Supplemental Materials for

Protein phosphatase 2A holoenzyme is targeted to peroxisomes by piggybacking and positively affects peroxisomal β-oxidation

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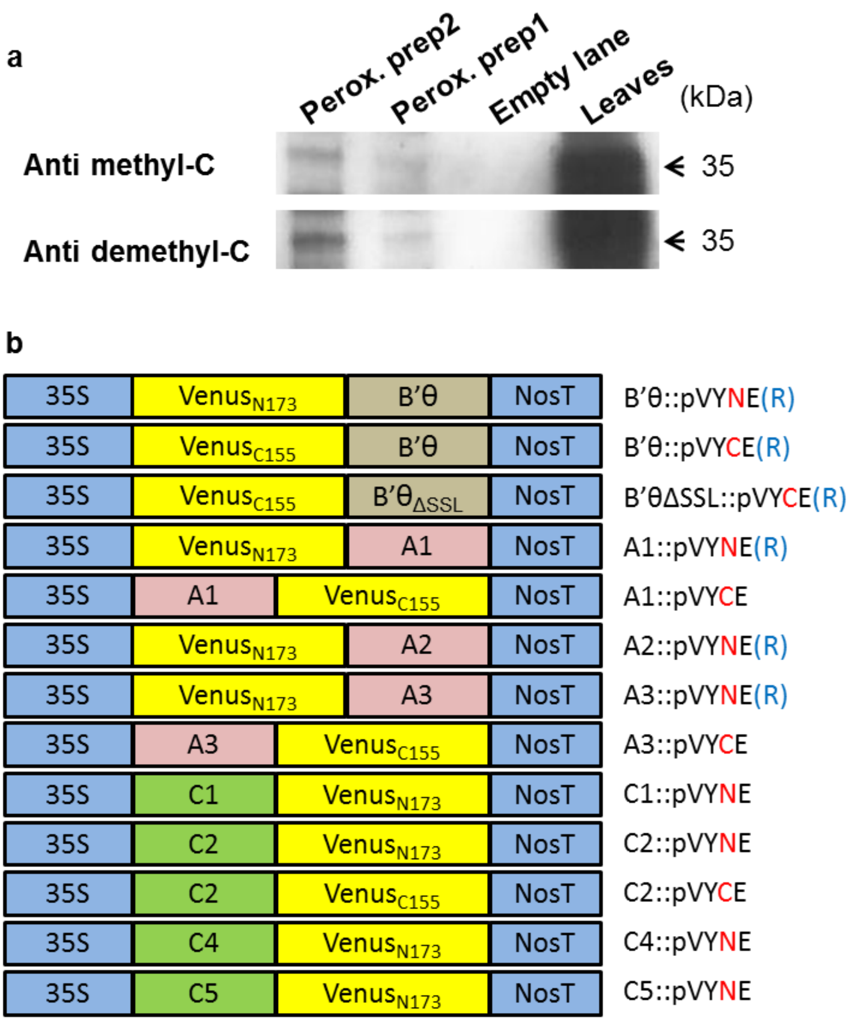
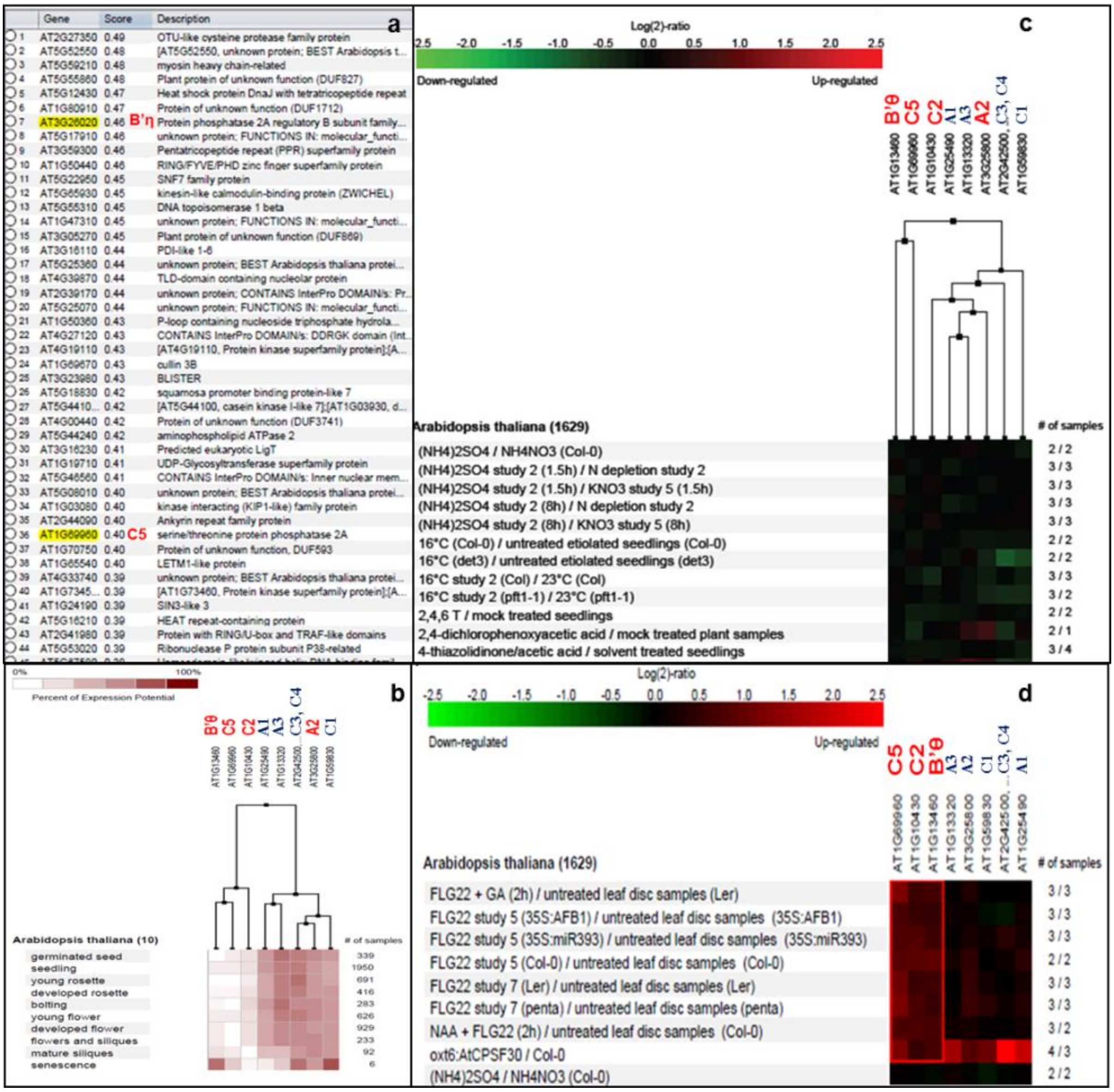


Supplemental Figure S1. Identification of PP2A in peroxisomes and constructing BiFC recombinant genes. (a) Catalytic subunit detection in isolated *A. thaliana* peroxisomes by Western blotting with specific antibodies against methylated (upper panel) and demethylated (lower panel) C-terminal end of PP2A-C. Two preparations of peroxisomes were used together with *A. thaliana* leaf extract (5-week-old plants) as a control. The detected band equals to 35 kDa. (b) Schematic representation of generated BiFC vectors. PP2A subunits (*B'θ*, *C*, *A*) were inserted in pVYNE, pVYCE, pVYNE(R) and pVYCE(R) (Waadt et al., 2008). 35S, promoter of the cauliflower mosaic virus (CaMV); Venus$_{N173}$, N-terminal fragment of YFP (Venus type) amino acids 1–173; Venus$_{C155}$, C-terminal fragment of YFP amino acids 156–239; NosT, terminator of the Nos gene; (R) indicates right and a free C-terminus of the protein of interest.



