSNCSWEDEGK--ETKEIL 94
gi | 18858925 | ref | NP_571784.1 | MADGPRCKRRK-----QANPRRTN-----VSNYSHVLEGGSDSDDEDDKLVHVEE--SITDADGADQDSDVAPDDPN--GTADPD-----GRWDDVK 77



gi | 291575192 | ref | NP_001167567.1 | GPEAQADEAGCTVKKDDECESDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDENGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGRDRHVTFQSGC--NRKFKC 243
gi | 73948810 | ref | XP_849865.1 | GPEAQADEAGCAVKKDDECDSDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDDSGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGRDRHVTFQSGG--NRKFKC 243
gi | 76670887 | ref | XP_615192.2 | GPEARADEVGCAVKKDDECDSDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDENGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGREORHVTFQSGG--NRKFKC 296
gi | 6756073 | ref | NP_035676.1 | -----DNECDSDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDDNGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGREORHVTFQSGG--NRKFKC 222
gi | 62899016 | ref | NP_037296.1 | -----DDECDSDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDDNGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGREORHVTFQSGG--NRKFKC 179
gi | 45384096 | ref | NP_990462.1 | GPEAQSDEVGCTVKKEDCDSDAENEQNHDPNVEEFLQOQDIAVIFPEAPEEDQRQGTPEASGHDENGTPDAFSQLLCPYCDRGYKRFITSLKEHIKYRHEKNEEDNFCSLCSYTFAYRTQLERHMTSHKSGRDRHVTFQSGG--NRKFKC 242
gi | 18858925 | ref | NP_571784.1 | -----EECVSD--EDERSRDALVEEMLQGDIAVIFPEAPEDEPRQGTPEASGHDENGTPDSFSQLLCPYCSRGYKRYITSLKEHIKYRHEKSEEDNFCSLCSYTFAYRTQLERHMTAHKAGREORHVTFQSGGGNRKFKC 211



gi | 291575192 | ref | NP_001167567.1 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLIPVNGRPRP-----GLKTSQCSSPPLSASPGSPTRPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 387
gi | 73948810 | ref | XP_849865.1 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLMPVNGRPRP-----GLKTPQCSSPPLSASPGSPTRPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 387
gi | 76670887 | ref | XP_615192.2 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLMPVNGRPRP-----GLKTSQCSSPPLSASPGSPTRPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 440
gi | 6756073 | ref | NP_035676.1 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLMPVNGRPRP-----GLKTSQCSSPPLSASPGSPTRPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 366
gi | 62899016 | ref | NP_037296.1 | TFCGKAFYKHHLKEHLRIHSG-----SPTRPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 266
gi | 45384096 | ref | NP_990462.1 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLMPVNGRPRP-----GLKTSQCSSPPLSASPGSPARPQIRQKIEN--KPLQEQLSVNOIKTEPVDYEFKPIVVASGINCSTPLONGVFTGGGFLQATSS 386
gi | 18858925 | ref | NP_571784.1 | TFCGKAFYKHHLKEHLRIHSGEKPVECPNCKKRFSSHSGSYSSHISKKKICISLIPVNGRPRPSPATGAAKTPQCSSPPLSASPGSPARVQVDRKIDNSKPLQEQLPITQIKSEPLDYEFKPIVVASVAP-----IARVGNVMTFGG-----AAAP 352



gi | 291575192 | ref | NP_001167567.1 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNQANLASKEQETINASSIQGGHVSIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--VATNSCKSEKLPEDLVKSEKDKSFEGGVNDSTCLLCD 536
gi | 73948810 | ref | XP_849865.1 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNQASLASKEQETINASSIQGGHVSIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--VPTNSCKSEKLPEDLVKSEKDKNFEGGVNDSTCLLCD 536
gi | 76670887 | ref | XP_615192.2 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNQANLASKEQETINASSIQGGHVSIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--VPTTNSCKSEKLPEDLVKSEKDKSFEGGVNDSTCLLCD 589
gi | 6756073 | ref | NP_035676.1 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNQANLASKEQAVSASPIQGGHVSIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--APTNSCKSEKLPEDLVKSEKDKSFEGGVNDSTCLLCD 515
gi | 62899016 | ref | NP_037296.1 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNQANLASKEQAVSASPIQGGHVSIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--APPKSCSEKSPEDLVKSEKDKSFEGGVNDSTCLLCD 415
gi | 45384096 | ref | NP_990462.1 | POGVVQAVVLPVTVGLVSPISINLSDIQNVLKVAVDGNVIRQVLENNHANLASKEQETINASSIQAGHSLISIAISLPLVDQDGTTKIINIYSLQPSQLOVVPQNLKKEKNEP--VPTNSCKNEKLPEDLVKSEKDKNFEGGVNDSTCLLCD 535
gi | 18858925 | ref | NP_571784.1 | LQGAQAVVLPVTVGLVSPISINLGDIQNVLKVAVDGNVIRQVLESTQAKQQAGTGIVGAGGIAATQVQVQATSLPILPDQGNKIFITVSELD--PSQAQAVLSPKKEPLGNTVEVCKGOKLPEDLVKSNRDK-----PILTVD 492



gi | 291575192 | ref | NP_001167567.1 | DCPGDINALPELKHYYDLKQPTOPPPLPAAEAKEPSSVSSAGDGNLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQISVOSSEPPSSPEPGKVNIPAKNNDQPSANANEPDSTVNLQSPKLMKN 686
gi | 73948810 | ref | XP_849865.1 | ECPGDINALPELKHYYDLKQPAQPPPLPAEAKEPSSVSSG--GDGNLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQISVOSSEPPSPETGKVNIPKNDQPSSTNANEPDSTVNLQSPKLMKN 685
gi | 76670887 | ref | XP_615192.2 | DCPGDINALPELKHYYDLKQPAQPPPPPTPEAAKPEAAASSGSDGSLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQISVOSSEPPSPGKANTPAKSNQPSAADADAQDSTGNRQSPKLRAS 739
gi | 6756073 | ref | NP_035676.1 | DCPGDINALPELKHYYDECPAQPPTPEAAKPEKPESSASSA--GNGDLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQIPGQSPDPPSPGTGSVNIPTKTDQPPADGNEPQEDSTRGQSPVKIRS 663
gi | 62899016 | ref | NP_037296.1 | DCPGDINALPELKHYYDEHPAQPPTPEAAKPEKPESSASSA--GNGDLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQIPGQSPDPPSPGSGNIPAKTEEQPPVDGNEPQEDSTRGQSPKLMKS 563
gi | 45384096 | ref | NP_990462.1 | DCPGDINALQELKHYYEKNPQIPQSSGTAEKPSAPSETEGNNLSPSQPPLKLLSLLKAYYALNAQPSABELSKIADSVNPLPLDVVKWFEKMQAGQISVOSSEPPSPQVLISSFTDNDQATNTSESEPNSTNSQNPANTK 685
gi | 18858925 | ref | NP_571784.1 | EKS--MLHNDILLKHCQGD-----EHRINGKNLEKMDLEGLCPGQPLKLLSLLKAYYALNPEPKELAKISEVSLPAEYVVKWFEKMQAGQISMDDPSQHE--EQTTFVDLDGKASPKPDLDEQMSKQEBECC 628



