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AT1G68185.1 -----MGGEDELEPLFDYRRVQ---PANFVCIDDDDD--DASVTPI--PKKAKTSQT----VEKLDLDDVVKV--IEV----TGDDDWLLPPP---KVFIDKSKDSVEDSTIKALRSKKMELMSFTKTVDVMQEVVEESA 114
POPTR_0010s12880.1 -----MADSVEDLDSLFDYRRVQ---PIAILDEDDDDDEYDKFPVPS--PKRRKISKHN----VEIVGGDREA--SQV---TNDDDWLLPPP---KDSSEPKQIDEDSTIKELRLRKQELK--ALTSKECLFQYLESP 116
GSVIVT01011822001 MGVGVS-----PALEKSTEELEPLFDYSRVQ---PFNFVPLDDDDSD--DSSPNLT--PKRRKLSNS----SEEKNE--NV--TQVIDCKENEEEDWLP PPP---KLSVDVQNLGEDSTIKQLRLKKQELLFAESAKDLVLRTEESA 124
Solyc03g013030.1.1 -----MDESNEELEPLFDYRRVQPPNFNVAFLDDDDTP--DSSPVIS--KKRRKMIDST--AEKKKDKNEA--VQIIDC--BEKEEDWLPSP---SISA--HTSSLLEDSTIKELRLKKKELATPAQSAKDELRDVEESV 121
LOC_Os01g42250-P7 MAAAG-----AEAEAEDEELEPLFDYSRVQ---PTMAFSFDDTDI--EKSDIFVHCNKRKRVADGGDANADEKGDKGQKAKA AAAVVLDGEEEDWLP PPPPKPKST--VTDESEQSSVLKELRLQKQAMAKFAESADDFLEKLAQTA 136
Bradi2g43070.2 MPTLDGEEVPPAAAAADSEELEPLFDYSRVQ---PTIDFCFDDSDL--EKSDIFVHCNKRKRVAAAAAD--ADAVGDEKDATTKKKATV VNLDEEDWLP PPP---TKFV--VRADIRKDKTLHEERLNKQEI EKLAE---DTFQKVAEAV 135
Sb03g027375_F MTTTGE-----VDSAAGGEDLEPLFDYKRVQ---PRMTFSFDDSDL--EAADIFKHCNKRPRVQATTEE--VETKPFDEA---AATTKVLLDEEDWLP PPP---PKAA--FRASAEEDSTFRELRLKRQEWAKFAESAQDILQKMDMT 129
GRMZM2G073404_T01 MTTAGE-----VDSAAGGEDLEPLFDYKRVQ---PRMTFCFDDSDL--EVADIFKHCNKRPKVHTSTEE--EGKPFDEE---VAAKVVVLDDEEDWLP PPP---PKAA--FRATAEEDSAFRELRLKRQEWAKFAESAEDILQKLDIT 128
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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AT1G68185.1 KREVEE---SRNPSSETAAQLPSEPT--NDRAKIVITIQDKDKGQKTLRVFADEKFERVVKLYT DKAKLDPQNLVFI FDGDKIDPSTPSELGMEDHDMIEVHTKKT- 215
POPTR_0010s12880.1 NRQ-SD---SVQADLESQAEQPSKPH--HERAKIVISIQDKDVKQFRVYKDEKFERLFKRYADKVKLQSLVFVFDGDKINPNATPSELGMEDDDIVEVHEKPSG 216
GSVIVT01011822001 KRELGS---SLQSSVESVASQPSKPF--CERAKIVISIQDKDGLKQPRIYMDKFERLFKMYADKVLKLDLKLIFCFDQDKISPATPDELGMEDNDIVEVHIKSS- 225
Solyc03g013030.1.1 KRDLGASLHSLQDEVADILSKPSKPS--TDHVKMVISIQDKDGKQFRVIADDFERLFKSFADKVKLELQNLVFCFDGDKINPNATPSELGMEDDDIVEVHEKPSG 226
LOC_Os01g42250-P7 RQKVEA----RIPTHEIDLDKSPERH--EAREKVVVTVQDKAGHHQFRLYKDEKFKLFRAYAKKVNLSVADLTFVFDGDKVDAESTPDELGLEDEDMVEVLHKTR- 236
Bradi2g43070.2 MKKLEA----KKQSEHIVLDEATEEVKKAREKILIMIEDKDGQRQFRISKDEKFKLFRVYAKKVVQSPDDLTFVFDGDKINPSTPQDLDEADMIEVRHKPR- 237
Sb03g027375_F NNEVGP---KEPPEQIILDSESEPPVEKAREKIVISIQDKDGHQQMRVYKDEKFKDLKLVYAKKAKLNPDDLDFVFDGDKINPSTPQDLDEADMIEVRRKRQ- 231
GRMZM2G073404_T01 NKEVGP---KEPPEQIILDSESEPPVEKAREKIVISIQDKDGQQMRVYKDEKFKDLKLVYAKKAKLNPDDLDFVFDGDKINPSTPQDLDEADMIEVRRKRQ- 230
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....

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Fig. S10 Sequence alignment of proteins with SUMO-like domain