	Gene	Score		Description
○ 1	AT2G27350	0.49		OTU-like cysteine protease family protein
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○ 3	AT5G59210	0.48		myosin heavy chain-related
○ 4	AT5G55860	0.48		Plant protein of unknown function (DUF827)
○ 5	AT5G12430	0.47		Heat shock protein DnaJ with tetratricopeptide repeat
○ 6	AT1G60910	0.47		Protein of unknown function (DUF1712)
○ 7	AT3G26020	0.46	B'η	Protein phosphatase 2A regulatory B subunit family...
○ 8	AT5G17910	0.46		unknown protein; FUNCTIONS IN: molecular_functi...
○ 9	AT3G59300	0.46		Pentatricopeptide repeat (PPR) superfamily protein
○ 10	AT1G50440	0.46		RING/FYVE/PHD zinc finger superfamily protein
○ 11	AT5G22950	0.45		SNF7 family protein
○ 12	AT5G65930	0.45		kinesin-like calmodulin-binding protein (ZWICHEL)
○ 13	AT5G55310	0.45		DNA topoisomerase 1 beta
○ 14	AT1G47310	0.45		unknown protein; FUNCTIONS IN: molecular_functi...
○ 15	AT3G05270	0.45		Plant protein of unknown function (DUF869)
○ 16	AT3G16110	0.44		PDI-like 1-6
○ 17	AT5G25360	0.44		unknown protein; BEST Arabidopsis thaliana protei...
○ 18	AT4G39870	0.44		TLD-domain containing nucleolar protein
○ 19	AT2G39170	0.44		unknown protein; CONTAINS InterPro DOMAIN/s: Pr...
○ 20	AT5G25070	0.44		unknown protein; FUNCTIONS IN: molecular_functi...
○ 21	AT1G50360	0.43		P-loop containing nucleoside triphosphate hydrola...
○ 22	AT4G27120	0.43		CONTAINS InterPro DOMAIN/s: DDRGK domain (Int...
○ 23	AT4G19110	0.43		[AT4G19110, Protein kinase superfamily protein];[A...
○ 24	AT1G69670	0.43		cullin 3B
○ 25	AT3G23980	0.43		BLISTER
○ 26	AT5G18830	0.42		squamosa promoter binding protein-like 7
○ 27	AT5G4410...	0.42		[AT5G44100, casein kinase I-like 7];[AT1G03930, d...
○ 28	AT4G00440	0.42		Protein of unknown function (DUF3741)
○ 29	AT5G44240	0.42		aminophospholipid ATPase 2
○ 30	AT3G16230	0.41		Predicted eukaryotic LigT
○ 31	AT1G19710	0.41		UDP-Glycosyltransferase superfamily protein
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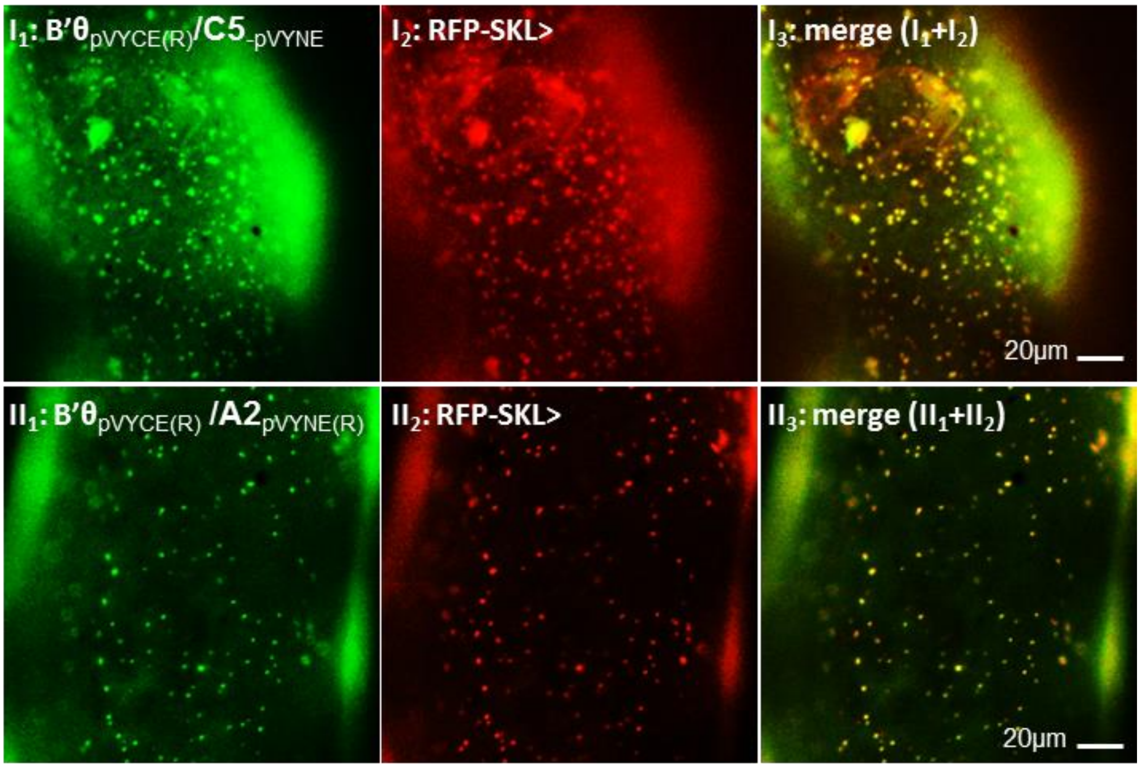
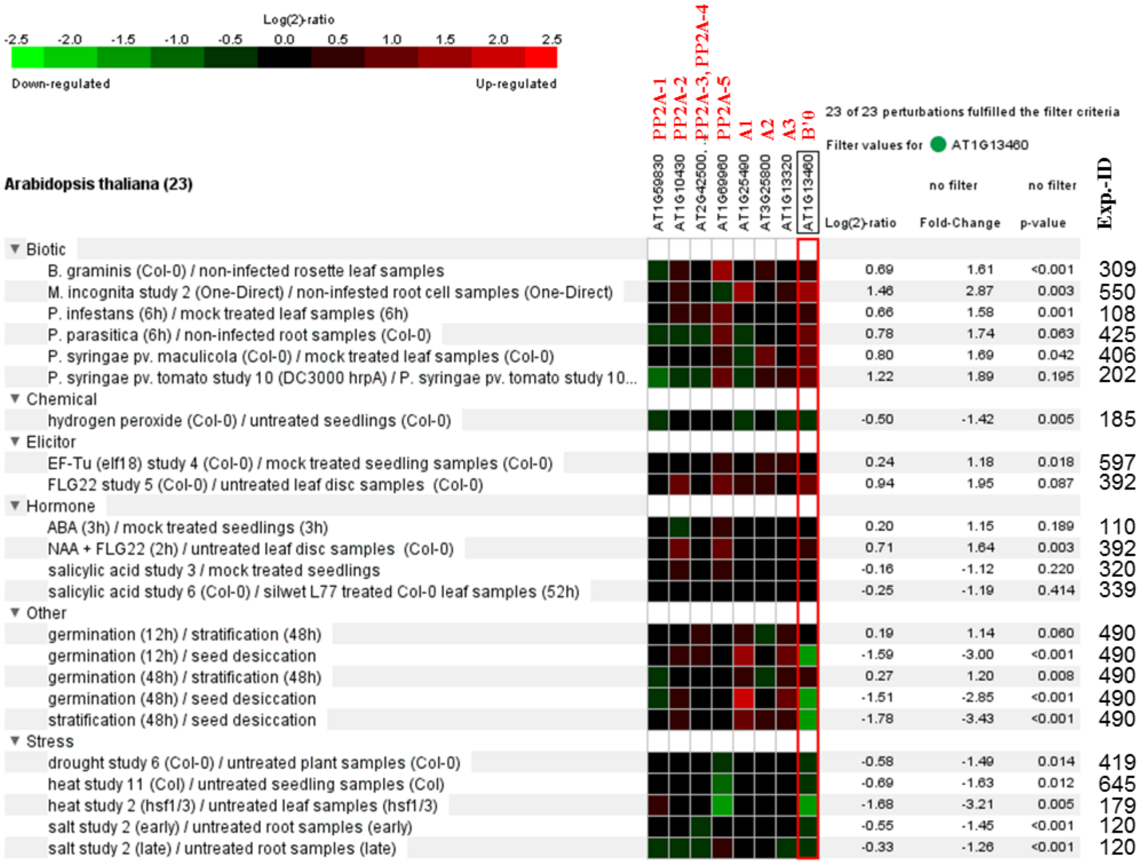
○ 34	AT1G03080	0.40		kinase interacting (KIP1-like) family protein
○ 35	AT2G44090	0.40		Ankyrin repeat family protein
○ 36	AT1G69960	0.40	C5	serine/threonine protein phosphatase 2A
○ 37	AT1G70750	0.40		Protein of unknown function, DUF593
○ 38	AT1G65540	0.40		LETM1-like protein
○ 39	AT4G33740	0.39		unknown protein; BEST Arabidopsis thaliana protei...
○ 40	AT1G7345...	0.39		[AT1G73460, Protein kinase superfamily protein];[A...
○ 41	AT1G24190	0.39		SIN3-like 3
○ 42	AT5G16210	0.39		HEAT repeat-containing protein
○ 43	AT2G41980	0.39		Protein with RING/U-box and TRAF-like domains
○ 44	AT5G53020	0.39		Ribonuclease P protein subunit P38-related

Supplemental Figure S2. Clustering and co-expression of *Arabidopsis* PP2A subunits C and A with B′θ. The expression analyses support the identification of C5 and C2 as interacting partners of B′θ. (a) List of genes co-expressed with *B′θ* according to the co-expression tool of external stimuli. (b-d) Gene expression profiles based on microarray data were clustered according to similarity in expression patterns. (b) Hierarchical clustering in the case of plant development and (c) Hierarchical clustering of various stimuli, (d) Biclustering. Hierarchical clustering is grouping genes based on similar expression in all conditions. Biclustering tool identifies groups of genes that exhibit similarity only in a subset of conditions, irrespective of their profiles in other conditions. The figures are from an output result of MetaAnalyzer of GENEVESTIGATOR (www.genevestigator.com (Zimmermann et al., 2004)). Clustering results were generated by default settings. Results are given as heat maps coding that reflect absolute signal values.



Supplemental Figure S3. Identification of PP2A complexes in peroxisomes of onion epidermal cells. Visualization of B′θ/C5 and B′θ/A2 complexes formation and localization into peroxisomes by BiFC. (I) Co-expression of C5-VYNE and B′θ-VYCE(R); (II) co-expression of A2-VYNE(R) and B′θ-VYCE(R). (I_2 and II_2) Peroxisomes were labeled with RFP-SKL (Matre et al., 2009). (I_3 and II_3) are the merged images.

