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AT5G48655.1 M-----NISEVVRVPRGNRRRKAV-----IDLNAV-P---VDQ@GTSAS-----VRLTLVPIITPSQPA-----PTMI DVDAI--EDDV-IESSASAFAEAKSKSRNRRRRPLM-VDV 88
POPTR_0002s24690.1 M-----SQGQGVKSPFL-RGYRKRKTV-----LDLNV-P-IDGRDDEBTSTTRI-----EPQATNETKDRICRLLLLM-LML 67
POPTR_0014s18890.1 M-----STQ@QGVKSPFL-RGYRKRKTV-----LDLNAV-P-TBGRDDEBTSSR-----TEPQGVQASQQGSLF-----PTTIDVDVF--DDDV-IESSPTAFPAEAKNSRRRARGRAVV-VDV 97
GSVIVT01007471001 M-----N-----PVP-----PAIDVEAI--DDEV-VESSATAFAAARNNSRRRGRVYVDVL 45
AT3G07200.1 M-----ASRVVRTSMRLRRRDGVTVQN-----EHQGGQVQVQAPTVPQI--VATPPIRNVVAIEDDDV-VBSTASAFQAQKNSRRRARGRAVV-VDV 84
GSVIVT01020997001 M-----STQDLS@QNGSERCIIEEETLL-----LDLNV-P-PPSDNVALESTFTS-----SSPLLELYAKQDRSNP-----QATNVDAS--DDDVILSSPRSLFLAARNSRRRARGRAVV-NDN 101
LOC_Os09g32690.1 M-----STVSGTRRAPRRQ@QDGSADKVVVN--LDAISS-PVVG-----SRRAVPTST--GARASPIDVEAL--DDEVQTL-SASQVPPRRNRNRTRRQPVAV-VDL 88
Bra1d4g34450.1 M-----STISGARRASGRQR--SADKVVVN--LDM-SS-QLQG-----SRGVSTST--GARTSPIDVEAL--DDEVQAI-LPSQV-PQRNRGRTRRQPVAV-VDL 85
Sb02g029150.1 M-----STVSGTRRAPRRQ@QDGSADKVLVI--IEA-SS-RVAG-----SRGPTTVPV--GARNSPI DEVAL--DDEVQAV-SPSRVPPRRNRNRTRRQPVAV-VDL 88
GRMZM2G013892_T01 M-----NTVSGTRRAPRRQ@QDGSADKLVVI--VEA-SS-RGVG-----SRGPHAPIP--GALNSPIDVEAL--EDEVQAV-SPSRVPLPRNRNRTRRQPVAV-VDL 88
Bra1d3g40940_F M-----SAVSTAAARSRRRAQEDGLAREKAVVVLEAAGS-PVAGGGD-----SRVAPIPGT@AGTQGSPI DEVAL-----VDG 68
LOC_Os01g69040.1 M-----SSHDFARRVPRKRRTNKLSQL-----PDLNSL-P-ARGADDGSPSSSVLVSHAQTSAVA--VAGTSQLVPAVVAGPHI--GMSSCFIIVDDI--DDVVYI-SASSFPQVRQAPRTEPV-VT-IED 116
Bra1d2g58870.1 M-----SSLGFARIIPKRRRTQVPSVLVNRQLDLMLL-PAAGGTGNGSFSPTNEVSHSRASGVV--VAGTSQLVPPGAESNI--RMNSFPIDVEVI--DDVVYI-SASSRSLFRARQSTRAVPVTVI-IDD 123
Sb03g043910.1 M-----NSHGAGRRTPKRRRTTKGHSQL-----LDLNV-P-ABGAGEGALPFNSMPLVHIQASSMPVQHIQASS--TPPATDEPRI--GMLSCPIDVEAI--DDVVYI-SASSLQARQOS--TRTAVVI-IDD 117
GRMZM2G359505_T01 M-----NSHGAG-----SHSRL--LDLNV-P-ABGAGEGASRFSPIVSHREGSSMPVQHIQASS--TPPATDEPRI--GMNSCFI DEVAL--DDDAVI-SSRPLFRARQQLTTESTIITII-IDD 107
