

AT5G41580.1	*MSTAAAARF-----VAGTGLREK-TAASLVNFRLASVTRQLRYHIQ--DGAKV-----DFKFEQ ICCISFAKGI DFIANNDIFPKVVEFPWLLKQLCRHQTIVY--TKTALMVLMISVKHACHLGWFSDESQ ELIALADEIRTC FSGSSTPSGIKSPGSFFSQIMERFY	158
AT1G08910.1	MVIPATSF-----GFR-----AEF-----MKFEQASCISLANEIDAIAIANNVEFGNIQLLALILNNVCRKCDQYTRAVVMLMISVSKACQGLWFPERETQLLAIIDLWNGVFSCPENVTSCVNSPVTLLISQVIERFY	128
POPTR_0003s13280.1	MVGMAGM--MPPFQVAGVTIRAAQO--MSASLANFRVHAAERLSLHIQ--PGFDS--NTEFFGLCSLARIGDFAVANNETLLKAGLELPLLKVQCVRGQVFR--LQAAIMVLMASVKNACMVGWFOEKETQLVTLATEIGKVFCTPGDINAQTSLSIIPTMISRFY	167
GSVVT01026971001	MAGESRM--ATIGSvGGGHH--SLLVASVADLLMH1Q--SGQLL--DSAEFSLMCLSLARIGYAVANNEIPVARDPLPLLKQVLRNMNDSS--LVAFFVLMISVKNACKI GWFDPHDANDLLALAKEIKGMFSTMEDINAVFPYS--LLNMWKMLRYI	153
GSVVT01019423001	MAG--MSY--TDDGGGRIRIFA-----SRLVAVYADLLAMHIQ--NGHFL--DSEAVADLFSLARIGYDHAVANNEIPVARDPLPLLKQVLRNMNDSS--LVAFFVLMISVKNACKI GWFDPHDANDLLALAKEIKGMFSTMEDINAVFPYSVSKIMSRIT	151
Soly08g008130.1.1	MGATISLF-----TSYINIAGVETITYS--ISASLANSFRLLNAVELERLAMHVR--SGHRLLDGRSGFEFHMCLSLARIGYDILSANGVEVRFVDDLPLRLQICQRKMLF--LGGIMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	169
LOC_0s06g06870.1	W-----PMYDGMFQISGKAM--TASYSFRISAADAKVTC--NQKWT--DPIEFLCLSLARIGYDILSANGVEVRFVDDLPLRLQICQRKMLF--LGAIMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	164
Bradi1g48426_F	M-----ASAAPLPTPPFPQQGQPQFKKQOQ--QNAVAMNARRLVMI GDLRLTHRFGQGGVTLF-----EPPDLAHLVYAFARIGDFALS GGDPVTASIEIIPSLKVLVYKQDF--LQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	170
Sb10g004470_F	MAGI AASLF--PTAPAPAQOQMGOQQA REQLQKAVEMNAKRAIGERIRGRHR--GGAAAL--PFAELSHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	172
GRMZM2G075582_T01	MATAARATPHFPPTPLQQOQHQDQKQ--QKALSMNAIRLKAIGDLRKAHR--GMNVP--PTAEFAHLVYAFARIGDIFAVSAGDIFDILKMGDIPDILRQLRREFF--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	170
	MTNAAATPHFPPTPLQQOQHQDQKQ--QKALALNAFRLKGI GDLRIFHLK--GMVVP--PVAELAHLVYAFARIGDIFAVSAGDIFDILKMGDIPDILRQLRREFF--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	169
	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150.....160.....170.....180	
AT5G41580.1	*FVKLGHVLSVEFKAGYTMLAHDFYISKNMPSHQEKIRLFAVQTDNI DTSACISNPPEVFSLLNGKVEKRVINAMDTPQLPFPMTAQLKYGTMLLQVMGKFNKGNII I IAFPQVLPVPEKPVLDLQSGVI EASPSDII EGPSR-----VSLSCPISRKRIKLPVKGQCKHL	332
AT1G08910.1	FCVKLGHVLSVEFKAGYTMLAHDFYISKNMPSHQEKIRLFAVQTDNI DTSACISNPPEVFSLLNGKVEKRVINAMDTPQLPFPMTAQLKYGTMLLQVMGKFNKGNII I IAFPQVLPVPEKPVLDLQSGVI EASPSDII EGPSR-----VSLSCPISRKRIKLPVKGQCKHL	302