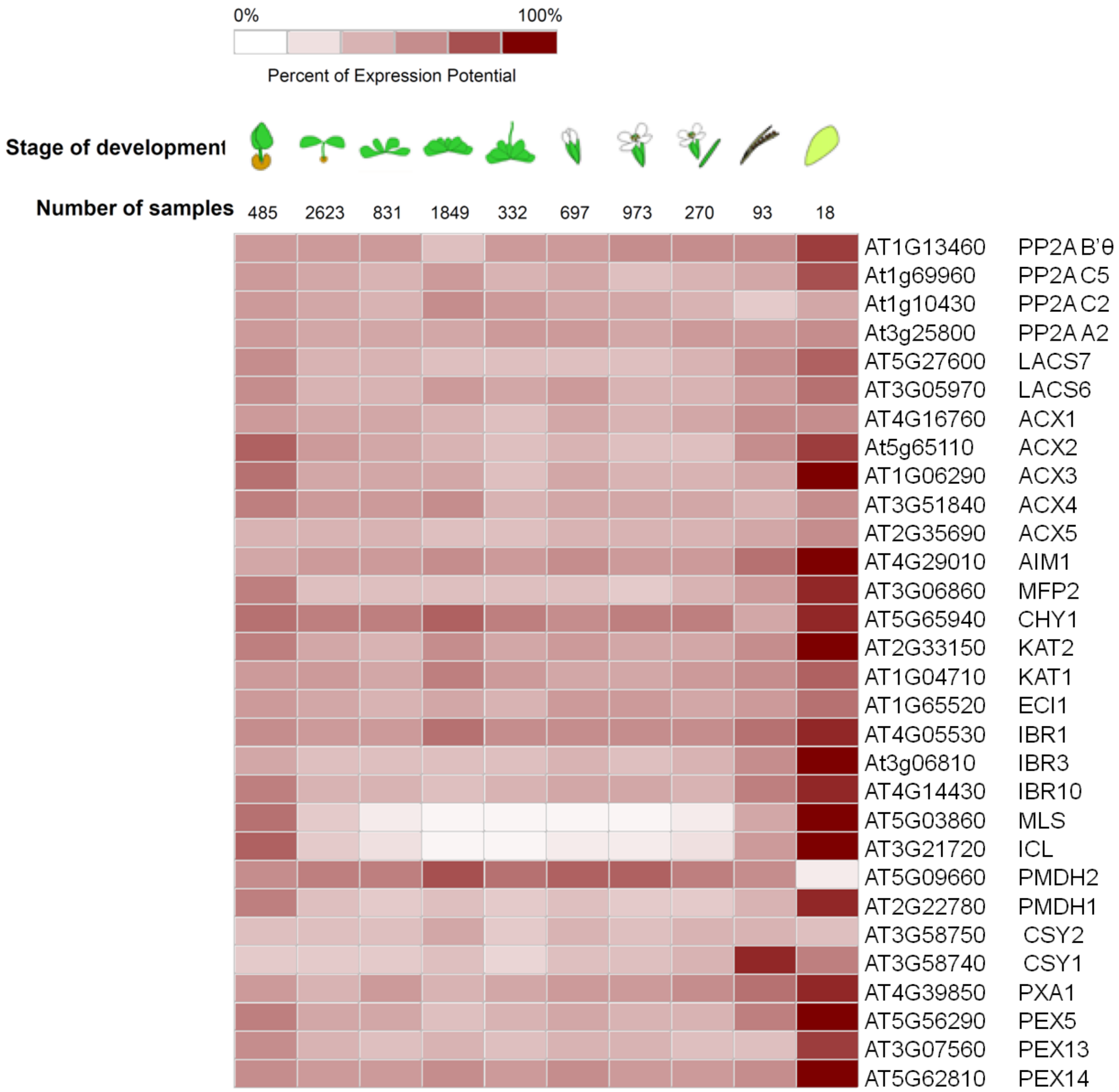


23 of 23 perturbations fulfilled the filter criteria

Filter values for ● AT1G13460

Arabidopsis thaliana (23)	Log(2)-ratio	no filter Fold-Change	no filter p-value	Exp.-ID
▼ Biotic				
B. graminis (Col-0) / non-infected rosette leaf samples	0.69	1.61	<0.001	309
M. incognita study 2 (One-Direct) / non-infested root cell samples (One-Direct)	1.46	2.87	0.003	550
P. infestans (6h) / mock treated leaf samples (6h)	0.66	1.58	0.001	108
P. parasitica (6h) / non-infected root samples (Col-0)	0.78	1.74	0.063	425
P. syringae pv. maculicola (Col-0) / mock treated leaf samples (Col-0)	0.80	1.69	0.042	406
P. syringae pv. tomato study 10 (DC3000 hrpA) / P. syringae pv. tomato study 10...	1.22	1.89	0.195	202
▼ Chemical				
hydrogen peroxide (Col-0) / untreated seedlings (Col-0)	-0.50	-1.42	0.005	185
▼ Elicitor				
EF-Tu (elf18) study 4 (Col-0) / mock treated seedling samples (Col-0)	0.24	1.18	0.018	597
FLG22 study 5 (Col-0) / untreated leaf disc samples (Col-0)	0.94	1.95	0.087	392
▼ Hormone				
ABA (3h) / mock treated seedlings (3h)	0.20	1.15	0.189	110
NAA + FLG22 (2h) / untreated leaf disc samples (Col-0)	0.71	1.64	0.003	392
salicylic acid study 3 / mock treated seedlings	-0.16	-1.12	0.220	320
salicylic acid study 6 (Col-0) / silwet L77 treated Col-0 leaf samples (52h)	-0.25	-1.19	0.414	339
▼ Other				
germination (12h) / stratification (48h)	0.19	1.14	0.060	490
germination (12h) / seed desiccation	-1.59	-3.00	<0.001	490
germination (48h) / stratification (48h)	0.27	1.20	0.008	490
germination (48h) / seed desiccation	-1.51	-2.85	<0.001	490
stratification (48h) / seed desiccation	-1.78	-3.43	<0.001	490
▼ Stress				
drought study 6 (Col-0) / untreated plant samples (Col-0)	-0.58	-1.49	0.014	419
heat study 11 (Col) / untreated seedling samples (Col)	-0.69	-1.63	0.012	645
heat study 2 (hsf1/3) / untreated leaf samples (hsf1/3)	-1.68	-3.21	0.005	179
salt study 2 (early) / untreated root samples (early)	-0.55	-1.45	<0.001	120
salt study 2 (late) / untreated root samples (late)	-0.33	-1.26	<0.001	120

Supplemental Figure S4. Gene expression profiles of *Arabidopsis* PP2A subunits C, A and B′θ in response to various stimuli. Expression table obtained from *Arabidopsis* microarray experiments as reported by Genevestigator (www.genevestigator.com (Zimmermann et al., 2004)). The examples of perturbations used for this analysis include hormones, stress (drought, heat, and salt treatments) and others (germination and stratification conditions). The color code is in the $\log_2$ scale where red represents up-regulation and the green represents down-regulation. Exp.-ID = Experiment Identifier.



Supplemental Figure S5. PP2A subunits *C5* and *B'θ* show high expression during senescence. Proteins which are involved in peroxisomal β-oxidation, glyoxylate cycle and PTS1 import, were subjected to gene expression analysis by Genevestigator (www.genevestigator.com (Zimmermann et al., 2004)). The expression pattern in the developmental map show that most of the genes are up-regulated during senescence (rightmost column), as are *C5* and *B'θ*. Expression levels are given as heat maps coding that reflect absolute signal values, darker color represents stronger expression as indicated by the scale.

Supplemental Table S6. Summary of phosphorylated peroxisomal proteins involved in β-oxidation, glyoxylate cycle and PTS1 import. S indicates Serine; T is for Threonine and Y for Tyrosine. Experimentally identified phosphoproteins are summarized in columns 4-6 and extracted from PhosPhAt 4.0 (Heazlewood et al., 2008).

AGI	Acronym	ANOTATION	Experimentally detected Phospho-peptides	Mod. aa	Experimental data sources : (PhosPhAt 4.0)
AT3G05970	LACS6	Long-chain acyl-CoA synthetase 6	IYAGIINAVK	Y363	PhosPhAt 4.0
AT3G51840	ACX4	Acyl-CoA oxidase 4	LGAMGVAGGSIK	S104	Nakagami et al., 2010
AT4G29010	AIM1	Enoyl-CoA hydratase/isomerase family	VAVIGGGLMGSGIATALLLSN AMNGMLLSESK	S331, T326 S712	Nakagami et al., 2010 PhosPhAt 4.0
AT3G06860	MFP2	Multifunctional protein 2	SMIIPLMQEDK SISGVKLDPK	S565 S611	PhosPhAt 4.0
AT1G04710	KAT1	Peroxisomal 3-ketoacyl-coa thiolase 4	AASATASGKFK	S219	PhosPhAt 4.0
AT1G65520	ECI1	Delta(2)-enoyl CoA isomerase 1	SDPSFSQSVLITTSDGK	S43, S54, S47 T51, T52	PhosPhAt 4.0
At3g06810	IBR3	Acyl-CoA dehydrogenase-related	DVSPSYESLVDGSGR	S387, S389 Y390	Nakagami et al., 2010 Sugiyama et al., 2008
AT3G21720	ICL	Isocitrate lyase	EARMSMSR	S154 S156	Engelsberger & Schulze 2012
AT3G58750	CSY2	Citrate synthase 2	FGQVSISNASR	S499, S501 S504	Nakagami et al., 2010 Sugiyama et al., 2008
AT4G39850	PXA1	Peroxisomal ABC transporter 1	LCNGQSDDDETLEK LIGLSVLQSGASSIIAPSLRHL IASLNGTTVKYVLEQDK	S59, T64, S806 T786, T787	Reiland et al., 2011 Engelsberger & Schulze 2012
AT5G56290	PEX5	Peroxin 5	LAHTLSQDGNPK DRSSIMAR	S173, S174 S308	Nakagami et al., 2010 Wang et al., 2013
AT3G07560	PEX13	Peroxin13	GGMLYGELAR	Y241	Nakagami et al., 2010
AT5G62810	PEX14	Peroxin 14	SASPPAAPADSSAPPHPK QRSWVPPQPPPVAMAEAVEAIR	S310, S312, S320, S321, S427	Wang et al., 2013 Reiland et al., 2009 Reiland et al., 2011 Sugiyama et al., 2008

