

Supplementary Information

Abscisic acid (ABA) signaling: Finding novel components off the beaten track

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The rationale behind using search motifs to detect hidden functional sites and the methods used to build them and test them are extensively detailed elsewhere (Zhou et al. 2021).

***Arabidopsis thaliana* proteins (including splice variants) retrieved with the Motif I - D.{7,8}R.{3,4}D.{5,6}Y.{6,7}H :**

ATG number	AA range			
AT1G10350.1	1	4	32	DYYNVLKVNRRNANEDDLKKSYYRRMAMKWH
AT1G24120.1	1	20	48	DPYEVVLGVLRNSTDQEIKSAYRKLALKYH
AT1G50190.1	1	214	239	DELSCGVCRKLVDVNYGQYACKKGCH
AT1G54130.1	1	451	477	DEIHDIHGLRLIVDNEKDCYKALGVVH
AT1G67040.1	1	330	358	DQMVKKALHRAQFKDEMSPGYRNRSEYH
AT1G67040.2	1	330	358	DQMVKKALHRAQFKDEMSPGYRNRSEYH
AT1G74300.1	1	299	327	DMLVPVTLQRYIADKLPWLHYHEVAGGGH
AT1G74300.2	1	200	228	DMLVPVTLQRYIADKLPWLHYHEVAGGGH
AT1G76730.1	1	87	116	DPKAWKWVIRKKMWDLMERNYAMSPRPVH
AT2G20560.1	1	4	32	DYYKVLQVDRSASDDDLKKAYRKLAMKWH
AT2G39360.1	1	69	95	DESTLFQTARVFSDESSSTYRFPIEEH
AT3G02850.1	1	560	586	DLYQLKSLIRAGGDPNKTDDYDGRSPLH
AT3G02850.2	1	560	586	DLYQLKSLIRAGGDPNKTDDYDGRSPLH
AT3G06150.1	1	193	220	DISGENWKSRRPVKDFGNGTYSFSLQVH
AT3G08910.1	1	4	32	DYYKVLQVDRNAKDDDLKKAYRKLAMKWH
AT3G14050.1	1	447	473	DEIHDIHGLRLIVDNEGDCYKALGVVH
AT3G17790.1	1	298	325	DGQGFMSARFTHSDAEIVFYDVFGIILH
AT3G20015.1	1	53	82	DESSSKYTLRLLHRDRFPSVTYRNHHHRLH
AT3G27710.1	1	332	358	DEKVRQLERAQRDLDRYTHYHYRYKAH
AT3G44720.1	1	238	265	DVLTPHAAREAFHDTAAAAEYISANDLH
AT3G51340.4	1	350	377	DDLMEKRRPVDPDFPFEEFCYDLRSCFH
AT4G08450.1	1	1141	1167	DYSEDYEDRDTSDLGNETDYSEEYEDH
AT4G08450.2	1	1141	1167	DYSEDYEDRDTSDLGNETDYSEEYEDH
AT4G27920.1	1	97	123	DNEHILGIRIVGGDHRLKNYSSTISLH
AT4G28480.1	1	4	32	DYYKVLQVDRSANDDDLKKAYRKLAMKWH
AT4G28480.2	1	4	32	DYYKVLQVDRSANDDDLKKAYRKLAMKWH
AT4G34370.1	1	334	360	DDKEKQMERAKRDLNRYTHYHHRYKAH
AT4G34370.2	1	167	193	DDKEKQMERAKRDLNRYTHYHHRYKAH
AT5G01390.1	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.2	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.3	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.4	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G19060.1	1	151	178	DLSGENWKSRRPVKDLGNGTYSLSLQIH
AT5G25530.1	1	4	32	DYYDILKVNRRNATEDDLKKSYYRKLAMKWH
AT5G25530.2	1	4	32	DYYDILKVNRRNATEDDLKKSYYRKLAMKWH
AT5G37500.1	1	543	569	DFYQLKSLIRSGADPNKTDDYDGRSPLH
AT5G39820.1	1	17	44	DDVVLPGFRRFHTDEELVSFYLRKRVLH
AT5G47650.1	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.2	1	296	322	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.3	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.4	1	295	321	DYEGFTPLRV SAPDQQGNLYYNTRDLH

AT5G47650.5	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G53160.2	1	101	127	DNEHILSIRIVGGDHRLKNYSSIISLH
AT5G60290.1	1	15	44	DKFGDANGLRFLSKDMSSYSAYLTGNYSAH

The principle of the gene ontology analyses and their applications to infer function are detailed elsewhere (Meier and Gehring, 2008; Meier et al., 2011).

Summary of the GO analysis:

GO:0006457	protein folding	11	275
	2.8e-16	1.1e-14	
GO:0044267	cellular protein metabolic process	12	3487
	1e-05	0.00013	
GO:0019538	protein metabolic process	13	4009
	7.1e-06	0.00013	
GO:0043170	macromolecule metabolic process	13	7127
	0.0026	0.024	
GO:0044260	cellular macromol. metabolic proc.	12	6447
	0.0035	0.026	

The numbers in "red" are the FDRs.

