

AT4G11140.1 -----METEKVSLP-----RILRISVTDPYATDSSSDEEEVDFMDFALSTKRRRVKRYVHEVWDS--VVSDEKPKM-KRKRKRVT-----
 VPVVVTTAT---- 88
 AT4G23750.1 -----MEAKKMVLPRIKFTEHKTNTTIVSELTNTHQTRILRISVTDPDATDSSSDEEE-EHQRFVSKRRRVKRFVHEVYLDGSAVVTGSCGQMESKKRQKRAVKSE-----
 STVSPVVSATTTTTTGE 119
 AT5G53290.1 --MDEYIDFPLKYTEHKTSMTKYTKKSS--EKLSGGKSLKKVSLCYTDPDATDSSSDEDEE----DFLPFRRVKRFVHEITVEPSCNNV--
 VTGVSMKDRKRLSSSDDETQSPASSRQRPNKVSVSQ-I 123
 AT4G27950.1 MMMDEFMDLRPVKYTEHKTVIRKYTKKSSMERKTSVRDSARLVRVSMTRDADTSSSDEEE----FLPFRRVKRLIHEITVEPSSSSTGDVVSASPTKDRKRINVDS-----TVQKP----
 SVSGQNQ 119
 AT2G46310.1 ----MKSRLKSKYTVHRKIT---STPPD-----GFPKIVKIVTDPDATDSSSDEE----NDNKSVAPEVKRYVHEITVECD-EDDEPKPARKAKKSP-AAAAEN-----
 GDDLKVS 101
 AT3G61630.1 ----MERRTRVKFTENRVTINVAATPSN-----GSPRLVRITVTDPFATDSSSDDDD----NNNVTVVPEVKRYVHEITVECDQGESSSSTAARKGKHEEESVVVED-----
 DVSTSVKP 107

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AT4G11140.1 RKFRGVRQRPWGKAAEIRDPSRRVRVWLGTFDATAEEAAIVYDAAIQLRGPAELNF-----PPPVTENVEEASTEVEKGVSD----
 FIIGGECRLRSPSVLSDFSGESTAVKEEFVGVST- 200
 AT4G23750.1 KKFRGVRQRPWGKAAEIRDPLKRVRLWLGTYNATAEEAAIVYDAAIQLRGPAALTNFSVTPPTTATEKKAPPPSPVKKKKKKNNKSKSVIASSSISRSSSNDCLCSPVSVLSPFA-----
 VDEFSGISS 252
 AT5G53290.1 KKFRGVRQRPWGKAAEIRDPEQRRRIWLGTFDATAEEAAIVYDAAIRLRGPAALTNFSIPPQEEEEEE--EPEVIEEKPVIMTPTPTSSSE-STEEDLQHLSSPSVLRHR-----
 SEE-IQQV 252
 AT4G27950.1 KKFRGVRQRPWGKAAEIRDPEQRRRIWLGTFDATAEEAAIVYDAAIKLRGPAALTNFTVQP-----EPEVQEQE--QEPESNMSVIS-ESMDSQHLSSPVSVLYQTY-----
 VSEPIDSL 235
 AT2G46310.1 VFRGVRQRPWGKAAEIRDPSRRTRWLGTFDATAEEAAIYDAAIRIKGHAQTNFLTTPP-----SPTTEVLPETPVIDLEIVSGCDSARESQISLCSPPVSVLFSHN--
 DETEYRTEPTTEEQ- 218
 AT3G61630.1 KKFRGVRQRPWGKAAEIRDPSRRTRWLGTFDATAEEAAIYDAAIHLKGPALTNFLTTPP-----TP-----TPVIDLQIVSACDYGRDSRQSLHSPVSVLFNVN--
 EETEHEIEAIELSP 216

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AT4G11140.1 --AEIVVKKEPSFNG----SDFSAPLFSDDVFGFSTSS-ESFGGLFGDNLF-ADMSFGSGFGFCSG-----SGFSSWHVEHFQDIDGLFGSDPVLTV 287
 AT4G23750.1 PVAVVVKEPSMTTVSETPDFSAPLFSDDVDFDRSSVDPYLGGLFGEDFTADMCTDMNFGDFG-----SGLSSWHVEHFQDIDGLFGSDPLLAV 343
 AT5G53290.1 QQPFSKAPPEPGVSNAPWWHTGNTGLGESDPSFPLDTPLDNYENESPPMESLFDQPMQIFCENDIFNDMLFLGGETMNIEDELTSSSIKDMGTFSDPDSLSISDLLVA- 354
 AT4G27950.1 IKPVKQEFLEPEQEPISWHLGEGNT--NTNDLSPFLDITLDNYENESLFDISLFDQPMSPIQPTENDFNDMLFLFDSN---AEEYSSSEIKELGTFSDPDSLSISDLLV- 335
 AT2G46310.1 -----NPFPLPDLFRSCDYFDSEITPDPLFLFLFHQSLLPNINNNNTVCDKDTNL-----SDSFLGVIGDES--WDVDFEQDHLDDK- 294
 AT3G61630.1 ERKSTVIKEEEESSAGLVFPDPYLLPDLSLAGECFWDEHAPDLFLDEETK-LQSTLLPNTEVSKQGENE-----TEDFEFGLIDRESPWVDVDFEDHHSFSD 315

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