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At_Btheta        1 --------MWKQILSKLPKKSSSK-----------NHSSSSSS---TSKSSDNGASKSGN
Al               1 --------MWKQILSKLPKKSSSK-----------SHSSSSSSNASTSKSSDNGAGKPGN
Cr               1 --------MWKQIISKLPKKSSSK-----------NHSSSTPS-ASTSKTSDNGAGKSGN
Es               1 --------MWKQIISKLPKKSSSK-----------NHSSANAV-ASTSKSSVNGAGKSGN
At_Beta          1 --------MWKQILSKLPNKKSSKHEHRGREHGGHSSSSSHTSGASTSKSTDNGAAKS--
Csi              1 --------MIKQILKKLPRKSSKTGDNREHG----RNSVTHSIASTGSRSSDLGKSKSGN
Pv               1 --------MFNKIFSKLPRKSSKGSEHGGSGKG--HHGVTTSSKNSDSVSVSPG-GTKPG
Cs               1 --------MIKQIFSKLPRKSSKGGESREHGGSHMAPSTAYASASSRGNDLASGKSANL-
Sl               1 --------MIKQIFGK--KKQSK-------------TAGSTSSKKSDGGGKKVGVSANTV
Vv               1 --------MIKQIFSKLPRKLSKAVENRELGG---TTAFSNNSNRSRGSDVESNQFANLN
Os               1 --------MIKQILGRFPKKPSKSGDKDPIGRS--SPSVPNPPLGPRGAERSSNLSSQTP
Zm               1 --------MIKQILGRLPRKPGKAGD----SRE--AAAAGNGTEPSNSYSVARSMDPGNK
Gm               1 --------MIKQILNRLPRKPSKSGESREGGAI--LTPSSTPSTSARSSDAAGYHYANAT
Cmsm             1 --------MIKQILNRLPRKPSKSTEHREGAGT--TISSSNASTSLRSNDLAANHHANTG
At_Bzeta         1 --------MIKQIFGKLPRKPSKSLQNDSN--GEGGVNNSYYASNSSTTSISKPSSTSSK
At_Bgamma        1 --------MIKQIFGKLPRKPSKSSHNDSNPNGEGGVN-SYYIPNSGISSISKPSSK---
At_Bdelta        1 --------MFKQILGKLPKKTSAK-----------------FWDNGESQTLDNNNNQGGG
Smo              1 ----------------MPGSTSVP-----------------SNPGSRSSSSSSGPVNGLL
At_Balpha        1 --------MFKKIMKGANRKASKAE--------------ANDSSMYGFDPP-GRSGPGSN
At_Bbeta         1 --------MFKKIMKGGHRKPSKSE--------------ANEPSSYGIGLPDNRSGPGSN
At_Bepsilon      1 --------MFNKIIKLGQKKFNKSDQ------------HHQDNNNNNNNTSTNTVVRGSR
Pp               1 ---------MQRGTKGKTDDKTDASA------------SAPDVVSQAAGSRVGNYAVGAP
M_RCC299         1 ------------------------------------------------------------
Vcfn             1 ---------MLKSMKQKFSGKKDASK------------NKDDSQPSTS-AKAGIP-ASSK
Cre              1 ---------MLKSMKQKFSGKKDASK------------NKDDSQPSTS-AKAGAPAASSK
At_Bkapa         1 --------MFKQFLSKLPRKSSKSD--------------SGELNRSSSGPVSSPVQRSGT
Hs_PPP2R5C       1 ----MPNKNKKEKESPKAGKSGKSSK-----------------EGQDTVESEQ-------
Dr_gppp2r5cb     1 ----MPNKTKKDKDSPKSAKVGKT-------------------AGQENSEHEQ-------
Hs_Bdelta        1 ----MPYKLKKEKEPPKVAKCTAKPSSSGKD------------GGGENTEEAQPQPQPQP
Sc_RTS1          1 MMRGFKQRLIKKTTGSSSSSSS-KKKDKEKE--KEKSSTTSSTSKKPASASSSSHGTTHS
Kl               1 MMRGFKQKLIKKTTGSTSSSSNQKRKDKEKEEKKEKEHSKRSPSTSGSSSARSSLDKTSH
Eg               1 MWGGCSAAGRARASGLLTGPAQLIKKT------TGSSSSTQKKKDKETGKKPGSANGAAG
Sp_par1          1 -MKGIKSKMLSRGKSQDTQKSSKKKESKKSNSHD---------SSKAPKESPSTD-----
Mo               1 -MRRFSQKVLSRGKDPNK-SSKKNKDSKDGASSPQTAGSSRDGSNQSPVLTPSSSSSTLN
Nc               1 -MKRFSQRVLSRTKDKDS-KSKKNKDAKDGTASPNSQGS-RE-ATQSPVLTPSSSTSTLV


At_Btheta       39 SQTQNAPPVKP-------------------------------------------------
Al              42 SHTKNAPAVKP-------------------------------------------------
Cr              41 SHAKNAPAVKPA------------------------------------------------
Es              41 SHTKNAPAAKPAA-----------------------------------------------
At_Beta         51 -HAKNASPAGKS------------------------------------------------
Csi             49 LNTVSPQMNDS-------------------------------------------------
Pv              50 NSSQNHGNRV--------------------------------------------------
Cs              52 VSSFAATNSVQDVG----------------------------------------------
Sl              38 ISAPYSVSAS--------------------------------------------------
Vv              50 VTSLAASNSTPITG----------------------------------------------
Os              51 V--ISSSGLSYGSG----------------------------------------------
Zm              47 R--AGNGDYPVPSG----------------------------------------------
Gm              51 ASPLSGTADSVP-G----------------------------------------------
Cmsm            51 TGSFSGPNSTLSVG----------------------------------------------
At_Bzeta        51 SSSASGSRVANG-T----------------------------------------------
At_Bgamma       49 -SSASNSNGANGTV----------------------------------------------
At_Bdelta       36 DEVLSQRTSSNG------------------------------------------------
Smo             28 P-----------------------------------------------------------
At_Balpha       38 MIVNHASRGSLVPS----------------------------------------------
At_Bbeta        39 VVVSHASRGALVNS----------------------------------------------
At_Bepsilon     41 TTTPAPSSVSNGES----------------------------------------------
Pp              40 ASAGVPAS-SKVGG----------------------------------------------
M_RCC299         1 ------------------------------------------------------------
Vcfn            38 APAPRPVS-ATREK----------------------------------------------
Cre             39 APAPRPIS-AIREK----------------------------------------------
At_Bkapa        39 SGGGSGPVRSNS------------------------------------------------
Hs_PPP2R5C      33 ---------ISVRK----------------------------------------------
Dr_gppp2r5cb    31 ---------ASNKK----------------------------------------------
Hs_Bdelta       45 QPQAQSQPPSSNKR----------------------------------------------
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Kl              61 RSGSTGSNAGSSRRVDSKSGSNNHNNHGSSNSN---ASGSGSSANNNQNDGVPR------
Eg              55 AVGGSGGRATVDKKEQKGSGAKQPKAKDAGKSGAGAAPKVKVAAKKEERS----------
Sp_par1         46 ---------PNGS---------------------------VIG----AQNDFL-------
Mo              59 -DIRNKPLPPNNASPHSTEGASPSGQPPMTQNQGGSDRFGLMGGLSPASNGGS-------
Nc              57 NDSRNKPLPPNNAA-HGDHGNSMLGPQGGNSNPGAADRFSSIGGQQQGANGGS-------
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At_Btheta       50 ------------------------------------------------------------
Al              53 ------------------------------------------------------------
Cr              53 ------------------------------------------------------------
Es              54 ------------------------------------------------------------
At_Beta         62 ------------------------------------------------------------
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Pv              60 ------------------------------------------------------------
Cs              66 ------------------------------------------------------------
Sl              48 ------------------------------------------------------------
Vv              64 ------------------------------------------------------------
Os              63 ------------------------------------------------------------
Zm              59 ------------------------------------------------------------
Gm              64 ------------------------------------------------------------
Cmsm            65 ------------------------------------------------------------
At_Bzeta        64 ------------------------------------------------------------
At_Bgamma       62 ------------------------------------------------------------
At_Bdelta       48 ------------------------------------------------------------
Smo             29 ------------------------------------------------------------
At_Balpha       52 ------------------------------------------------------------
At_Bbeta        53 ------------------------------------------------------------
At_Bepsilon     55 ------------------------------------------------------------
Pp              53 ------------------------------------------------------------
M_RCC299         1 ------------------------------------------------------------
Vcfn            51 ------------------------------------------------------------
Cre             52 ------------------------------------------------------------
At_Bkapa        51 ------------------------------------------------------------
Hs_PPP2R5C      38 ------------------------------------------------------------
Dr_gppp2r5cb    36 ------------------------------------------------------------
Hs_Bdelta       59 ------------------------------------------------------------
Sc_RTS1        118 KKTSSRKGQEQSKQSQQPSQSQKQGSSSSSAAIMNPTPVLTVTKDDKSTSGEDHAHPTLL
Kl             112 ------------------------------------TPSVNITKADSNAVG----KPTLI
Eg             105 -------------------------------------------------------YPTMI
Sp_par1         59 -------------------------------------------------------TVPKH
Mo             111 -------------------------------------------------------TPVRH
Nc             109 -------------------------------------------------------TPVRH