POPTR_0003s14810.1 MDLLENFDSNMVFMK-----AENTMDLIGVDLLVENLWEAERSYFQH-FDLNFPVPPVENNIPCGPWFV-----AQPQIFQAEAYGLT--RQRTARDVEVI--DDDAII-SPNFDQARKARRNPDAEVR-ENI 122
POPTR_0001s11540.1 MNLLENFDNMMI FVENLDDNKVFLVHGDNMTDLIGNTDRLLEDLWEAERSYFQH-SNLNFPVPPVQNNMPLHGMVFP-----CHPRNFQAEVYGLT--RQHTAQDVEVI--DDDAII-SPNFDQARKARRNPDAEVR-ENI 131
solyc06g007870.1.1 F M-----SSQESSAQPIRRTRRSQRNRYLNLN--VDLNA--PPAENRIQEGDPIH-----VVSQDTPQGRNGSSLT--AGALDEVAL--DDDV-IISSPRAFVAKNSRRRQGRVIV-LDV 101
solyc09g059450.1.1 F M-----STQDRRAPMRYTRNOSRRKTVLD--VDLNV-P-PPSDNRDDEBTSSR-----VVGVDVPPAQRGASST-----PAPIDVEAL--DDDVMISSPRALAEANNSMTRRQVIL-VDE 102
GRMZM2G039968_T01 M-----QLHQNMQLQTFSSNCSSIEGRS VNEFVDACKK-----ATGVNKK--INFVLTWCASLQSPDRHHLMPKANKLL-KNK 72
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150.....160

AT5G48655.1 E--SGGTRFRPANISNKR-----RRIPSSSEVIDCE-HASVNDVEMMSRVSRSK-----APAPP--PEEPKFTCPICMCPFTEEMSTKGGHIFCKKCI KMAISROGKQPTCRKKVITAKELIRVFLPTTR--- 203
POPTR_0002s24690.1 S--TTTTT--SSNRR-----PERLLRN-----VQTLF--PKEPTFNGPIGLCLPLVEMSTKGGHIFCKKCI SDAIKRQAKQPTCRKRVTTKELIRVFLPATS--- 155
POPTR_0014s18890.1 E--SGRTSRLSHNLLNKR-----RRVPPNQTIIINCLDYINLEGGSSSSSRKREN-----VQTLF--PKEPTFNGPIGLCLPLVEMSTKGGHIFCKKCI ADAIKRQAKQPTCRKRVTTKELIRVFLPATS--- 213
GSVIVT01007471001 E--VQTRFPL--NRRNKR-----RRAPPNQTIIINDRYINLESSNLSL--LRNKPPPEQVHWVPLP--PKEPTFNGPIGLCLPLVEMSTKGGHIFCKKCI KAAISAQKQPTCRKRVTMKDTRIYVLPAS-- 163
AT3G07200.1 E--SAGA--NRSTR-----RR--SDQTSVD-----SVELNKPKRKSK-----AVAPP--VEEPKFSPIGLCPFTQEVSTKGGHIFCKKCI KNAISLQAKQPTCRKKIIVKDLIRVFLPTTR--- 182
GSVIVT01020997001 D--IEMPGHLGIVFDDIEMQG-----HQEIAQONKIITDLKLCLELNFKTETENVQIP--TEVFS--PETPTFCPIGMQDLTETSTKGGHIFCKKCI EGAMAVSQRCPPTCRKKLKKDRIYVLPKPK-- 220
LOC_Os09g32690.1 E--VDASRE--GNKR-----QRVAVPIHCLSP--RGESSL--K-----TSNEPK--AKEPVFNGPVCWNKLEPSTTIIGHIFCTTCIKQAIQIKKQPTCRKSLRANFHRVYLPNSDS-- 191
Bra1d4g34450.1 E--VDASOE--GNKR-----RRVAVPIN--ISPE--TGESSLQSKNAVK-----TKKPAKVPKPEPIFTCPVVCWNKLEPSTTIIGHIFCTTCIKOSIQVKKQPTCRKSLRANFHRVYLPNSVASG 197