The following retrieved ABA-binding candidates are annotated as "associated with responses to ABA":

AT3G17790.1	ATACP5, ATPAP17, PAP17, PURPLE ACID PHOSPHATASE 17
AT3G20015.1	Eukaryotic aspartyl protease family protein
AT3G27710.1	ARIADNE 3, ARARI3, ARI3 ubiquitin-dep. Prot. catabolism
AT3G44720.1	ADT4, AROGENATE DEHYDRATASE 4 - phenylalanine biosynthesis
AT4G08450.1	Disease resistance protein (TIR-NBS-LRR) - cyclic ADP ribose generating.
AT4G27920.1	PYL10, PYR1-LIKE 10, RCAR4, REGULATORY COMPONENT RECEPTOR 4
AT4G28480.1	DNAJ heat shock family protein
AT4G34370.1	ARABIDOPSIS ARIADNE 1, ARI1, ARIADNE 1, ATARI1
AT5G01390.1	DNAJ heat shock family protein
AT5G19060.1	cytochrome P450 family protein (monooxygenase)
AT5G25530.1	DNAJ heat shock family protein
AT5G37500.1	Shaker family K ⁺ channel - AKT5 - like GORK and SROR
AT5G39820.1	ANAC094, NAC DOMAIN CONTAINING PROTEIN 94, NAC094
AT5G47650.1	ADP-ribose pyrophosphorylation for enhanced tolerance to oxidative stress

***Arabidopsis thaliana* proteins (including splice variants) retrieved with the Motif II - [D].{7,8}[R].{8,10}[Y].{6,7}[H]:**

ATG number		AA Range		AA Sequence
AT3G48190.1	2	1336	1362	DRINIFRPDRVFMFITEMHYRMSAACH
AT3G48190.1	2	1477	1503	DSSLNEDIRDLEPLPDLKYFQVIRESH
AT3G48190.2	2	1336	1362	DRINIFRPDRVFMFITEMHYRMSAACH
AT3G48190.2	2	1477	1503	DSSLNEDIRDLEPLPDLKYFQVIRESH
AT3G48190.3	2	1312	1338	DRINIFRPDRVFMFITEMHYRMSAACH
AT3G48190.3	2	1453	1479	DSSLNEDIRDLEPLPDLKYFQVIRESH
AT5G57260.1	2	228	255	DWFTGLHARRERSVRDLDAFYEQMIDLH
AT5G57260.1	2	265	290	DDFVDLLLRLEKEEAVLGYGKLTRNH
AT1G06900.1	1	333	359	DLTWTLPPLRSAYVKKPEDYLAHLLGH
AT1G08310.1	1	258	286	DKVVPFQLQRCILQKQPLINYHEIPQGGH
AT1G08310.2	1	261	289	DKVVPFQLQRCILQKQPLINYHEIPQGGH
AT1G08660.1	1	135	162	DGWL DY AAMRIAQLGADKCYNRTLCEEH
AT1G08660.2	1	135	162	DGWL DY AAMRIAQLGADKCYNRTLCEEH
AT1G08660.3	1	84	111	DGWL DY AAMRIAQLGADKCYNRTLCEEH
AT1G09010.1	1	580	606	DGFIKEVPNRMWDYHKYIPYSNPGKVH
AT1G10350.1	1	4	32	DYYNV LKVN RNANEDDLKKS YRRMAMKWH
AT1G10940.1	1	202	228	DQEDPKNFRKTIQKIMAVQYKIPDYVH
AT1G10940.2	1	210	236	DQEDPKNFRKTIQKIMAVQYKIPDYVH
AT1G11680.1	1	404	431	DPERFSPGREEDKAAGAFSYIAFGGGRH
AT1G12420.1	1	202	228	DSMMHIERRLHQLMFEDRDYERRSKKH
AT1G12420.2	1	130	156	DSMMHIERRLHQLMFEDRDYERRSKKH
AT1G13350.1	1	181	207	DKGREFQSDREKHKSLDDGYGEVRHKKH
AT1G13350.2	1	208	234	DKGREFQSDREKHKSLDDGYGEVRHKKH
AT1G13350.3	1	208	234	DKGREFQSDREKHKSLDDGYGEVRHKKH
AT1G19565.1	1	110	138	DWAAPPLKIRDGRHQELFLLYAEITLFSH
AT1G19670.1	1	37	63	DSTAPPKPV RITCPTVAGTYPVV LFFH
AT1G21700.1	1	246	272	DIEDFARVFRFLDHWGI INYCATAQSH
AT1G23340.1	1	82	108	DHPLLQGQRPM DPPEMPIGYSQENESH
AT1G23340.2	1	82	108	DHPLLQGQRPM DPPEMPIGYSQENESH
AT1G23340.3	1	82	108	DHPLLQGQRPM DPPEMPIGYSQENESH
AT1G24120.1	1	20	48	DPYEV L GVL RNSTDQE IKSAYRKLALKYH
AT1G27700.1	1	176	202	DEPVVRPPRKVPSFSGFLNYMDPVSKH
AT1G27860.1	1	29	55	DGFDSEDIRSPV VLTGLFH YDCQSGRH
AT1G27880.1	1	591	618	DNDTYLKL RSLAHS DGVDEYAVGKFLTH