At_Btheta       50 ------------------------------------------------------------
Al              53 ------------------------------------------------------------
Cr              53 ------------------------------------------------------------
Es              54 ------------------------------------------------------------
At_Beta         62 ------------------------------------------------------------
Csi             60 ------------------------------------------------------------
Pv              60 ------------------------------------------------------------
Cs              66 ------------------------------------------------------------
Sl              48 ------------------------------------------------------------
Vv              64 ------------------------------------------------------------
Os              63 ------------------------------------------------------------
Zm              59 ------------------------------------------------------------
Gm              64 ------------------------------------------------------------
Cmsm            65 ------------------------------------------------------------
At_Bzeta        64 ------------------------------------------------------------
At_Bgamma       62 ------------------------------------------------------------
At_Bdelta       48 ------------------------------------------------------------
Smo             29 ------------------------------------------------------------
At_Balpha       52 ------------------------------------------------------------
At_Bbeta        53 ------------------------------------------------------------
At_Bepsilon     55 ------------------------------------------------------------
Pp              53 ------------------------------------------------------------
M_RCC299         1 ------------------------------------------------------------
Vcfn            51 ------------------------------------------------------------
Cre             52 ------------------------------------------------------------
At_Bkapa        51 ------------------------------------------------------------
Hs_PPP2R5C      38 ------------------------------------------NSLVAVPSTVSAK-----
Dr_gppp2r5cb    36 ------------------------------------------GGNSVPPATQLLK-----
Hs_Bdelta       59 ------------------------------------------PSNSTPPPTQLSK-----
Sc_RTS1        178 GAVSAVPSSPISNASGTAVSSDVENGNSNNNNMNINTSNTQDANHASSQSIDIPRSSHSF
Kl             132 GAAAQVTPPPTS--------PKAQPASLNTPSSATGSTTVLKDSQRSPTSIEIPRSSHSF
Eg             110 --AAAVSPGSTS-----------------------GPPSPKEAEAASPNGIDIPRSSHSF
Sp_par1         64 ------------------------------------------SGKKVPIDTTP-------
Mo             116 GQLPPTVIISPSG---------------------APHVPPPGAAETMPHDLAPPKAGQNS
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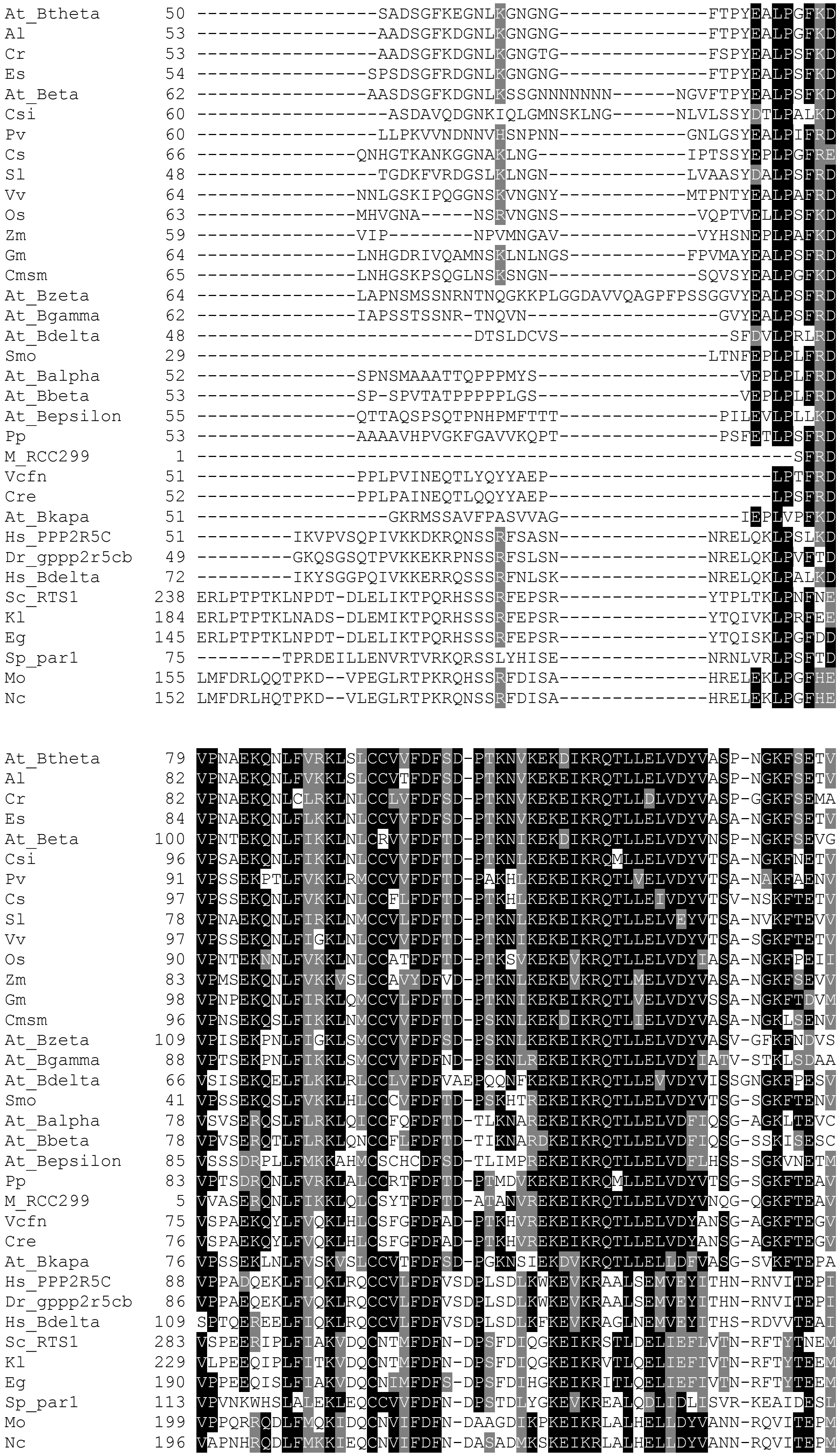

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Al              53 -----------------AADSGFKDGNLKGNGNG--------------FTPYEALPGFKD
Cr              53 -----------------AADSGFKDGNLKGNGTG--------------FSPYEALPSFKD
Es              54 ----------------SPSDSGFRDGNLKGNGNG--------------FTPYEALPSFKD
At_Beta         62 ----------------AASDSGFKDGNLKSSGNNNNNNN------NGVFTPYEALPSFKD
Csi             60 ------------------ASDAVQDGNKIQLGMNSKLNG------NLVLSSYDTLPALKD
Pv              60 -----------------LLPKVVNDNNVHSNPNN------------GNLGSYEALPIFRD
Cs              66 ---------------QNHGTKANKGGNAKLNG--------------IPTSSYEPLPGFRE
Sl              48 -----------------TGDKFVRDGSLKLNGN-------------LVAASYDALPSFRD
Vv              64 ---------------NNLGSKIPQGGNSKVNGNY------------MTPNTYEALPAFRD
Os              63 ---------------MHVGNA-----NSRVNGNS-------------VQPTVELLPSFKD
Zm              59 ---------------VIP--------NPVMNGAV-------------VYHSNEPLPAFKD
Gm              64 ---------------LNHGDRIVQAMNSKLNLNGS-----------FPVMAYEALPSFRD
Cmsm            65 ---------------LNHGSKPSQGLNSKSNGN--------------SQVSYEALPGFKD
At_Bzeta        64 ---------------LAPNSMSSNRNTNQGKKPLGGDAVVQAGPFPSSGGVYEALPSFRD
At_Bgamma       62 ---------------IAPSSTSSNR-TNQVN------------------GVYEALPSFRD
At_Bdelta       48 --------------------------DTSLDCVS----------------SFDVLPRLRD
Smo             29 ------------------------------------------------LTNFEPLPLFRD
At_Balpha       52 ---------------SPNSMAAATTQPPPMYS-------------------VEPLPLFRD
At_Bbeta        53 ---------------SP-SPVTATPPPPPLGS-------------------VEPLPLFRD
At_Bepsilon     55 ---------------QTTAQSPSQTPNHPMFTTT---------------PILEVLPLLKD
Pp              53 ---------------AAAAVHPVGKFGAVVKQPT---------------PSFETLPSFRD
M_RCC299         1 --------------------------------------------------------SFRD
Vcfn            51 ---------------PPLPVINEQTLYQYYAEP---------------------LPTFRD
Cre             52 ---------------PPLPAINEQTLQQYYAEP---------------------LPSFRD
At_Bkapa        51 ------------------GKRMSSAVFPASVVAG-----------------IEPLVPFKD
Hs_PPP2R5C      51 ---------IKVPVSQPIVKKDKRQNSSRFSASN--------------NRELQKLPSLKD
Dr_gppp2r5cb    49 ---------GKQSGSQTPVKKEKRPNSSRFSLSN--------------NRELQKLPVFTD
Hs_Bdelta       72 ---------IKYSGGPQIVKKERRQSSSRFNLSK--------------NRELQKLPALKD
Sc_RTS1        238 ERLPTPTKLNPDT-DLELIKTPQRHSSSRFEPSR--------------YTPLTKLPNFNE
Kl             184 ERLPTPTKLNADS-DLEMIKTPQRHSSSRFEPSR--------------YTQIVKLPRFEE
Eg             145 ERLPTPTKLNPDT-DLELIKTPQRHSSSRFEPSR--------------YTQISKLPGFDD
Sp_par1         75 --------TPRDEILLENVRTVRKQRSSLYHISE--------------NRNLVRLPSFTD
Mo             155 LMFDRLQQTPKD--VPEGLRTPKRQHSSRFDISA--------------HRELEKLPGFHE
Nc             152 LMFDRLHQTPKD--VLEGLRTPKRQNSSRFDISA--------------HRELEKLPGFHE

