

gi | 21361553 | ref | NP_003168.2 | MASSGMADSANHLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 114625493 | ref | XP_520123.2 | MASSGMADSANHLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 56550045 | ref | NP_035648.2 | MAGS-AVDNANHLTYFFFGNIITREAEADYLVGGMTDGLYLLRQSRNYLGGFALSVAHNRKAHHTIERELNGTYAISGGRAHASPADLCHYHSQEPDGLICLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 6981620 | ref | NP_036890.1 | MAGN-AVDNANHLTYFFFGNIITREAEADYLVGGMTDGLYLLRQSRNYLGGFALSVAHNRKAHHTIERELNGTYAISGGRAHASPADLCHYHSQEPDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 73946720 | ref | XP_850411.1 | MAGS-MADSANHLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 82697355 | ref | NP_001032542.1 | ----MCDGANLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQEPDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 71895287 | ref | NP_001026601.1 | MASN-MANPANHLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQEPDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
gi | 47086347 | ref | NP_998008.1 | ----MVDKVLPPFFFGNIITREAEADYLVGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAIAAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPGVQPKTGPFDLKENLIREYVKOTWNLGGQALBQAIISQ 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 21361553 | ref | NP_003168.2 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----NVNFGGRPLPGSHPATW 300
gi | 114625493 | ref | XP_520123.2 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----NVNFGGRPLPGSHPATW 300
gi | 56550045 | ref | NP_035648.2 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----SGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----MGHPGSPNAHPVTW 300
gi | 6981620 | ref | NP_036890.1 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----MGHPGSPNAHPVTW 300
gi | 73946720 | ref | XP_850411.1 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----MGHPGSPNAHPVTW 300
gi | 82697355 | ref | NP_001032542.1 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRAKD-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----NINFRPLPSHPGTR 300
gi | 71895287 | ref | NP_001026601.1 | KPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----NVNFGGRPLPGSHPATW 300
gi | 47086347 | ref | NP_998008.1 | RPQLEKLIATTAHEKMPWFHFKIIRSESEIIVLIGSKTNGKFLIRARDN-----NGSYALCLLHEGKVLHYRIDDKDTGKLSIPGKKFDFLWQLVEHYSYKADGLLRVLTVPCOKIGTGG-----PSHISE-- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 21361553 | ref | NP_003168.2 | SAGGIISRIKSYSPKPKGHRKSSPAQGNRQESIVSNFNYEPE--LAPWAADKGPORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 114625493 | ref | XP_520123.2 | SAGGIISRIKSYSPKPKGHRKSSPAQGNRQESIVSNFNYEPE--LAPWAADKGPORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 56550045 | ref | NP_035648.2 | SPGGIISRIKSYSPKPKGHRKSSPAQGNRQESIVSNFNYEPE--GGPWGDRGLORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 6981620 | ref | NP_036890.1 | SPGGIISRIKSYSPKPKGHRKSSPAQGNRQESIVSNFNYEPE--GGPWGDRGLORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 73946720 | ref | XP_850411.1 | SAGGIISRIKSYSPKPKGHRKSSPAQGNRQESIVSNFNYEPE--LAPWAADKGPORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 82697355 | ref | NP_001032542.1 | TS-----SNGVDSSTTEFNPEYD--RGPWANEREAORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 71895287 | ref | NP_001026601.1 | TP-----IGAPSDDDTPFPNVLQARGLLGAEGKQORALPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
gi | 47086347 | ref | NP_998008.1 | TP-----GSAENFYKITSNGKD--NWSKGNFLDSAMPMDTEVYESPYADPEIRPKKVVLDRLKLLLEDKELGSGNFGTVKKGYYQMKVVKTVAVKILKNEANDPALKDELLAEANVMQOLDNPIYI 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 21361553 | ref | NP_003168.2 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 114625493 | ref | XP_520123.2 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 56550045 | ref | NP_035648.2 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 6981620 | ref | NP_036890.1 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 73946720 | ref | XP_850411.1 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 82697355 | ref | NP_001032542.1 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 71895287 | ref | NP_001026601.1 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
gi | 47086347 | ref | NP_998008.1 | VRMIGICEAESWMLVMEMAEGLPLNKYLQONRHVKDKNIIELVHQVSMGMKYLEESNFVHRDLAARNVLLVTOHYAKISDFGLSKALRADENYKQATHGKWPVKWYAPCEINYYKFSKSDVVSFGVLMWEAFSYGQKPYRGMKGSSEVT 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 21361553 | ref | NP_003168.2 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 114625493 | ref | XP_520123.2 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 56550045 | ref | NP_035648.2 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 6981620 | ref | NP_036890.1 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 73946720 | ref | XP_850411.1 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 82697355 | ref | NP_001032542.1 | AMLEKGERMCCPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 71895287 | ref | NP_001026601.1 | QMTERGERMECPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
gi | 47086347 | ref | NP_998008.1 | QMTERGERMECPAGCPREMYDLMLNCWTYDVENRPGFAAVALRRLRNYYDDVNV 653
.....610.....620.....630.....640.....650

