

gi | 145610181 | ref | XP_366588.2 | MQRPEQAYGQSPPLHHP-----VPHQVSTVPQLRSPPPPVSOQAQS-----GGYGGSPYPQQQGGAGPQNMFGQYQGFQMDPAQVAHFGSTAFRGGIIDDININRYLSVHLLKHYPNVTNSVIVNK 120
gi | 32408647 | ref | XP_324804.1 | MQRSE-GYQSPPLHHP-----VPHQVSTVPQLRSPPPPTSQPHS-----GYDGGSPY--QQQGRAPSGNMFQYGNFINDPAAQLASQFGQAFKGGQBYLEQNVNRFVSVSALKHYFNVTNSVIVNK 114
gi | 19113152 | ref | NP_596360.1 | -----MPPKLYHP-----QPHTAIPVSNMR-----VNIITYEP-----TAGFSGSIVP-SVQAAANPSAYLFP-----NSAAQMGFQLGKNAVAGQEVVEVNFQKWLSTTRLLHHYFTVTNSVIVAK 99
gi | 170932464 | ref | NP_065203.2 | -----MAVHSYGGAHG-----SKHRARAAADPP--PPLFDDTSGG-----YSSQPGGYPATGADVAFS--VNHLLGDPMANVAMAYGSSIASHGKDMVHKELHRFVSVSKLKYFFAVDIADVAKK 105
gi | 114638673 | ref | XP_001171098.1 | -----MAVHSYGGAHG-----SKHRARAAADPP--PPLFDDTSGG-----YSSQPGGYPATGADVAFS--VNHLLGDPMANVAMAYGSSIASHGKDMVHKELHRFVSVSKLKYFFAVDIADVAKK 105
gi | 73982992 | ref | XP_852515.1 | -----MAVHSYGGAHG-----SKHRARAAADPP--PPLFDDTSGA-----YSSQPGGYPATGADVAFN--VNHLLGDPMANVAMAYGSSIASHGKDMVHKELHRFVSVNKLKYFFAVDIADVAKK 105
gi | 77735493 | ref | NP_001029441.1 | -----MAVHSYGGAHG-----SKHRARAAADPP--PPLFDDTSGG-----YSSQPGGYPATGADVAFN--VNHLLGDPMANVAMAYGSSIASHGKDMNKLHRFVSVNKLKYFFAVDIADVAKK 105
gi | 25282409 | ref | NP_080829.1 | -----MAVHSYAGVHG-----SKHRARAAADPP--PPLFDDTSGG-----YSSQPGGYPATGADVAFS--VNHLLGDPMANVAMAYGSSIASHGKDMVHKELHRFVSVNKLKYFFAVDIADVAKK 105
gi | 41282065 | ref | NP_956225.1 | -----MNFQQ-QGVR-----TKPRARASPTTGGPMLFDDTSSGPF-----PFMNNQNYYS--GYNMAEMPAGGQEPG-----VGNIFADPMANAMMYGSTLANQKDIVNKEINRFMSVNLKLYFFAVDIADVAKK 115
gi | 115533208 | ref | NP_001041126.1 | -----MNEWGNDWNTDTSWNTGYSQPQPSAPPAAPAAAPDQGGYGGYYSQSSNOGFDGYYGQOSPTONQYGGYQQQQQSYQONNGFGGFPPQQLMSDPMNAAKQFGGQFAEQK-----EKLTKLYLGTFNLYFFAVDIADVAKK 141
gi | 50304711 | ref | XP_452311.1 | -----MSYNPYVSEIGSDSNVG-----MAAAGKKNISATGKQYGMQPPS-----LGPOTFQQQQQNGSYLPSASTNMAFQFGQAFNPFVQGENISQFQELMSKATG--ATNSSVAHYFQVNSVVFHK 114
gi | 45199177 | ref | NP_986206.1 | -----MTYNPYV-EQSQAQAR-----YPCQGRQMQQTTPADPRVYQQQYQ-----TAPQGPAYAG-----FADPRASMAFQFGQALNPFIGENFNQFQVQRAITG--GGD--LSHYFQVNSVVFQK 105
gi | 6324066 | ref | NP_014136.1 | -----MSYNPYVAMASEQNGVNDRF--HTPQQQRPMQIPRNTFVNQOQNG-----MNANVNGSGG-----GFFPQDPRGSMFAFQGSASFNSFQGDNFNQFQELVTKATANAAGSQQISTYFQVSRVIVNK 118
gi | 115468982 | ref | NP_001058090.1 | -----MAAMNDLQ-----GLGGRPAISQANPFFSALYCG-----AGPGLIRSLGAYGKFLGSSSEFMQSNITLYLSNP--DYFQVNSVIVNK 79
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 145610181 | ref | XP_366588.2 | IYLVLEPWRH--KPWSRKPAMG--PGGQEG--VLPRDLDVNSPDMYIPVMSLVYIILLSTAIAGLRG-----QFQPELLGNTAGTALIVVAAEIILKLCYVMSI--SNNSQLLDLVAYSQYKFGVIVVAVAEVMNGGK 250
gi | 32408647 | ref | XP_324804.1 | LYLVLFPWRH--KPWSRKPAMG--PGGQEG--VLPRDLDVNSPDMYIPVMSLVYIIFLQTLIAGLRG-----QFQPELLGNTAGTALIVVAAEIILKLCYVMSI--SNNSQLLDLVAYSQYKFGVIVVAVAEVMNGGK 245
gi | 19113152 | ref | NP_596360.1 | LLLIIFPWRH--RSWAKLRREINGSAERG--KCPAEDLNSGDMYIPLMAFTTHILLCALAGLID-----DFQPELLGLRASKACAVVVEFLATRLGCYLLNI--SQSQVLDLLAFSGYVGLIIT--SLSKLFEFMP-- 228