AT1G27880.2	1	591	618	DNDTYLKLRLSLAHS DGVDEYAVGKFLTH
AT1G33360.1	1	260	286	DKFVIGQSRAKKVLSVAVYNHYKRIYH
AT1G33420.1	1	215	243	DRLCSSLAVRKASVMDVSRKYGMDYRLLH
AT1G33420.2	1	110	138	DRLCSSLAVRKASVMDVSRKYGMDYRLLH
AT1G36510.1	1	152	179	DVSTCVTIARVCFIETMPKWYYIACKAH
AT1G48090.1	1	1780	1807	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G48090.2	1	1780	1807	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G48090.3	1	1761	1788	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G48090.4	1	1739	1766	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G48090.5	1	1739	1766	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G48090.6	1	1739	1766	DPTNDPITRSRGIVLSEPLYKQTEDVVH
AT1G50190.1	1	214	239	DELSCGVCRKLV DVNYGQYACKKGCH
AT1G54130.1	1	451	477	DEIHDIHGLRLIVDNEKDCYKALGVVH
AT1G56290.1	1	219	245	DSEKKPKERISEKGN NREYLKGESLNH
AT1G57780.1	1	223	249	DIYEEIDKDRNVSLNPITDYEKEMAKH
AT1G64330.1	1	48	75	DIEEDES KRLVVAELVKDFYKEYESLYH
AT1G65910.1	1	95	120	DRKVTSHSRMVGT KKT LVYYRGRAPH
AT1G66320.1	1	215	241	DNVNVLRVRSQSLLSFNYYGPSSRDLH
AT1G66550.1	1	138	165	DQNCNATKRVQKIKDNPPVYRTTYLGKH
AT1G66550.2	1	133	160	DQNCNATKRVQKIKDNPPVYRTTYLGKH
AT1G66560.1	1	133	160	DQNCNARKRVQMIQDNPPVYRTTYLGKH
AT1G66600.1	1	133	160	DQNCYATKRVQMIQDSPPVYRTTYLGQH
AT1G66640.1	1	189	215	DNVNVLRVRSQSLLSFNYYGPSSRDLH
AT1G67570.1	1	378	404	DVESMDHYMRMPVTN QFPSYMSMSSYH
AT1G67570.2	1	378	404	DVESMDHYMRMPVTN QFPSYMSMSSYH
AT1G69670.1	1	105	132	DHNKALQMIRDILMYMDRTYVSTTKKTH
AT1G69670.2	1	105	132	DHNKALQMIRDILMYMDRTYVSTTKKTH
AT1G70380.1	1	343	370	DKATTNLRRFDIEGMDDQHYSFHTFLDH
AT1G71010.1	1	1186	1213	DSAIRFQERI QKGLPPSSLYLSTLRSFH
AT1G74280.1	1	316	344	DMLVPAKLQRYLAHQLPWVHYHEVPRSGH
AT1G74290.1	1	317	345	DMLVPVKLQRYLAHQLPWVHYHEVPRSGH
AT1G74300.1	1	299	327	DMLVPVTLQRYIADKLPWLHYHEVAGGGH
AT1G74300.2	1	200	228	DMLVPVTLQRYIADKLPWLHYHEVAGGGH
AT1G79050.2	1	315	340	DIGLRARVRVQKSKVSRPYKQEERKH
AT1G80590.1	1	115	142	DQNCDATKRVQKIQDNPPVYRNTYVGQH
AT2G02300.1	1	169	196	DIRGVLNTRIISP GTHYSAYIVYTKTSH
AT2G02580.1	1	229	256	DWLTGLQRRREKSVKDL DVFYQQMFDLH
AT2G03360.1	1	301	328	DVGFEVITFRPSKTTSLREAYKLIKSSH
AT2G03360.2	1	305	332	DVGFEVITFRPSKTTSLREAYKLIKSSH
AT2G03370.1	1	302	329	DVGFEVIIFRPSKTTNLKEAYKLIKSSH
AT2G03370.2	1	304	331	DVGFEVIIFRPSKTTNLKEAYKLIKSSH