Sb02g029150.1 E--VESSRE--GNKR-----QRVVPVGHLLSD--SGASSLQS-NAVQ-----TKKPAKVPKPEPFTFCPIGWKMEPSTTIIGHIFDTCIKQAIKIKKQPTCRKGLKMSAHRVYLPKASS-- 198
GRMZM2G013892_T01 E--VEASRE--GSKR-----QRVEPVGRHLVYD--WRASSLQS-NAAQ-----TSKPAKVPKPEPFTFCPIGWKMEPSTTIIGHIFDTCIKQAIKVKKKQPTCRKGLKMSAHRVYLPNGSS-- 198
Bra1d3g40940_F E-----RNNDVRLSRSSANVAPKNILK-----KVAPP--PKEPAFTCSVGLNKLQASTTIIGHIFDTCIKQAIKVKKKQPTCRKGLKMSAHRVYLPNTD-- 159
LOC_Os01g69040.1 D--SETTFQAGDAVDEHVILLSLTLGRYFRHGHQRSSNISTSPVLIHIDTFSN-----ALPEPEKAVPKPEFTFCPIGMNLEVPSTTIIGHIFCKKCI KASIQAKKQPTCRKLLMNNFHRVYLPNSAE-- 241
Bra1d2g58870.1 D--SETTAGPAGEALDEHVNTLLSL--GTNPRHHHSAG--VDNLVNIADTPEVNRVLPKVMQ-----APPEPVKEVPKPEFTFCPIGMNLEVPSTTIIGHIFCKKCI KLSIQTKKQPTCRKLLMNNFHRVYLPNTD-- 254
Sb03g043910.1 D--SETNPEAGDALDEHVNTLLSL--GINRRHESPRAG--NARPVISIVDPEVNTFK-----APPEPVKEVPKPEFTFCPIGMNLEVAESTVGGHIFCKKCI KAAIQAKKQPTCRKLLMNNFHRVYLPNTD-- 242
GRMZM2G359505_T01 D--SETNLETAGDALDEHVNTLLSL--GIERSHEPSTAT--NTFPGISMVDTPKVNTFK-----VPEPVKEVPKPEFTFCPIGMNLEVAESTVGGHIFCKKCI KAAIQAKKQPTCRKLLMNNFHRVYLPNSP-- 231
POPTR_0003s14810.1 NMANQVHAAGSVFPLPG--SSQAV-----PPSFPFGSSQTVPPQSLGSLTVPPPHFSGLS-----QTAPP--PPAPMFCPIGMNLEVAESTVGGHIFCKKCI KALAVKQKQPTCRMKCI AKSIRVFLPFL-- 245
POPTR_0001s11540.1 NIVMQ--ARVLIQFHLLSQPV-----PSPQLPQLQTMPPQPFQSQTEPPAQVSLGSL-----QAVFP--PAAPAFRCPIGMNLEVAESTVGGHIFCKKCI KALAVKQKQPTCRMKCI AKSIRVFLPFL-- 252
solyc06g007870.1.1 F D--SEDRAS--RGNRRNRH-----RRVSTNQAANNGDIHIDLEGHSCPKRVDLRS-----AIPAP--PKEPTFSCPIGMNLEVAESTVGGHIFCKKCI KASIAAQKQPTCRKLLMNNFHRVYLPNTD-- 215
solyc09g059450.1.1 F D--BEDHLP--MFRNRNRH-----RRVSTNQAANNGDIHIDLEGHSCPKRVDLRS-----EPTTPK--PIQPTFSCPIGMNLEVAESTVGGHIFCKKCI KASIAAQKQPTCRKLLMNNFHRVYLPNTD-- 225
GRMZM2G039968_T01 LYFPEGVSDSTIELKNAIKDSF-----YMKNOPLVSNSE-----HASLSQSEVLEPKFSGLIWNSELTEATSLVGGHIFCKKCI KASIAAQKQPTCRKLLMNNFHRVYLPNTD-- 173
.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300.....310.

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Fig. S11 Alignment of proteins with multiple SUMO interaction motifs and a RING domain