POPTR_0003s13280.1	FLMKMGQIVSLELVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	295
GSVVT01026971001	PRFRMGHMLASLDVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	325
GSVVT01026973001	PRRIMGSHVLASLELVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	325
GSVVT01019423001	PRRIMGQILASRELVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	325
Soly08g008130.1.1	PRMKMGQIVSLELVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	338
LOC_0s06g06870.1	LoC_0s06g06870.1 PRLKMGQIVSLELVKPGFAGVYDFHTISKITRMSYEDYI--RAI SPALVRSGNFIPT-----PFAEFAHLVYAFARIGDIFALS GGDPVKMAPVEPDLIRKVTQLRREFS--IQSSVMVLMISVKNACKI GWFTEKDAKELD LA NEI SSGFTMLDIPMFS NSSSTII STIMSRF	341
Bradi1g48426_F	PRLKFDRLI I SLEAKAGVD ILMADFFIHRML--PKNEKILNLI VVQKELGVSVCISINP PHSVFLVNGKGVDRKTMSVQETGQFPDITIKMLKYGANII QAVGYNAST I IAVAFVNLTSFDAPKLDYDAPQVTI D--VPSDVLVLEGPSK-----VSLKCPISFRRIKTIKGRLCKHY	343
Sb10g004470_F	PRLKFDRLI I SLEAKAGVD ILMADFFIHRML--PKNEKILNLI VVQKELGVSVCISINP PHSVFLVNGKGVDRKTMSVQETGQFPDITIKMLKYGANII QAVGYNAST I IAVAFVNLTSFDAPKLDYDAPQVTI D--VPSDVLVLEGPSK-----VSLKCPISFRRIKTIKGRLCKHY	343
GRMZM2G075582_T01	PRLKFDRLI I SLEAKAGVD ILMADFFIHRML--PKNEKILNLI VVQKELGVSVCISINP PHSVFLVNGKGVDRKTMSVQETGQFPDITIKMLKYGANII QAVGYNAST I IAVAFVNLTSFDAPKLDYDAPQVTI D--VPSDVLVLEGPSK-----VSLKCPISFRRIKTIKGRLCKHY	343
	1.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150.....160.....170.....180	
AT5G41580.1	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	501
AT1G08910.1	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	435
POPTR_0003s13280.1	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	441
GSVVT01026971001	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	489
GSVVT01026973001	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	497
GSVVT01019423001	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	368
Soly08g008130.1.1	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	512
LOC_0s06g06870.1	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	502
Bradi1g48426_F	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	500
Sb10g004470_F	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	497
GRMZM2G075582_T01	QCDFDfSNVHINMRRPTWRCPhCQmQ FVCYFDIRLDQNMARLKVDEHNAAVDI DAGGTWVTKMTEDETE-PVREI I H-----DLEPMSILLNSGFVFDLNGDDA--ELVFQDNKVDREKPSMDAQSQMNNMNTN--KHPNSDNYSSIFDISDVI ALDPEILS--SAGTAPQPH	496
370.....380.....390.....400.....410.....420.....430.....440.....450.....460.....470.....480.....490.....500.....510.....520.....530.....540	