At_Btheta       79 VPNAEKQNLFVRKLSLCCVVFDFSD-PTKNVKEKDIKRQTLLELVDYVASP-NGKFSETV
Al              82 VPNAEKQNLFVKKLSLCCVTFDFSD-PTKNVKEKEIKRQTLLELVDYVASP-NGKFSETV
Cr              82 VPNAEKQNLCLRKLNLCCLVFDFSD-PTKNVKEKEIKRQTLLDLVDYVASP-GGKFSEMA
Es              84 VPNAEKQNLFLKKLNLCCVVFDFSD-PTKNVKEKEIKRQTLLELVDYVASA-NGKFSETV
At_Beta        100 VPNTEKQNLFIKKLNLCRVVFDFTD-PTKNIKEKDIKRQTLLELVDYVNSP-NGKFSEVG
Csi             96 VPSAEKQNLFIKKLNLCCVVFDFTD-PTKNLKEKEIKRQMLLELVDYVTSA-NGKFNETV
Pv              91 VPSSEKPTLFVKKLRMCCVVFDFTD-PAKHLKEKEIKRQTLVELVDYVTSA-NAKFAENV
Cs              97 VPSSEKQNLFVKKLNLCCFLFDFTD-PTKHLKEKEIKRQTLLEIVDYVTSV-NSKFTETV
Sl              78 VPNAEKQNLFIRKLNMCCVLFDFTD-PTKNLKEKEIKRQTLLELVEYVTSA-NVKFTEVV
Vv              97 VPSSEKQNLFIGKLNLCCVVFDFTD-PTKNIKEKEIKRQTLLELVDYVTSA-SGKFTETV
Os              90 VPNTEKNNLFVKKLNLCCATFDFTD-PTKSVKEKEVKRQTLLELVDYIASA-NGKFPEII
Zm              83 VPMSEKQNLFVKKVSLCCAVYDFVD-PTKNLKEKEVKRQTLMELVDYVASA-NGKFSEVV
Gm              98 VPNPEKQNLFIRKLQMCCVLFDFTD-PTKNIKEKEIKRQTLVELVDYVSSA-NGKFTDVM
Cmsm            96 VPNSEKQSLFIKKLNMCCVVFDFTD-PSKNLKEKDIKRQTLIELVDYVASA-NGKLSENV
At_Bzeta       109 VPISEKPNLFIGKLSMCCVVFDFSD-PSKNLKEKEIKRQTLLELVDYVASV-GFKFNDVS
At_Bgamma       88 VPTSEKPNLFIKKLSMCCVVFDFND-PSKNLREKEIKRQTLLELVDYIATV-STKLSDAA
At_Bdelta       66 VSISEKQELFLKKLRLCCLVFDFVAEPQQNFKEKEIKRQTLLEVVDYVISSGNGKFPESV
Smo             41 VPSSEKQSLFVKKLHLCCCVFDFTD-PSKHTREKEIKRQTLLELVDYVTSG-SGKFTENV
At_Balpha       78 VSVSERQSLFLRKLQICCFQFDFTD-TLKNAREKEIKRQTLLELVDFIQSG-AGKLTEVC
At_Bbeta        78 VPVSERQTLFLRKLQNCCFLFDFTD-TIKNARDKEIKRQTLLELVDFIQSG-SSKISESC
At_Bepsilon     85 VSSSDRPLLFMKKAHMCSCHCDFSD-TLIMPREKEIKRQTLLELVDFLHSS-SGKVNETM
Pp              83 VPTSDRQNLFVRKLALCCRTFDFTD-PTMDVKEKEIKRQMLLELVDYVTSG-SGKFTEAV
M_RCC299         5 VVASERQNLFIKKLQLCSYTFDFTD-ATANVREKEIKRQTLLELVDYVNQG-QGKFTEAV
Vcfn            75 VSPAEKQYLFVQKLHLCSFGFDFAD-PTKHVREKEIKRQTLLELVDYANSG-AGKFTEGV
Cre             76 VSPAEKQYLFVQKLHLCSFGFDFAD-PTKHVREKEIKRQTLLELVDYANSG-AGKFTEGV
At_Bkapa        76 VPSSEKLNLFVSKVSLCCVTFDFSD-PGKNSIEKDVKRQTLLELLDFVASG-SVKFTEPA
Hs_PPP2R5C      88 VPPADQEKLFIQKLRQCCVLFDFVSDPLSDLKWKEVKRAALSEMVEYITHN-RNVITEPI
Dr_gppp2r5cb    86 VPPAEQEKLFVQKLRQCCVLFDFVSDPLSDLKWKEVKRAALSEMVEYITHN-RNVITEPI
Hs_Bdelta      109 SPTQEREELFIQKLRQCCVLFDFVSDPLSDLKFKEVKRAGLNEMVEYITHS-RDVVTEAI
Sc_RTS1        283 VSPEERIPLFIAKVDQCNTMFDFN-DPSFDIQGKEIKRSTLDELIEFLVTN-RFTYTNEM
Kl             229 VLPEEQIPLFITKVDQCNTMFDFN-DPSFDIQGKEIKRVTLQELIEFIVTN-RFTYTEEM
Eg             190 VPPEEQISLFIAKVDQCNIMFDFS-DPSFDIHGKEIKRITLQELIEFIVTN-RFTYTEEM
Sp_par1        113 VPVNKWHSLALEKLEQCCVVFDFN-DPSTDLYGKEVKREALQDLIDLISVR-KEAIDESL
Mo             199 VPPQRRQDLFMQKIDQCNVIFDFN-DAAGDIKPKEIKRLALHELLDYVANN-RQVITEPM
Nc             196 VAPNHRQDLFMKKIEQCNVIFDFN-DASADMKSKEIKRLALHELLDYVANN-RQVITEPM
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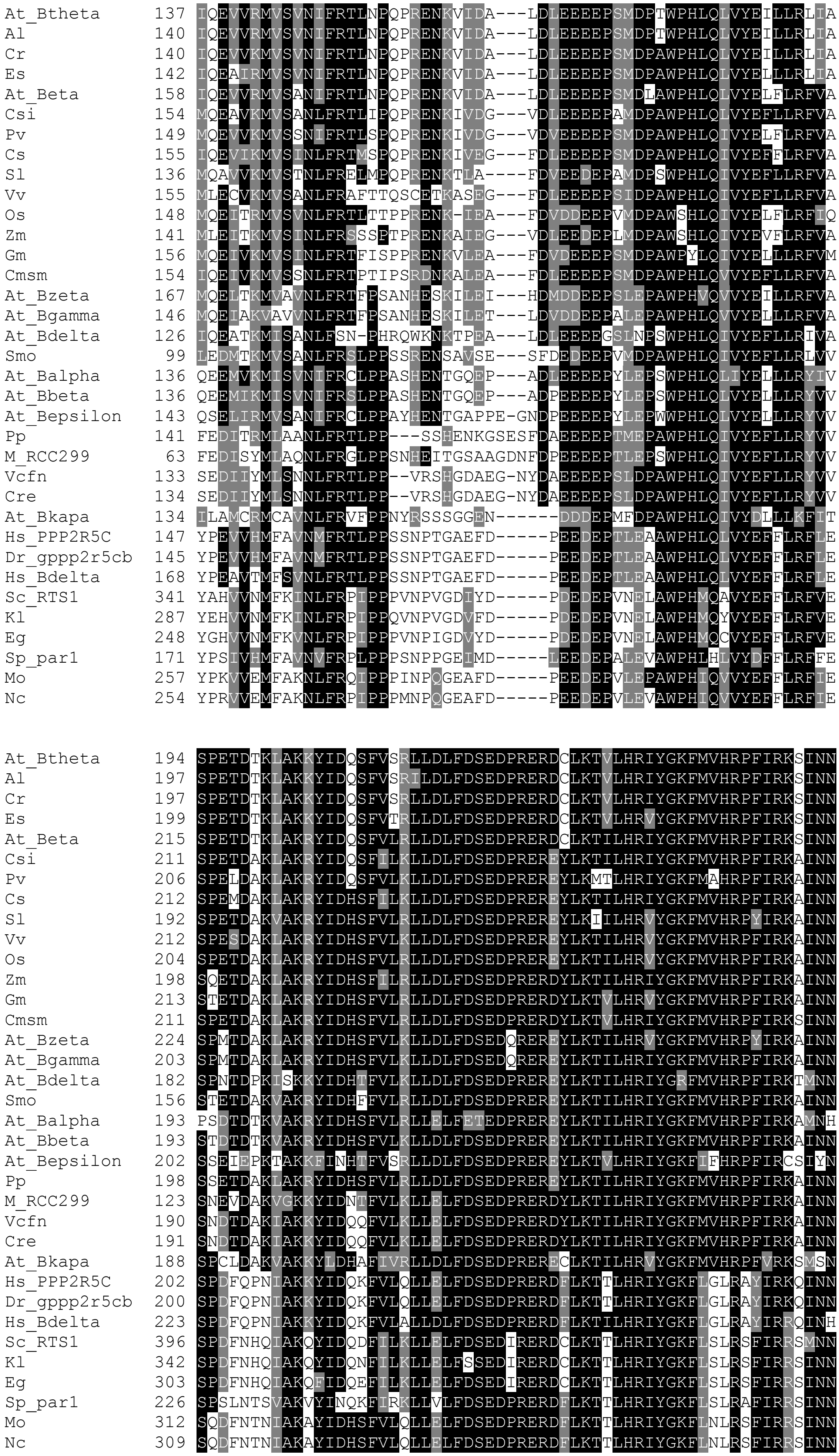

