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*****.:*****:***.*****:.:*****.*****: * *
AT5G55160.1 -----MSATPEEDKKP---DQGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDFNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGGAKNGLKLF CF 103
AT4G26840.1 -----MSANQEEDKKPG---DGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGSGGATA---- 100
POPTR_0014s18990.1 MSASAGGGGGGQEEDKKPG--GDQSAHINLKVKGQDNEVFFRIKRSTQLRKLMTAYCDRQSVFNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGGASLD---- 108
POPTR_0002s21690.1 ----MSEATGQPQEEDKKPN---DQSAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVINSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGAVKASDYA--- 105
POPTR_0002s21680.1 ----MSGATGQPQEEDKKPN---DQSAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVFNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGAVKTSN---- 103
POPTR_0014s15650.1 ----MSGVTGQPQEEDKKPN---DQSAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVFNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGAMKTSN---- 103
GSVIVT01030502001 ---MSGVANPSSQEDKKN---DQSGHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDLNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGACV----- 101
GSVIVT01003301001 -----M-----DQGAHINLKVKGQDNEVFFRIKRSTQLRKLMSAYCDRQSVELNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGVANMCLTAN-- 91
GSVIVT01003307001 ---MSATGGAAGGQEEDKKPT---DQGAHINLKVKGQDNEVFFRIKRSTQLRKLMSAYCDRQSVELNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGVANM----- 103
Solyc12g006010.1.1 ----MSGVAGGEEDKKPA---GDQSGHINLKVKKSQDNEVFFRIKRSTQLKKLMNAYCDRQSVDFNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGTTI----- 99
Solyc07g064880.1.1 ----MSGVTQEEKKA---GDQGGHINLKVKKSQDNEVFFRIKRSTQLKKLMNAYCDRQSVDFNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGSLA----- 99
Solyc09g059970.1.1 ----MSASGGTGDEDKKN---DQMVHINLKVKGQDNEVFFRIKRSTQMRKLMSAYCDRQSVDMNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGSCCTCF SNF-- 105
Solyc07g049360.1.1 ----MSQAAEEDKKPG---GDQVHINLKVKNKDNEVFFRIKRSTQLKKLMNAYCDRQSVDFNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGSTI----- 96
LOC_Os01g68940.1 ----MSSPAGEDEKPKPAGGEGGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDIKSI AFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGSLPA----- 101
LOC_Os01g68950.1 ----MSAAGEEDKPKPAGGEGGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGCLPA----- 100
Bradi2g58830.1 ----MSAAGGEEDKPKPAGGEGGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRAEQTPDELEMEDGDEIDAMLHQTGGFLLPPNA---- 104
Sb03g043870.1 ----MSGAGEEDKKA---EAGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGVPGA----- 99
GRMZM2G053898_T01 ----MSGAGEEDKKA---EGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRGEQTPDEVT-----QFGRSQH----- 85
GRMZM2G082390_T01 ----MSGAGEEDKKA---EGGAHINLKVKGQDNEVFFRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRRLRGEQTPDELEMEDGDEIDAMLHQTGGVPSST----- 99
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....

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Fig. S4 Alignment of SUMO protein sequences