

gi|6680512|ref|NP_032442.1| MCTKMEQPFYHDDSYAAAGYGRSPGSLSLHDYKLLKPTLALNLADP-YRGLKGPARGPGPEGSAGSYFSGGSDTGASLKLASTEERLIVPNSNGVITTPPPGQYFPRGGSGGGTG--GGVTEEGEGFADGFVKALDDLHKM 146
gi|40254775|ref|NP_068608.2| MCTKMEQPFYHDDSYAAAGYGRSPGSLSLHDYKLLKPTLALNLADP-YRGLKGPARGPGPEGSAGSYFSGGSDTGASLKLASTEERLIVPNSNGVITTPPPGQYFPRGGSGGGTG--GGVTEEGEGFADGFVKALDDLHKM 146
gi|4504809|ref|NP_002220.1| MCTKMEQPFYHDDSYATGYGRAPGGLSLHDYKLLKPSLAVNLADP-YRSLKAPGARGPGPEGGGGSYFSGGSDTGASLKLASSELERLIVPNSNGVITTPPPGQYFPRGGSGGGAGGAGGGVTEEGEGFADGFVKALDDLHKM 149
gi|114675615|ref|XP_524126.2| MCTKMEQPFYHDDSYTTTGGRAPGGLSLHDYKLLKPSLAVNLADP-YRSLKAPGARGPGPEGGGGSYFSGGSDTGASLKLASSELERLIVPNSNGVITTPPPGQYFPRGGSGGGAGGAGGGVTEEGEGFADGFVKALDDLHKM 149
gi|57101922|ref|XP_542043.1| MCTKMEQPFYHDDSYAAAGYGRAPGGLSLHDYKLLKPSLALNLADP-YRSLKAPGARGPGPEGSAGSYFSGGSDTGASLKLASSELERLIVPNSNGVITTPPPGQYFPRGGSGGGAGGAGGGVTEEGEGFADGFVKALDDLHKM 149
gi|115497082|ref|NP_001069124.1| MCTKMEQPFYHDDSYAAAGYGRTPGGSLSLHDYKLLKPSLALNLSDP-YRNLKAPGARGPGPEGGGGSYFSGGSDTGASLKLASSELERLIVPNSNGVITTPPPGQYFPRGGSGGGAGGAGGGVTEEGEGFADGFVKALDDLHKM 149
gi|47174747|ref|NP_998721.2| MSTKMEQPFY-DDSFLSA-YGHP--DAALHDYKLLKQNMVSFAEP-YRNLKTLRSE-----IDFYLAATGDVG-SLKLASPELERLIQNGNGVITS-PTP-GQYLYGRS-----ITTEEGEGFADGFVKALDDLHKM 120
gi|47086549|ref|NP_997915.1| MSTKMEQPFYHDDSFLLG-YGHN--DAALHDYKLOKPGMNLNVEPPYRSLKS-----DLYQASSADVG-SLKLASPELERLIQNGNGVITS-PTP-GQYLYGRS-----ITTEEGEGFADGFVKALDDLHKM 117



gi|6680512|ref|NP_032442.1| NHVTTPNVSLGASGGPQAGPGG-VYAG--PEPPPVYTNLSSYSPASAPSGGSGTAVGTGSSYPTATISYLPHAPPFAG-----GHPAQLG--LSRGSAFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 280
gi|40254775|ref|NP_068608.2| NHVTTPNVSLGASGGPQAGPGG-VYAG--PEPPPVYTNLSSYSPASAPSGGSGTAVGTGSSYPTATISYLPHAPPFAG-----GHPAQLG--LSRGSAFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 280
gi|4504809|ref|NP_002220.1| NHVTTPNVSLGATGGPPAGPGG-VYAG--PEPPPVYTNLSSYSPASASSGGAGAAGVTGSSYPTTISYLPHAPPFAG-----GHPAQLG--LGRGASTFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 283
gi|114675615|ref|XP_524126.2| NHVTTPNVSLGATGGPPAGPGG-VYAG--PEPPPVYTNLSSYSPASASSGGAGAAGVTGSSYPTTISYLPHAPPFAG-----GHPAQLG--LGRGASTFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 283
gi|57101922|ref|XP_542043.1| NHVTTPNVSLGASGGPAGPGG-VYAG--PEPPPVYTNLSSYSPASAPSGGAGAAGVTGSSYPTATISYLPHAPPFAG-----GHPAQLG--LGRGASTFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 283
gi|115497082|ref|NP_001069124.1| NHVTTPNVSLGASGGPAGPGG-VYAG--PEPPPVYTNLSSYSPASAPSGGAGAAGVTGSSYPTATISYLPHAPPFAG-----GHPAQLG--LGRGASTFKEEPTVPEARSRDATPPVSPINMEDQERIKVERKRLNRRLAAT 283
gi|47174747|ref|NP_998721.2| NMPPPNVSI GAPVSSCSVAS-VFGASLPPETPVYITLNSCNPNINLT-----PAANYPTATISYLPHHHHHQQYHHHHHQPTPHPHFQHS-LHPQRLVTLKEEPTVDPDQSDGSPPMSPIDMEDQERIKVERKRLNRRLAAT 261
gi|47086549|ref|NP_997915.1| NMPPPNVSI GAPVTTCTTASVFGSSLQSEPIYITLNAFCP-----APSHPTTISYLPSTHQSSQ-----HPEI--AHAFQHPGVLPQRFLPLKEEPTVDPDQSDGSPPMSPIDMEDQERIKVERKRLNRRLAAT 246



gi|6680512|ref|NP_032442.1| KCRKRKLERIARLEDKVKTLKAENAGLSAAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 344
gi|40254775|ref|NP_068608.2| KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 344
gi|4504809|ref|NP_002220.1| KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 347
gi|114675615|ref|XP_524126.2| KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 347
gi|57101922|ref|XP_542043.1| KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 347
gi|115497082|ref|NP_001069124.1| KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSNQCQLLLGVKGHAF 347
gi|47174747|ref|NP_998721.2| KCRRRKLERISRLLEDKVKVLKSDNAGLSSTASLLREQVAQLKQKVMTHVSSGCQLMLTPKIKSF 325
gi|47086549|ref|NP_997915.1| KCRRRKLERIARLEEKVKVLKSDNAGLSNTASVLRREQVAQLKQKVLRHMNSSGCQLMLTKMEAF 310