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Al             140 IQEVVRMVSVNIFRTLNPQPRENKVIDA---LDLEEEEPSMDPTWPHLQLVYEILLRLIA
Cr             140 IQEVVKMVSVNIFRTLNPQPRENKVIDA---LDLEEEEPSMDPAWPHLQLVYEILLRLIA
Es             142 IQEAIRMVSVNIFRTLNPQPRENKVIDA---LDLEEEEPSMDPAWPHLQLVYELLLRLIA
At_Beta        158 IQEVVRMVSANIFRTLNPQPRENKVIDA---LDLEEEEPSMDLAWPHLQLVYELFLRFVA
Csi            154 MQEAVKMVSANLFRTLIPQPRENKIVDG---VDLEEEEPAMDPAWPHLQLVYEFLLRFVA
Pv             149 MQEVVKMVSSNIFRTLSPQPRENKIVDG---VDVEEEEPSMDPAWPHLQIVYELFLRFVA
Cs             155 IQEVIKMVSINLFRTMSPQPRENKIVEG---FDLEEEEPSMDPAWPHLQIVYEFFLRFVA
Sl             136 MQAVVKMVSTNLFRELMPQPRENKTLA----FDVEEDEPAMDPSWPHLQIVYEFLLRFVA
Vv             155 MLECVKMVSANLFRAFTTQSCETKASEG---FDLEEEEPSIDPAWPHLQIVYEFLLRFVA
Os             148 MQEITRMVSVNLFRTLTTPPRENK-IEA---FDVDDEEPVMDPAWSHLQIVYELFLRFIQ
Zm             141 MLEITKMVSINLFRSSSPTPRENKAIEG---VDLEEDEPLMDPAWSHLQIVYEVFLRFVA
Gm             156 MQEIVKMVSINLFRTFISPPRENKVLEA---FDVDEEEPSMDPAWPYLQIVYELLLRFVM
Cmsm           154 IQEIVKMVSSNLFRTPTIPSRDNKALEA---FDLEEEEPSMDPAWPHLQVVYEFLLRFVA
At_Bzeta       167 MQELTKMVAVNLFRTFPSANHESKILEI---HDMDDEEPSLEPAWPHVQVVYEILLRFVA
At_Bgamma      146 MQEIAKVAVVNLFRTFPSANHESKILET---LDVDDEEPALEPAWPHLQVVYELLLRFVA
At_Bdelta      126 IQEATKMISANLFSN-PHRQWKNKTPEA---LDLEEEEGSLNPSWPHLQIVYEFLLRIVA
Smo             99 LEDMTKMVSANLFRSLPPSSRENSAVSE---SFDEDEEPVMDPAWPHLQIVYEFLLRLVV
At_Balpha      136 QEEMVKMISVNIFRCLPPASHENTGQEP---ADLEEEEPYLEPSWPHLQLIYELLLRYIV
At_Bbeta       136 QEEMIKMISVNIFRSLPPASHENTGQEP---ADPEEEEPYLEPSWPHLQLVYELLLRYVV
At_Bepsilon    143 QSELIRMVSANIFRCLPPAYHENTGAPPE-GNDPEEEEPYLEPWWPHLQLVYELLLRYVV
Pp             141 FEDITRMLAANLFRTLPP---SSHENKGSESFDAEEEEPTMEPAWPHLQIVYEFLLRYVV
M_RCC299        63 FEDISYMLAQNLFRGLPPSNHEITGSAAGDNFDPEEEEPTLEPSWPHLQIVYEFLLRYVV
Vcfn           133 SEDIIYMLSNNLFRTLPP--VRSHGDAEG-NYDAEEEEPSLDPAWPHLQIVYEFLLRYVV
Cre            134 SEDIIYMLSNNLFRTLPP--VRSHGDAEG-NYDAEEEEPSLDPAWPHLQIVYEFLLRYVV
At_Bkapa       134 ILAMCRMCAVNLFRVFPPNYRSSSGGEN------DDDEPMFDPAWPHLQIVYDLLLKFIT
Hs_PPP2R5C     147 YPEVVHMFAVNMFRTLPPSSNPTGAEFD-----PEEDEPTLEAAWPHLQLVYEFFLRFLE
Dr_gppp2r5cb   145 YPEVVHMFAVNMFRTLPPSSNPTGAEFD-----PEEDEPTLEAAWPHLQLVYEFFLRFLE
Hs_Bdelta      168 YPEAVTMFSVNLFRTLPPSSNPTGAEFD-----PEEDEPTLEAAWPHLQLVYEFFLRFLE
Sc_RTS1        341 YAHVVNMFKINLFRPIPPPVNPVGDIYD-----PDEDEPVNELAWPHMQAVYEFFLRFVE
Kl             287 YEHVVNMFKINLFRPIPPQVNPVGDVFD-----PDEDEPVNELAWPHMQYVYEFFLRFVE
Eg             248 YGHVVNMFKVNLFRPIPPPVNPIGDVYD-----PDEDEPVNELAWPHMQCVYEFFLRFVE
Sp_par1        171 YPSIVHMFAVNVFRPLPPPSNPPGEIMD-----LEEDEPALEVAWPHLHLVYDFFLRFFE
Mo             257 YPKVVEMFAKNLFRQIPPPINPQGEAFD-----PEEDEPVLEPAWPHIQVVYEFFLRFIE
Nc             254 YPRVVEMFAKNLFRPIPPPMNPQGEAFD-----PEEDEPVLEVAWPHIQVVYEFFLRFIE

