

PtARF3.1	MVGMIDLNTTDEDE....TTPSSGSLSSFSSSAASALASASGSGSSTP..VCELEWACAGPLISLPRKGSVWVYFQGHLECLPDLF.....LG	85
PtARF3.2	MVGMIDLNTTDEDE....TTPSCGSLSSFSSSAASALASASGSGSSTSS..VCELEWACAGPLISLPRKGSVWVYFQGHLECLPDLF.....IA	85
AtARF3	MGGLIDLNVMTTEDEDTQTQTPSSASGSVSFTSSSEASVSVSSNAGGG..VCELEWACAGPLISLPRKGSVWVYFQGHLECLPDLF.....AA	90
AtARF5	..MASLSCVSDRMKTSCLVNGGTTITTTTSCSTLLEEMKLLKDCSGTRKPVINSLEWACAGPIVCLQVGSVWVYFQGHLECLPDLF.....AVSTRREATTQVFN	98
PtARF5.1MGSPPEEKIKTGGGIING....AQTNLLEEMKLLKEFDQCSGTRK.AINSELWACAGPIVSLQVGSVWVYFQGHLECLPDLF.....AVSTRREATTQVFN	88
PtARF3.1	IYVLEPHVFCRVDVLELFAASDEVACVSHVESEIECKLREGVEGEGEEDVEATVKTTPHMFCKLTIASDTSTHGGFSVPRFAADCFPPLDY	185
PtARF3.2	VYDLESHVFCRVDVLELFAASDEVACVSHVESEIECKLREGVEGEGEEDVEATVKTTPHMFCKLTIASDTSTHGGFSVPRFAADCFPPLDY	185
AtARF3	IYGLPHVFCRILDVLELFAETTTDEVACVSHVESEIECKLREGVEGEGEEDVEATVKTTPHMFCKLTIASDTSTHGGFSVPRFAADCFPPLDY	190
AtARF5	YPNLESQMLCVHNVLEADKDDTDEIFAQSIQVNSSEK.....VEFVDFGM...LRGSKHPEHFCRLLIASDTSTHGGFSVPRFAADCFPPLDY	189
PtARF5.1	YPNLESQMLCVHNVLEADKDDTDEIFAQSIQVNSSEK.....VEFVDFGM...LRGSKHPEHFCRLLIASDTSTHGGFSVPRFAADCFPPLDY	178
PtARF3.1	TQGRFSQELVARDLHGSEKFRHYYRGQFRHLLTTGWSFVNKRLVSGIAVLEHREGDGLRIGVRFACQVKCGPTFFALWNQQLNGSSLADVAARIS	285
PtARF3.2	TQGRFSQELVARDLHGSEKFRHYYRGQFRHLLTTGWSFVNKRLVSGIAVLEHREGDGLRIGVRFACQVKCGPTFFACWNHQLNQLISPGDVAAARIS	285
AtARF3	SGQFSSQELVARDLHGSEKFRHYYRGQFRHLLTTGWSFVNKRLVSGIAVLEHREGDGLRIGVRFACQIEGTAALSAQYNQNMNNHNSSEVAARIS	290
AtARF5	SAGPFSQELVARDLHENVTFRHHYYRGQFRHLLTTGWSFVSGRRLFAQGSVLEHREDEKSCQIMVGVRFANRQQIALPSSVLSADSMHIGVLAARAFIA	289
PtARF5.1	SMQFSSQELVARDLHENVTFRHHYYRGQFRHLLTTGWSFVSGRRLFAQGSVLEHREDEKSCQIMVGVRFANRQQITLPSVLSADSMHIGVLAARAFIA	278
B3 DBD		
PtARF3.1	MREAFRIMYNFASSESEIIFENREKRSLL.QSFSAGMRVKMREPEELAARRMTGLINGISELDFRWPGSKWKQLVWRDDTEAN.RHSRVSWVEVEP	383
PtARF3.2	TRSFPHIMYNFASSESEIIFENREKRSLL.QSFSAGMRVKMREPEELAARRMTGLINGISELDFRWPGSKWKQLVWRDDTEAN.RLSRVSWVEVEP	383
AtARF3	THSVESISYNFASWNSNHIARRELRVVD.YFCIGMRFARVVESELASDRRSGFISGSELDFRWPGSKWKQLVWRDDIVANGHQCRVSWVEVEP	389
AtARF5	NRTFPHIMYNFACFAEVYIHLARYRAICGSQLSVGMREGMPEDEDSGRRRMGLINGISELDFRWPGSKWRNLQVWDEFGCNDRETRVSWVDIET	389
PtARF5.1	NRSFPHIMYNFACPEIEVYIHLKRETRVFGTQVSVGMREGMPEDESGRPRMGLINGISELDFRWPGSKWRNLQVWDEFGCSDKQNRVSWVDIET	378
PtARF3.1	SGSVSGSGSGSISSSNNSVAFG..LKRSRSGLPSLRAEFPIDG.....IGASDFRVSSRFQEVLGQGEIMR.....	448
PtARF3.2	SG.....SGSISSSNNSVAFG..LKRSRSGLPSLRAEFPIDG.....IGAPGFRESSRSQEVLGQGEIMSFNALYDGVGQNHPEIRSCFFPGYH	446
AtARF3	SG.....SISNSGFSVTTG..PKRSRIGFSSGKPDIPVSEG.....IPATDEEESLRFQVVLGQGEIIF.....	446