gi | 170932464 | ref | NP_065203.2 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 114638673 | ref | XP_001171098.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 240
gi | 73982992 | ref | XP_852515.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 77735493 | ref | NP_001029441.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 25282409 | ref | NP_080829.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 41282065 | ref | NP_956225.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 115533208 | ref | NP_001041126.1 | LGLLVFPYTH--QNWEE--VOYS-RDAPLPPRODLNAPDLYIPTMAFIYVLLLAGMALGIQK-----RFSPEVLGLCASTALVWVVMVEVLALLGLYLATV--RSDLSTFHLLAYSQYKFGVIVVAVAEVMNGGK 228
gi | 50304711 | ref | XP_452311.1 | LKLVLLPMLH--KQWR-----IPDTSNSQPFRIDVNSPDMYIPVMSLVYIILAVNVVQGLNG-----SFDPENLYFKLSSSLAFVFLDLIILRLGLYLLVLS--NITVFTSLVELCYVGYKFGVIVVAVAEVMNGGK 240
gi | 45199177 | ref | NP_986206.1 | LKLVLLPMLH--KQWR-----IPDTSNSQPFRIDVNSPDMYIPVMSLVYIILAVNVVQGLNG-----SFDPENLYFKLSSSLAFVFLDLIILRLGLYLLVLS--NITVFTSLVELCYVGYKFGVIVVAVAEVMNGGK 230
gi | 6324066 | ref | NP_014136.1 | LKLVLLPMLH--KQWR-----IPDTSNSQPFRIDVNSPDMYIPVMSLVYIILAVNVVQGLNG-----SFDPENLYFKLSSSLAFVFLDLIILRLGLYLLVLS--NITVFTSLVELCYVGYKFGVIVVAVAEVMNGGK 246
gi | 115468982 | ref | NP_001058090.1 | LKLVLLPMLH--KQWR-----IPDTSNSQPFRIDVNSPDMYIPVMSLVYIILAVNVVQGLNG-----SFDPENLYFKLSSSLAFVFLDLIILRLGLYLLVLS--NITVFTSLVELCYVGYKFGVIVVAVAEVMNGGK 206
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 145610181 | ref | XP_366588.2 | TGGVSGVSVFYIFLANSFLMRSLKYVLLPENADNR-----MQLDTRAKNRQTFQFFVYVYVLLFFMWILSRP----- 322
gi | 32408647 | ref | XP_324804.1 | TGGVIGWVTFGYEFFANALFLMRSLKYVLLPENADNR-----MQLDTRAKNRQTFQFFVYVYVLLFFMWILSRP----- 322
gi | 19113152 | ref | NP_596360.1 | -----WVTRFVFLMYLAIAFFLLRSKYAVLPSMAIN-----AITSHQRSRRIRYFLFFIA-ASQILFMYVLS----- 293
gi | 170932464 | ref | NP_065203.2 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 293
gi | 114638673 | ref | XP_001171098.1 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 305
gi | 73982992 | ref | XP_852515.1 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 293
gi | 77735493 | ref | NP_001029441.1 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 293
gi | 25282409 | ref | NP_080829.1 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 293
gi | 41282065 | ref | NP_956225.1 | -----GYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 307
gi | 115533208 | ref | NP_001041126.1 | -----FYVVALAWTS--SALMYFIVRSLRATAALG--PDSMG-----GPVPRQRLQVLYTLGAAAFPLIYWLTFHLVR----- 349
gi | 50304711 | ref | XP_452311.1 | -----LNRLAKLYLFAVGVFLRSIKFNFLA-----DMGN--SADFSFKKGTVKKVNFVYVYVLLFFMWILSRP----- 305
gi | 45199177 | ref | NP_986206.1 | -----ATVLGKFLYLFMAFGIFLLRSVKFNLFN-----DTAN--DVN--TVKKSVMKCNVFLFYVYVLLFFMWILSRP----- 294
gi | 6324066 | ref | NP_014136.1 | -----LNILKFLYLFMAFGIFLLRSVKFNLFN-----DTAN--DVN--TVKKSVMKCNVFLFYVYVLLFFMWILSRP----- 314
gi | 115468982 | ref | NP_001058090.1 | -----YFVLVWFLVYVYVLLFFMWILSRP-----APRS-----YERHPSRNHYVLLFLAVVQFPLMFLWGLNLSG----- 267
.....310.....320.....330.....340.....350.....360.....370.....380.....390