AT2G03820.1	1	155	183	DQWVASIQLRQHVSHRRTFFYLEQLILRH
AT2G04810.1	1	185	212	DYAVAWTFMRQYLFSYIKGDYSWCNLNH
AT2G05170.1	1	460	487	DVETAIRVCRAANYHEHAMYVAKKAGKH
AT2G07820.1	1	55	81	DRIRGLQQRISGLLQERNYLIVCTIEH
AT2G16500.1	1	546	573	DNNGCSGGRYLGMFLGGAYEEALGGVH
AT2G17930.1	1	327	355	DERVLVGTGRACFESLRPLAYSLLAEIVH
AT2G19220.1	1	280	307	DKLATIFKGRIEPGKTKTRRYRKRVIDH
AT2G20560.1	1	4	32	DYYKVLQVDRSASDDDLKKAYRKLAMKWH
AT2G21600.1	1	31	59	DKTTPHSTNRWIGTLVFFLIYCLRVYSIH
AT2G22740.1	1	705	733	DAASKGNVGRFINHSCSPNLYAQNVLYDH
AT2G22740.2	1	705	733	DAASKGNVGRFINHSCSPNLYAQNVLYDH
AT2G23030.1	1	202	228	DPK DPRNFRKTVQKIMAVNYKIPGYVH
AT2G24150.1	1	23	51	DCGEETRIVRRMLKFEDLPEYLDNEFIH
AT2G24180.1	1	234	261	DRISGLDSSRRKSFQDLDTFYQKAIVDH
AT2G25850.1	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.2	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.3	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.4	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.5	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.6	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.7	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.8	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G25850.9	1	480	508	DVHVSHVRRRQLPSFVFPNGYKRSRQSRH
AT2G26910.1	1	888	914	DVYISGFPKRQETFARISGYCEQNDVH
AT2G28700.1	1	127	152	DFVMNDNDRLDLCKFIDHYLRNLYHH
AT2G29090.1	1	403	429	DPEKFDPSRFEVAPKPYTYMPFGNGVH
AT2G29090.2	1	403	429	DPEKFDPSRFEVAPKPYTYMPFGNGVH
AT2G29090.3	1	308	334	DPEKFDPSRFEVAPKPYTYMPFGNGVH
AT2G29690.1	1	531	557	DMDIALALRTMVFPNTNTRYDTLYSYKH
AT2G33360.1	1	146	172	DSGSPVISRAIIGCKRVTYMLDKPTLH
AT2G34490.1	1	411	437	DPDRFSETRQEDQVFKRNYLAFGWGAH
AT2G36290.1	1	312	340	DVLVPVTLQRYIAKKLPWIHYHEIPGAGH
AT2G36290.2	1	298	326	DVLVPVTLQRYIAKKLPWIHYHEIPGAGH
AT2G39360.1	1	69	95	DESTLFQTARVFSDESSSTYRFPIEEH
AT2G40750.1	1	116	142	DSGESKKKRLGVGKGKRGCYTRKTRSH
AT2G40955.1	1	380	406	DESHKPKQRLAPKSWMFKYRRDHKILH
AT2G42430.1	1	188	215	DVTTTANVRETHHQTGGGVYGHGIGGFH
AT3G02850.1	1	560	586	DLYQLKSLIRAGGDPNKTDYDGRSPLH
AT3G02850.2	1	560	586	DLYQLKSLIRAGGDPNKTDYDGRSPLH
AT3G03200.1	1	95	120	DRRVSWRDRAIGTKKTLVYYRGRAPH
AT3G03680.1	1	559	586	DEKKPYSGRIHVKVCLEGGYHVLDEAAH

AT3G06150.1	1	193	220	DISGENWKS RPPVKDFGNGTYSFSLQVH
AT3G08910.1	1	4	32	DYYKVLQVDRNAKDDDLKKAYRKLAMKWH
AT3G09060.1	1	272	298	DDCLKIWERMKQNEREKDLYTYSSLIH
AT3G09060.2	1	272	298	DDCLKIWERMKQNEREKDLYTYSSLIH
AT3G09530.1	1	544	570	DPKLLDEMRLISIGRKLLPVYRDFYNAH
AT3G10630.1	1	39	66	DLYKVQSLRFTFTVNRFYSYLQFLLGFH
AT3G11920.1	1	398	424	DHTSV DYMRLISQSEEFRRYLNLAQDFH
AT3G12120.1	1	283	309	DSSEWDWLRGALATVDRDYGILNKV FH
AT3G12120.2	1	283	309	DSSEWDWLRGALATVDRDYGILNKV FH
AT3G13350.1	1	234	261	DTQKPKCHRSGYNFFFAEQYARLKPEYH
AT3G14050.1	1	447	473	DEIHDIHGLRLIVDNEGDCYKALGVVH
AT3G14950.1	1	322	348	DPNFARAHRLASLLLRLGYVDNAGIH
AT3G15510.1	1	157	184	DFGNKKNSLRLDDWVLCRIYKKNNASRH
AT3G16320.1	1	517	542	DTALKMFQRAIQLNERFTYAHTLCGH
AT3G16320.2	1	506	531	DTALKMFQRAIQLNERFTYAHTLCGH
AT3G16320.3	1	506	531	DTALKMFQRAIQLNERFTYAHTLCGH
AT3G16320.4	1	517	542	DTALKMFQRAIQLNERFTYAHTLCGH
AT3G16340.1	1	884	910	DIRISGFPRQETFARISGYCEQNDIH
AT3G16340.2	1	879	905	DIRISGFPRQETFARISGYCEQNDIH
AT3G16350.1	1	97	122	DSPLSDHARYSNLHHNEGYSLDDPAH
AT3G17790.1	1	298	325	DGQGFMSARFTHSDAEIVFYDVFG EILH
AT3G17830.1	1	63	91	DHYSTLNVNRNATLQEIKSSYRKLARKYH
AT3G24715.1	1	93	120	DAYDFGRDPRSTIRLENGGYMPHFNAYH
AT3G24715.2	1	93	120	DAYDFGRDPRSTIRLENGGYMPHFNAYH
AT3G24715.3	1	93	120	DAYDFGRDPRSTIRLENGGYMPHFNAYH
AT3G26290.1	1	229	256	DKFNGLQGWRKKSFRLDAFYEQIFDLH
AT3G26290.2	1	242	269	DKFNGLQGWRKKSFRLDAFYEQIFDLH
AT3G26300.1	1	229	256	DLTGLQGRRERSMRDLDAFYEQMF DLH
AT3G26320.1	1	229	256	DWLTGLHGQRERSVRALDAFYEQMF DLH
AT3G26330.1	1	229	256	DWLTGLQGQRERSVRGLDAFYEQMF DLH
AT3G26410.1	1	325	351	DPYTPDDKRTDHI PSTGAYSLVECVH
AT3G27710.1	1	332	358	DEKVRQLERAQRDLDRYTHYHYRYKAH
AT3G29400.1	1	595	621	DEGLREDVRTKASMWVIQAYWTFYSRH
AT3G33520.1	1	224	251	DLRLDLRLARNGNTLIKSTYVLPDGVTH
AT3G44300.1	1	287	313	DLDLGDVARAKLYFDSVGHYSRPDVLH
AT3G44310.1	1	294	320	DIDLGDIAKLYFDSVGHYSRPDVLH
AT3G44310.2	1	172	198	DIDLGDIAKLYFDSVGHYSRPDVLH
AT3G44310.3	1	294	320	DIDLGDIAKLYFDSVGHYSRPDVLH
AT3G44310.4	1	172	198	DIDLGDIAKLYFDSVGHYSRPDVLH
AT3G44510.1	1	156	184	DKVMPFQLQRCLCRKLPWIRYHEVPKG GH
AT3G44510.2	1	262	290	DKVMPFQLQRCLCRKLPWIRYHEVPKG GH