AT5G41580.1	ASMGQQGQQYSNLSQ-----IPMSIDMPF-----VPVFFSQTSPRDRPATTSTVTFINPSPQYQSVHASFVPTPTGTLGRITS-----FRWNQTY--CQSQAPFMTF-----	593
AT1G08910.1	TLNADFQGGQVNLQ-----IINTRDPSASQALPMFSFPTSPQDILATNANAGTSMPPAQSSQFGSHVTSLGNCGNCSDLML--ARWNHITGVRVQTQFPFAPLASHHHYSMQ--QSPS-----PAQQRFPVSYIAHPQTFHVNY	568
POPTR_0003s13280.1	FWS--PTWSSASDAQMNVGFSEPTTFMT--SPVITDVSFALMC DVYGGYNT--TTSVMHMGLSASITLQSLQNFVN-----SVLAGE--GTFPEIHYD-----RSPF-----AVQALRFPQTAPQQRSR	528
GSVVT01026971001	VSYNFVLPPTMSNGQRMFGVSRTPSSFM--SHVLTDAIPSLW-----EATGVHR--ETQMPISSLQNYFRFAGMEIQQTRFGLSSTNEYRMCVCLPMRPTAVIKSRN	591
GSVVT01026973001	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	368
GSVVT01019423001	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	611
Soly08g008130.1.1	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	615
LOC_0s06g06870.1	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	619
Bradi1g48426_F	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	625
Sb10g004470_F	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	622
GRMZM2G075582_T01	QFIAVLEINFPSSD-----TRQCICITASLN-----VTELEPTGQWPSMTKSTVSSRCLQNFIRASNMTDFDTITTTISGK-----DTFKPIE ICSSSLTVPSSARRCFR-----SCTPCSWHMWPKCSA	620
550.....560.....570.....580.....590.....600.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720	
AT5G41580.1	-----YTSRKVSV-----FVTSQS FANVSSVQSQ-----HVPRLVLS-----PNNYGRGLTSSH-----	639
AT1G08910.1	-----GENADQHWPFSSIAH-----FPTIPVNGGNTWRF-----PSSIAHPTLPLVNRMGMDHR-----STPYSITHLQTL-----NYGGNADQRFMPSSITNLOTLPATYGGYAHQRPMSSS-----ITHFPTSPVMGGPDP	687
POPTR_0003s13280.1	-----TFNPATISGASLSSHGTFEARMALSPVSGMNDQ--QQFARSLMTSSSSSQMMNDQDHPFHHGQSAAQVAVTFSSQLAGAHARASSPNLLYQQFPLRVPSRHSFNVVRSSLFLAPAQTOQGAAQVGVGMSAGATNSG--QSRLVMAQLAARARQFSS	686
GSVVT01026971001	-----IVHFSIRIQFQVQ--RRSSVQVTAAGQER-----QMSMPPSVFVQLPQRTGT-----	642
GSVVT01026973001	-----YGCSSASS-----PDDFNALACSKNIQNR-----LERHFSLDL DLVQTRMSTSAL-----PQKRSFLHVQFSQHSVGRQSPSMRTPIPMNQQSQFSQATWDRWEALKQSSQAGVNRALPGQ HARVVITQ-----	368
GSVVT01019423001	-----AMNPLLHAGPAAAQ--DLPIASLSGS NLRSE-----LERHFSLDL DLVQTRMSTSAL-----PQKRSFLHVQFSQHSVGRQSPSMRTPIPMNQQSQFSQATWDRWEALKQSSQAGVNRALPGQ HARVVITQ-----	736
Soly08g008130.1.1	-----PSSPASAYVHQVTTN--ADSVITAMSGVLSLRAPD--AASFLQHQSTQETRAQTNRHGGFGLGTAPEQFNGMTRFPFVGQAIGAM--AHGAPPA-----QQSHHVRL--VSNLMLMGQATVAQPSATAFVLPSPQGGTSAVNFIRGHLFPAQQRSSQAMRQAVVPRTIS--	784