AtARF5	FES.LFIFPSLISGLKRLQHPSEYAGETEWGSLIKRPLIRVDSANGIMFYASFPSASEQLMKMMRFRHNNQNVFPMSEMCCQINVMGNGGLLGDMMRQ	488
PtARF5.1	FES.LFIFPSLISGLKRLQCSG.FLGDTEWGLVKKPLALLLPGSGNASLPHYASMSNMYSEQLINMLMRFQAVN.YFGICGALFEVSAVKVGSGLDVRNMQ	475
PtARF3.1SGIRGSIPTSENSFKGIGFN.....ESYRFHKVLOGQEIFFRSPYRRIFN.ANFARENCGLGLSDGVQRSSSRNGWSTMMQGYNTQMRPFTQ	534
PtARF3.2	SSGIAALGSGIRDSIATSNNYSYKIGIFN.....ESYRFHKVLOGQEIFFRSPYGRIFN.ANEARENCSLGFSDGVQRSSSRNGWSTMLQGYNTQIRPFAQ	562
AtARF3	...GFINTCSDGACARRGREKGTFFG....DSYGEHKVLOGQETVPE...AYS.....ITDHPQCHGL.....SQRNWCQGFQNFSTRILPESV	521
AtARF5	QPLMNN...QKSEMVQFNK...LTVN.FSASNTSGGQCNLQCSMSARAFENSTLSCSSGRVCHGLEQSMCAQSVTSTVTCNEEK.VNQLLQKREGA	579
PtARF5.1	RAINQTPQLNCSGITPIENQYSQICLDQSNAMNSYSSFANVAGKSLSLSRVENCAVGGVDGRFFAKPEHLPDQLSQPTSTGECIVQKPISCPMTQCA	575
PtARF3.1	VSPSSVLMFQHASNQSNSPT.....SIFNSNDHEEQTT.....NTQSWFY.FETHGGKFKLSHSDPFLRGDQCCSTNPFVLSHEHLQH	613
PtARF3.2	VSPSSVLMFQHASNVFPRRS.....SNFNFNHVVQTA.....TTRSWFCGFEMQGGNFKLSAHSPEPVKRDQWNSNPFGLSHEHLQH	642
AtARF3	SSPSSVLLTNSNS...PNG.....RLEDHGGSG.....RCRLPFG.FLTDDETAVASATAVPCVEGNSMKASAVGQSNHHSSGG	593
AtARF5	SGFEVCAQCCLLITHQYQFQS...DFINGEFLTDELTSQVS.....SFGSLAGSYKCFEILS...SQDSSAVVLPDSTNSLEFHEVWDTQLNL	664
PtARF5.1	TNHLVFNQNGGCSQLCASLWFMCALETSSLLNSQQIFASIALATTFNCLSPFLLAGEWISFMSIDSMCRSGFLSMFGLQDPSLFFMHQIADWQMSNL	675
PtARF3.1	GIS.....QFVVAQS.....AFRSSQDMVLCKSSCR....LFGFSLTEDRHVNKEEDNIASITSPINP..ESSFLPRVGEQLH	680
PtARF3.2	GVS.....QFIVACS.....AFRSGQDLVSCRSSCR....LFGFSLTEDKLVNKEEDNMTLITSPINP..GSSFLPPAGEHFH	709
AtARF3RDIYAMR.....DMLLDIAL.....	608
AtARF5	KFD...QFSFLMQCD.....LYASQNICMSNSTTNSILDFFLSNTVLDLDFCAIKDTEFNHPSGCLVGNNTSFAQDVCSQIT	739
PtARF5.1	RILSEANGLIFLACQEPFCFNSGAVKDSDESNDQSGYGLNIIASNGGGS.VYDRVTSYSAIILDEFCTLKIADLQN.ASDCLVGL..NLSSSQDVCSQIT	771
PtARF3.1	PKFFAINNAVGSCTFAIRQHAENYRIY.....	709
PtARF3.2	CSLQG.....	714
AtARF3	608
AtARF5	SASEADSCAFSRQDFPDNSGGTGTSSNVDFDDCSLRQNSKGSWGIATPRVRYTYKVTGTSVGRSIVDVTDFKDYELKSAETECMFGLEGLLTHPQSS	839
PtARF5.1	SASLADSCAFSRQDFPDNSG..GTSSNIEFDNSNLLQNN...SWQCVA.FRVRYTYKVKCTGSVGRSIVDVSFKNYEELCSAETECMFGLDGLLNNPRGS	865
Domain III		
PtARF3.1	709
PtARF3.2	714
AtARF3	608
AtARF5	GWKLVYVDYESDVLVGGDFWEEFVGCVRICIRILSFTEVQCMSEEGMKLLNSAGINDLKTYSV....	902
PtARF5.1	GWKLVYVDYENDVLLIGDDFWEEFVGCVRICIRILSFTEVQCMSEEGMKLLNSANIQQINTPITEGIH	932
Domain IV		

Fig. S1 Sequence alignment of PagARF3.1, PagARF3.2, PagARF5.1, Arabidopsis ARF3 and ARF5. PagARF3.1, PagARF3.2 and ARF3 are lack of the C-terminal dimerization domain (domain III and IV).