AT3G44510.4	1	156	184	DKVMPFQLQRCLCRKLPWIRYHEVPKGGH
AT3G44510.5	1	156	184	DKVMPFQLQRCLCRKLPWIRYHEVPKGGH
AT3G46710.1	1	110	137	DDIKTLKRRTLDVTRKLEMYGIGNFNEH
AT3G47170.1	1	308	334	DLVISVSIRSSIEPPLPEGYYGNAFTH
AT3G48410.1	1	326	354	DKFVPVKLQRYVASKLPWIRYHEISGSGH
AT3G48410.2	1	368	396	DKFVPVKLQRYVASKLPWIRYHEISGSGH
AT3G49530.1	1	11	38	DSLVPGLRFRPTDEELIRYYLRRKINGH
AT3G49530.2	1	11	38	DSLVPGLRFRPTDEELIRYYLRRKINGH
AT3G49900.2	1	234	260	DAVQQRFPRHDLRYRIVDAYVKVKREH
AT3G50500.1	1	221	247	DPQEPRDYRKTIQRILSVTYSIPEDLH
AT3G50500.2	1	228	254	DPQEPRDYRKTIQRILSVTYSIPEDLH
AT3G50670.1	1	337	362	DRTSRDHDRDRSRKKERDYEKGGEYEH
AT3G51160.1	1	91	118	DLTDASSLRRWIDVIKPDEVYNLAAQSH
AT3G52540.1	1	56	84	DVYEPEPPPSFSFSSSPSSSSYSSFSSTSH
AT3G54070.1	1	205	232	DVPLWMLERVDLYRKELALYPNSNKALH
AT3G54240.1	1	299	327	DRLVPIQLQRIIAQKLTWIKYHEIPGAGH
AT3G56990.1	1	562	589	DEADDGDATRPSKKARTPKLYEVKDERH
AT3G61120.1	1	80	106	DTLEDTQGLRQEVTKLKCKYESLLRTH
AT3G61670.1	1	283	310	DPHRFPIHGRGPHYPFSGQYVGNNGH
AT3G61670.2	1	283	310	DPHRFPIHGRGPHYPFSGQYVGNNGH
AT3G61760.1	1	263	290	DYFQTSPEYRHLTERMGEYLGKMLSKH
AT3G61760.2	1	263	290	DYFQTSPEYRHLTERMGEYLGKMLSKH
AT3G61760.3	1	263	290	DYFQTSPEYRHLTERMGEYLGKMLSKH
AT3G62120.1	1	144	170	DLEVPIAIRPTSETVMYPYYSKWIRGH
AT3G62120.2	1	144	170	DLEVPIAIRPTSETVMYPYYSKWIRGH
AT3G62120.3	1	131	157	DLEVPIAIRPTSETVMYPYYSKWIRGH
AT3G63350.1	1	110	137	DLLKSIKRRTSSSSPSSLNYSQSQPEAH
AT4G02100.1	1	392	419	DYYALMGIRRDCSRSELDLAYLLNLKH
AT4G08450.1	1	1141	1167	DYSEDYEDRDTSDLGNETDYSEEYEDH
AT4G08450.2	1	1141	1167	DYSEDYEDRDTSDLGNETDYSEEYEDH
AT4G09060.1	1	7	33	DSDEAETKSRTNLSQEVEEYIKDTIDH
AT4G09060.2	1	7	33	DSDEAETKSRTNLSQEVEEYIKDTIDH
AT4G14860.1	1	128	154	DLTRDVVADREYLHELLFCYLYLNPKH
AT4G18020.1	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.10	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.11	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.2	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.3	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.4	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.5	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.6	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH

AT4G18020.7	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.8	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18020.9	1	359	385	DHNHRWIQSRENHRPNQRNYNVFQQQH
AT4G18130.1	1	223	248	DTVVEDVQRLTGYDRVMVYQFHEDDH
AT4G19220.1	1	26	52	DSL R H S I S R W N S P S G Y C S N Y Y F S K R K H
AT4G19420.1	1	200	227	DAGFFLNTRDVSGVQYIKTYFEDVVTLH
AT4G19420.2	1	200	227	DAGFFLNTRDVSGVQYIKTYFEDVVTLH
AT4G19420.3	1	200	227	DAGFFLNTRDVSGVQYIKTYFEDVVTLH
AT4G19420.4	1	200	227	DAGFFLNTRDVSGVQYIKTYFEDVVTLH
AT4G21410.1	1	383	410	DSGQTMTHRFTSRIAGTYGYMAPEYAMH
AT4G21410.3	1	508	535	DSGQTMTHRFTSRIAGTYGYMAPEYAMH
AT4G22680.1	1	237	262	DFPIWSPERINDEKMFLDYCQDFGVH
AT4G27010.1	1	1230	1257	DLIIHCINRASITRAKILFYLVESSPLH
AT4G27010.2	1	1402	1429	DLIIHCINRASITRAKILFYLVESSPLH
AT4G27920.1	1	97	123	DNEHILGIRIVGGDHRLKNYSSTISLH
AT4G28480.1	1	4	32	DYYKVLQVDRSANDDDLKKAYRKLAMKWH
AT4G28480.2	1	4	32	DYYKVLQVDRSANDDDLKKAYRKLAMKWH
AT4G28990.1	1	39	65	DYEPGEVSRDRPSFNRS DRYKGDNGGH
AT4G30870.1	1	478	506	DNRYRDQKLRLQRSGFKKLIYILEGDPNH
AT4G31580.1	1	83	109	DRGGGGGGRGGRGGS DLKCYECGETGH
AT4G31580.2	1	83	109	DRGGGGGGRGGRGGS DLKCYECGETGH
AT4G32180.1	1	105	133	DKRKRTIKERLGITNGNLRSYPVLGGRLH
AT4G32180.2	1	105	133	DKRKRTIKERLGITNGNLRSYPVLGGRLH
AT4G32180.3	1	105	133	DKRKRTIKERLGITNGNLRSYPVLGGRLH
AT4G32850.1	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.10	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.11	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.12	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.13	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.14	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.15	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.16	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.17	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.2	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.3	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.4	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.5	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.6	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.7	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.8	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H
AT4G32850.9	1	478	506	DV F V S H V R R R Q L P P F V F P N G Y R R P R Q S R H