LOC_0s06g06870.1	-----QSSAASSNQGASHVFN--ADSVITAMSGVLSLRAPD--AASFLQHQSTQETRAQTNRHGGFGLGTAPEQFNGMTRFPFVGQAIGAM--AHGAPPA-----QQSHHVRL--VSNLMLMGQATVAQPSATAFVLPSPQGGTSAVNFIRGHLFPAQQRSSQAMRQAVVPRTIS--	765
Bradi1g48426_F	-----SSPSSTTQQTQVKN--PDSVIAPMNSGSQPLPRT--AASLHLQSTAREINMSTSHLSRVLGLPAPH--LMGARFPFGISGGQGGAM--AYRPI-----QQTPTLDLRHTRMMNQATLAAAGQTSAAHVRFPT-----ADIQSHLFPVQ--SQAPRSQVPPRAA5PFL	776
Sb10g004470_F	-----SSPSSTTQQTQVKN--PDSVIAPMNSGSQPLPRT--AASLHLQSTAREINMSTSHLSRVLGLPAPH--LMGARFPFGISGGQGGAM--AYRPI-----QQTPTLDLRHTRMMNQATLAAAGQTSAAHVRFPT-----ADIQSHLFPVQ--SQAPRSQVPPRAA5PFL	777
GRMZM2G075582_T01	-----SSPSSTTQQTQVKN--PDSVIAPMNSGSQPLPRT--AASLHLQSTAREINMSTSHLSRVLGLPAPH--LMGARFPFGISGGQGGAM--AYRPI-----QQTPTLDLRHTRMMNQATLAAAGQTSAAHVRFPT-----ADIQSHLFPVQ--SQAPRSQVPPRAA5PFL	776
730.....740.....750.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	
AT5G41580.1	-----ASTSRQHPGSPVQVSSRLSD--LVDVVDLIVPDSMRRF--RMRGSLVPGSHSTALDH-----IIRFSQQ-----SQTPSRNLMSQVQVT--PVSQTSQAQSPFPTTAYRTEIVLGNRHHVFAFPAGIVRFPGPTS-----	760
AT1G08910.1	-----QRMPSSITHPTQLVSYGGTTQDILNPGGAMQFSS--REFMNLNFAENMRFGRSMRGS--AFQGVYDM-----IHPTRFVHPQAPFPAPFATS YDGADEIQAFIGHPSYFVSNMNETACTS SLVPAEGLGYSQFMSPPEWT--	829
POPTR_0003s13280.1	-----VYFQITSGAGASYLTSADGRAPAT--EQRGNAGGALPAYSTGTE--LVLD-----ASQMGPRFLMGRMRSLSGRAYSAALKEF--MVQFTQQ--TQTFRPFPNLPFSQSMSM--PHLQFLFARNAGVQPAQ-----SSPVTGSAIENSSSSILP-----	822
GSVVT01026971001	-----RFSYAMVAEQLRTAAEEERNNMGRTGMAYEQLGT--AWSSFGADALAEWQPGTMRGLTGEADSAAISQF--MLQF-----PTSLTATLESGLFAFW--FPSSSTHNNAMESQTE-----TQGLRSNMAQTGSSGGLPEMTFNI P	776
GSVVT01026973001	-----WERTLLM-----LCSCKCQWG-----	375
GSVVT01019423001	-----SADRFRFLPPDQRSSSTGGT--PVTTRDS--SVDP--QLDPMRPTGRMRGSLGRAYSEALQF--ILKFTQQ--AAARP--SIPNLS--POLQVLLANRGAHSTQP--VNFPSAPANASISGLILPERSGMO	646
Soly08g008130.1.1	-----QAPFRAGSPFLPATARFPST--PPTGTSDD--LQEL--PVDSWRPTGMRGLTGAYSAVIGRYNPSVNIAGQTSHTVSQARPAAGPARR--	883
LOC_0s06g06870.1	-----QAPFRAGSPFLPATARFPST--PPTGTSDD--LQEL--PVDSWRPTGMRGLTGAYSAVIGRYNPSVNIAGQTSHTVSQARPAAGPARR--	872
Bradi1g48426_F	-----QAPFRAGSPFLPATARFPST--PPTGTSDD--LQEL--PVDSWRPTGMRGLTGAYSAVIGRYNPSVNIAGQTSHTVSQARPAAGPARR--	841
Sb10g004470_F	-----QAPFRAGSPFLPATARFPST--PPTGTSDD--LQEL--PVDSWRPTGMRGLTGAYSAVIGRYNPSVNIAGQTSHTVSQARPAAGPARR--	859
GRMZM2G075582_T01	-----QAPFRAGSPFLPATARFPST--PPTGTSDD--LQEL--PVDSWRPTGMRGLTGAYSAVIGRYNPSVNIAGQTSHTVSQARPAAGPARR--	860
910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050.....1060.....1070.....	

Fig. S7 Alignment of SUMO ligase PIAL sequences