AT4G33950.1	1	219	245	DPEEPKNFRKTIHRILNVQYAIIPDYVH
AT4G33950.2	1	219	245	DPEEPKNFRKTIHRILNVQYAIIPDYVH
AT4G34370.1	1	334	360	DDKEKQMERAKRDLNRYTHYHHRYKAH
AT4G34370.2	1	167	193	DDKEKQMERAKRDLNRYTHYHHRYKAH
AT4G36280.1	1	440	467	DFERSSLFQRLEARLKKIVYSYWYSHCH
AT4G36350.1	1	89	117	DGDVKPKKKRGHASTSSYRFYDYTSGFLH
AT4G36690.1	1	105	132	DHSRERGERRERGGRDDDDYRRSRDRDH
AT4G36690.2	1	105	132	DHSRERGERRERGGRDDDDYRRSRDRDH
AT4G36690.3	1	105	132	DHSRERGERRERGGRDDDDYRRSRDRDH
AT4G37720.1	1	62	87	DDEDCLVRRTLTAHLDYIYTHKNNHH
AT5G01390.1	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.2	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.3	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01390.4	1	4	32	DFYKVLEVDRSANDDELKKAYRKLAMKWH
AT5G01490.1	1	227	253	DGSDVVVLSRASFFVMLIAYLAFLIFH
AT5G01490.2	1	227	253	DGSDVVVLSRASFFVMLIAYLAFLIFH
AT5G03160.1	1	370	398	DWYKILGISRTASISEIKKAYKKLALQWH
AT5G03430.1	1	299	325	DSVSEEVDRQRSTSDMVFIYGGVGPLH
AT5G04810.1	1	399	424	DYWFDEAKRIHKTNLASIYGKIIYAH
AT5G04810.2	1	399	424	DYWFDEAKRIHKTNLASIYGKIIYAH
AT5G05490.1	1	279	306	DRPQPAKKRARKTATSAMDYEQTIAGH
AT5G05490.2	1	269	296	DRPQPAKKRARKTATSAMDYEQTIAGH
AT5G08590.1	1	202	228	DPNDPKNFRKTIQRIMAVQYKIPDYVH
AT5G08590.2	1	126	152	DPNDPKNFRKTIQRIMAVQYKIPDYVH
AT5G10630.1	1	293	318	DESAEERERGITMTVAVAYFNSKRHH
AT5G10630.2	1	294	319	DESAEERERGITMTVAVAYFNSKRHH
AT5G10630.3	1	364	389	DESAEERERGITMTVAVAYFNSKRHH
AT5G10630.4	1	369	394	DESAEERERGITMTVAVAYFNSKRHH
AT5G10630.5	1	294	319	DESAEERERGITMTVAVAYFNSKRHH
AT5G13620.1	1	194	220	DEQAREDDRTVFLTFSRGYPLSEAEVH
AT5G14430.1	1	292	319	DGILLLELDRLLRPGGYFVYSSPEAYAH
AT5G14430.2	1	292	319	DGILLLELDRLLRPGGYFVYSSPEAYAH
AT5G14950.1	1	1146	1172	DSSQPREGRVSI SPMEIRAYKLELRPH
AT5G16740.1	1	203	229	DDGKIPVLRLENIPTVSGIYLFSGGH
AT5G17260.1	1	95	120	DRRVSWRDRAIGTKKTLVYYRGRAPH
AT5G17370.1	1	407	434	DGTIKLYDQRMVKRGVGVQTYEGHVNSH
AT5G17370.2	1	407	434	DGTIKLYDQRMVKRGVGVQTYEGHVNSH
AT5G17880.1	1	566	593	DITRKWCFYRHAFAMMRDLRYLKIYSTH
AT5G17880.2	1	566	593	DITRKWCFYRHAFAMMRDLRYLKIYSTH
AT5G17980.1	1	589	616	DEKRGNRSRVHIRLCFDGGYHVMDEAAH
AT5G19060.1	1	151	178	DLSGENWKS RPPVKDLGNGTYSLSLQIH

AT5G19400.1	1	966	992	DGYQAQSSRGVGLNSSLNYATSGKPEH
AT5G19400.2	1	966	992	DGYQAQSSRGVGLNSSLNYATSGKPEH
AT5G19400.3	1	966	992	DGYQAQSSRGVGLNSSLNYATSGKPEH
AT5G19400.4	1	934	960	DGYQAQSSRGVGLNSSLNYATSGKPEH
AT5G19400.5	1	934	960	DGYQAQSSRGVGLNSSLNYATSGKPEH
AT5G19520.1	1	482	509	DADTGKITRKTFTWVNVYTSRKTIGH
AT5G19520.2	1	482	509	DADTGKITRKTFTWVNVYTSRKTIGH
AT5G20710.1	1	107	134	DAGLYSVLRIGPYVCAEWNYGGFPVWLH
AT5G22460.1	1	293	321	DRIIPYEINRYISEKLPWIKYHEVLGYGH
AT5G22460.2	1	293	321	DRIIPYEINRYISEKLPWIKYHEVLGYGH
AT5G22460.3	1	293	321	DRIIPYEINRYISEKLPWIKYHEVLGYGH
AT5G23240.1	1	50	78	DLYDLLGIDRSSDKSQIKSAYRALQKRCH
AT5G25150.1	1	83	109	DLYKHELLRVMYPVFIHCYMDLVGKGH
AT5G25150.2	1	83	109	DLYKHELLRVMYPVFIHCYMDLVGKGH
AT5G25220.1	1	149	176	DGVVSWQNARHKAIEILSHPLYEQLLSAH
AT5G25220.2	1	149	176	DGVVSWQNARHKAIEILSHPLYEQLLSAH
AT5G25360.3	1	15	41	DKFCYLNCRCLCFRTYCLWIIYIGCCLH
AT5G25530.1	1	4	32	DYYDILKVNARNATEDDLKKSyrKLAMKWH
AT5G25530.2	1	4	32	DYYDILKVNARNATEDDLKKSyrKLAMKWH
AT5G26190.1	1	277	304	DVLIRDENQRCYACVLPFYDACYICTH
AT5G37370.1	1	286	313	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37370.2	1	278	305	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37370.4	1	231	258	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37370.5	1	153	180	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37370.6	1	153	180	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37370.7	1	153	180	DYGNDRRSRRDYDSRSRRNDYEDDRSRH
AT5G37500.1	1	543	569	DFYQLKSLIRSGADPNKTDYDGRSPLH
AT5G39230.1	1	72	98	DKASSISFRVSSPSCCSHYALLEVEVH
AT5G42390.1	1	1150	1176	DRAKRTLMLRHEAELKSNAYWLNLLAH
AT5G43850.1	1	139	166	DASNYIKLMRLFVGEPVWTPYNRPQEEH
AT5G47650.1	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.2	1	296	322	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.3	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.4	1	295	321	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G47650.5	1	249	275	DYEGFTPLRV SAPDQQGNLYYNTRDLH
AT5G53160.2	1	101	127	DNEHILSIRIVGGDHRLKNYSSIISLH
AT5G54530.1	1	48	75	DSYILHNDGRLEVFLAAPCYAKFETNVH
AT5G55100.1	1	712	737	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.10	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.11	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.12	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH

AT5G55100.2	1	712	737	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.3	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.4	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.5	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.6	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.7	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.8	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G55100.9	1	527	552	DNEGEHRHRSSKHSKDVDYSKDKRSH
AT5G63650.1	1	202	228	DPDDPRNFRKTIQRIMAVQYKIPDYVH
AT5G66280.1				DLSDASSLRRWLDVIKPDEVYNLAAQSH

Summary of the GO analysis:

GO:0043631	RNA polyadenylation	13	22
	7.6e-21 3.9e-18		
GO:0031123	RNA 3'-end processing	13	27
	6e-20 1.6e-17		
GO:0006396	RNA processing	23	453
	9.6e-15 1.7e-12		
GO:0016070	RNA metabolic process	36	1657
	1.5e-11 2e-09		
GO:0006457	protein folding	15	275
	1.9e-10 2e-08		
GO:0006807	nitrogen comp. metab. process	51	3826
	1.7e-08 1.5e-06		
GO:0006139	nucleobase metabolic proc.	44	3198
	8.7e-08 6.4e-06		
GO:0044260	cellular macromol. metab. process	69	6447
	1.7e-07 1.1e-05		
GO:0009987	cellular process	102	11684
	1.3e-06 7.3e-05		
GO:0043170	macromolecule metabolic process	71	7127
	1.6e-06 8.4e-05		
GO:0009737	response to ABA stimulus	8	220
	0.002 0.034		

The numbers in "red" are the FDRs.

GO:0009737

AT1G12420.1	ACR8, ACT DOMAIN REPEAT 8 ACR8 mRNA are increased by ABA & NaCl
AT4G21410.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 29
AT3G50500.1	SNRK2.2
AT3G02850.1	SKOR
AT5G37500.1	GORK
AT4G33950.1	OST1-open stomata 1, SnRK2.6, calcium-indep. ABA-activated protein kinase
AT4G33950.2	OST1 - SnRK2.6
AT3G14050.1	AT-RSH2, ATRSH2, maintenance of the (p)ppGp level in plastids

GO:0000398

	nuclear mRNA splicing, via spliceosome
	3.4e-06 0.00016
AT3G50670.1	U1SNRNP
AT4G36690.1	Splicing fac. like prot. expressed in pollen
AT4G36690.3	
AT4G36690.2	
AT4G31580.1	RSZ22 - Serine/arginine-rich splicing factor
	RSZ22 ... is an RBP
AT4G31580.2	

H. sapiens proteins retrieved with the Motif I - D.{7,8}R.{3,4}D.{5,6}Y.{6,7}H

Swiss-Prot Identifiers:

O60504
O60575
O94875
P12318
P25685
P31994
P49888
P59910
Q07890
Q14C86
Q16394
Q7RTN6
Q8N5S9
Q8WXX5
Q92839
Q9H4B6
Q9HAC8
Q9NXW2
Q9NYQ8
Q9UKJ3
Q9Y2K2

Note that the following of the above proteins are associated with immune defense or tumorigenesis:

P12318

>sp|P12318|FCG2A_HUMAN Low affinity immunoglobulin gamma Fc region receptor II-a
OS=Homo sapiens (Human) OX=9606 GN=FCGR2A PE=1 SV=4

P31994

>sp|P31994|FCG2B_HUMAN Low affinity immunoglobulin gamma Fc region receptor II-b
OS=Homo sapiens (Human) OX=9606 GN=FCGR2B PE=1 SV=2

Q07890

>sp|Q07890|SOS2_HUMAN Son of sevenless homolog 2 OS=Homo sapiens (Human)
OX=9606 GN=SOS2 PE=1 SV=2

Q16394

>sp|Q16394|EXT1_HUMAN Exostosin-1 OS=Homo sapiens (Human) OX=9606
GN=EXT1 PE=1 SV=2 tumor suppressor protein

Supplementary References

- Meier S and Gehring C (2008). A guide to the integrated application of on-line data mining tools for the inference of gene functions at the systems level. *Biotech. J.* 3, 1375-1387. doi: 10.1002/biot.200800142.
- Meier S, Tzfadia O, Vallabhaneni R, Gehring C and Wurtzel ET (2011). A transcriptional analysis of carotenoid, chlorophyll and plastidial isoprenoid biosynthesis genes during development and osmotic stress responses in *Arabidopsis thaliana*. *BMC Systems Biol.* 5, 77. doi: 10.1186/1752-0509-5-77.
- Zhou W, Chi W, Shen W, Dou W, Wang J, Tian X, Gehring C and Wong A (2021). Computational identification of functional centers in complex proteins: A step-by-step guide with examples. *Front. Bioinform.* 1, 652286. doi: 10.3389/fbinf.2021.652286.