At_Btheta      194 SPETDTKLAKKYIDQSFVSRLLDLFDSEDPRERDCLKTVLHRIYGKFMVHRPFIRKSINN
Al             197 SPETDTKLAKKYIDQSFVSRILDLFDSEDPRERDCLKTVLHRIYGKFMVHRPFIRKSINN
Cr             197 SPETDTKLAKKYIDQSFVSRLLDLFDSEDPRERDCLKTVLHRIYGKFMVHRPFIRKSINN
Es             199 SPETDTKLAKKYIDQSFVTRLLDLFDSEDPRERDCLKTVLHRVYGKFMVHRPFIRKSINN
At_Beta        215 SPETDTKLAKRYIDQSFVLRLLDLFDSEDPRERDCLKTILHRIYGKFMVHRPFIRKSINN
Csi            211 SPETDAKLAKRYIDQSFILKLLDLFDSEDPREREYLKTILHRIYGKFMVHRPFIRKAINN
Pv             206 SPELDAKLAKRYIDQSFVLKLLDLFDSEDPREREYLKMTLHRIYGKFMAHRPFIRKAINN
Cs             212 SPEMDAKLAKRYIDHSFILKLLDLFDSEDPREREYLKTILHRIYGKFMVHRPFIRKAINN
Sl             192 SPETDAKVAKRYIDHSFVLRLLDLFDSEDPREREYLKIILHRVYGKFMVHRPYIRKAINN
Vv             212 SPESDAKLAKRYIDHSFVLKLLDLFDSEDPREREYLKTILHRVYGKFMVHRPFIRKAINN
Os             204 SPETDAKLAKRYIDHSFVLRLLDLFDSEDPREREYLKTILHRVYGKFMVHRPFIRKAINN
Zm             198 SQETDAKLAKRYIDHSFILRLLDLFDSEDPRERDYLKTILHRIYGKFMVHRPFIRKAINN
Gm             213 STETDAKLAKRYIDHSFVLRLLDLFDSEDPRERDYLKTVLHRVYGKFMVHRPFIRKAINN
Cmsm           211 SPETDAKLAKRYIDHSFVLRLLDLFDSEDPRERDYLKTVLHRIYGKFMVHRPFIRKSINN
At_Bzeta       224 SPMTDAKLAKRYIDHSFVLKLLDLFDSEDQREREYLKTILHRVYGKFMVHRPYIRKAINN
At_Bgamma      203 SPMTDAKLAKRYIDHSFVLKLLDLFDSEDQREREYLKTILHRIYGKFMVHRPFIRKAINN
At_Bdelta      182 SPNTDPKISKKYIDHTFVLKLLDLFDSEDPREREYLKTILHRIYGRFMVHRPFIRKTMNN
Smo            156 STETDAKVAKRYIDHFFVLRLLDLFDSEDPREREYLKTILHRIYGKFMVHRPFIRKAINN
At_Balpha      193 PSDTDTKVAKRYIDHSFVLRLLELFETEDPREREYLKTILHRIYGKFMVHRPFIRKAMNH
At_Bbeta       193 STDTDTKVAKRYIDHSFVLKLLDLFDSEDPREREYLKTILHRIYGKFMVHRPFIRKAINN
At_Bepsilon    202 SSEIEPKTAKKFINHTFVSRLLDLFDSEDPREREYLKTVLHRIYGKFIFHRPFIRCSIYN
Pp             198 SSETDAKLAKRYIDHSFVLRLLDLFDSEDPREREYLKTILHRIYGKFMVHRPFIRKAINN
M_RCC299       123 SNEVDAKVGKKYIDNTFVLKLLELFDSEDPRERDYLKTILHRIYGKFMVHRPFIRKAINN
Vcfn           190 SNDTDAKIAKKYIDQQFVLKLLELFDSEDPRERDYLKTILHRIYGKFMVHRPFIRKAINN
Cre            191 SNDTDAKIAKKYIDQQFVLKLLELFDSEDPRERDYLKTILHRIYGKFMVHRPFIRKAINN
At_Bkapa       188 SPCLDAKVAKKYLDHAFIVRLLDLFDSEDPREREСLKTILHRVYGKFMVHRPFVRKSMSN
Hs_PPP2R5C     202 SPDFQPNIAKKYIDQKFVLQLLELFDSEDPRERDFLKTTLHRIYGKFLGLRAYIRKQINN
Dr_gppp2r5cb   200 SPDFQPNIAKKYIDQKFVLQLLELFDSEDPRERDFLKTTLHRIYGKFLGLRAYIRKQINN
Hs_Bdelta      223 SPDFQPNIAKKYIDQKFVLALLDLFDSEDPRERDFLKTILHRIYGKFLGLRAYIRRQINH
Sc_RTS1        396 SPDFNHQIAKQYIDQDFILKLLELFDSEDIRERDCLKTTLHRIYGKFLSLRSFIRRSMNN
Kl             342 SPDFNHQIAKQYIDQNFILKLLELFSSEDIRERDCLKTTLHRIYGKFLSLRSFIRRSINN
Eg             303 SPDFNHQIAKQFIDQEFILKLLELFDSEDIRERDCLKTTLHRIYGKFLSLRSFIRRSINN
Sp_par1        226 SPSLNTSVAKVYINQKFIRKLLVLFDSEDPRERDFLKTTLHRIYGKFLSLRAFIRRSINN
Mo             312 SQDFNTNIAKAYIDHSFVLQLLELFDSEDPRERDFLKTTLHRIYGKFLNLRSFIRRSINN
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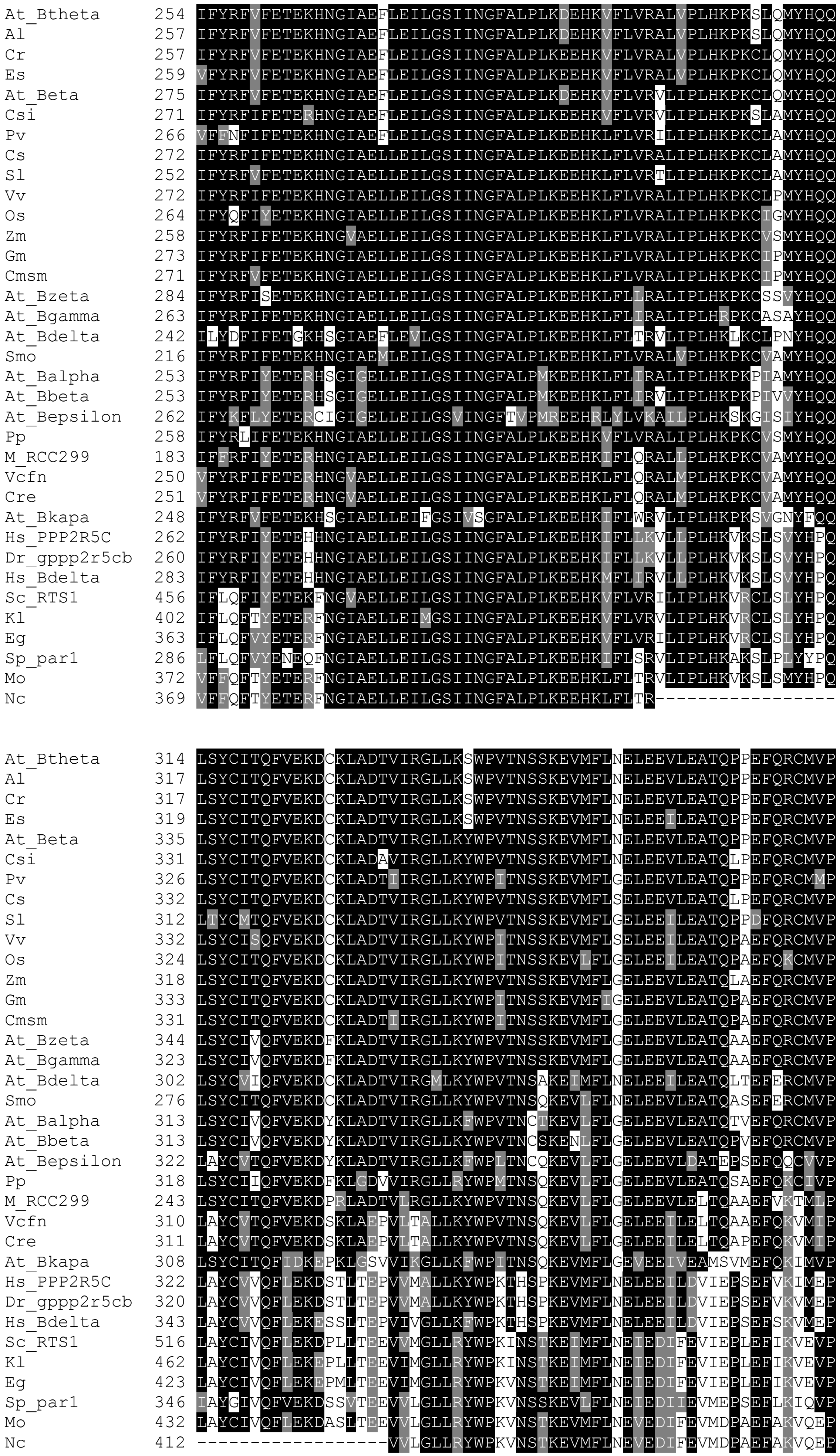

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Al            257 IFYRFVFETEKHNGIAEFLEILGSIINGFALPLKDEHKVFLVRALVPLHKPKSLQMYHQQ
Cr            257 IFYRFVFETEKHNGIAEFLEILGSIINGFALPLKEEHKVFLVRALVPLHKPKCLQMYHQQ
Es            259 VFYRFVFETEKHNGIAEFLEILGSIINGFALPLKEEHKVFLVRALVPLHKPKCLQMYHQQ
At_Beta       275 IFYRFVFETEKHNGIAEFLEILGSIINGFALPLKDEHKVFLVRVLIPLHKPKCLQMYHQQ
Csi           271 IFYRFIFETERHNGIAEFLEILGSIINGFALPLKEEHKVFLVRVLIPLHKPKSLAMYHQQ
Pv            266 VFFNFIFETEKHNGIAEFLEILGSIINGFALPLKEEHKLFLVRILIPLHKPKCLAMYHQQ
Cs            272 IFYRFIFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCLAMYHQQ
Sl            252 IFYRFVFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRTLIPLHKPKCLAMYHQQ
Vv            272 IFYRFIFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCLPMYHQQ
Os            264 IFYQFIYETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCIGMYHQQ
Zm            258 IFYRFIFETEKHNGVAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCVSMYHQQ
Gm            273 IFYRFIFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCIPMYHQQ
Cmsm          271 IFYRFVFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLVRALIPLHKPKCIPMYHQQ
At_Bzeta      284 IFYRFISETEKHNGIAELLEILGSIINGFALPLKEEHKLFLLRALIPLHKPKCSSVYHQQ
At_Bgamma     263 IFYRFIFETEKHNGIAELLEILGSIINGFALPLKEEHKLFLIRALIPLHRPKCASAYHQQ
At_Bdelta     242 ILYDFIFETGKHSGIAEFLEVLGSIINGFALPLKEEHKLFLTRVLIPLHKLKCLPNYHQQ
Smo           216 IFYRFIFETEKHNGIAEMLEILGSIINGFALPLKEEHKLFLVRALVPLHKPKCVAMYHQQ
At_Balpha     253 IFYRFIYETERHSGIGELLEILGSIINGFALPMKEEHKLFLIRALIPLHKPKPIAMYHQQ
At_Bbeta      253 IFYRFIYETERHSGIGELLEILGSIINGFALPMKEEHKLFLIRVLIPLHKPKPIVVYHQQ
At_Bepsilon   262 IFYKFLYETERCIGIGELLEILGSVINGFTVPMREEHRLYLVKAILPLHKSKGISIYHQQ
Pp            258 IFYRLIFETEKHNGIAELLEILGSIINGFALPLKEEHKVFLVRALIPLHKPKCVSMYHQQ
M_RCC299      183 IFFRFIYETERHNGIAELLEILGSIINGFALPLKEEHKIFLQRALLPLHKPKCVAMYHQQ
Vcfn          250 VFYRFIFETERHNGVAELLEILGSIINGFALPLKEEHKLFLQRALMPLHKPKCVAMYHQQ
Cre           251 VFYRFIFETERHNGVAELLEILGSIINGFALPLKEEHKLFLQRALMPLHKPKCVAMYHQQ
At_Bkapa      248 IFYRFVFETEKHSGIAELLEIFGSIVSGFALPLKEEHKIFLWRVLIPLHKPKSVGNYFQQ
Hs_PPP2R5C    262 IFYRFIYETEHHNGIAELLEILGSIINGFALPLKEEHKIFLLKVLLPLHKVKSLSVYHPQ
Dr_gppp2r5cb  260 IFYRFIYETEHHNGIAELLEILGSIINGFALPLKEEHKIFLLKVLLPLHKVKSLSVYHPQ
Hs_Bdelta     283 IFYRFIYETEHHNGIAELLEILGSIINGFALPLKEEHKMFLIRVLLPLHKVKSLSVYHPQ
Sc_RTS1       456 IFLQFIYETEKFNGVAELLEILGSIINGFALPLKEEHKVFLVRILIPLHKVRCLSLYHPQ
Kl            402 IFLQFTYETERFNGIAELLEIMGSIINGFALPLKEEHKVFLVRVLIPLHKVRCLSLYHPQ
Eg            363 IFLQFVYETERFNGIAELLEILGSIINGFALPLKEEHKVFLVRILIPLHKVRCLSLYHPQ
Sp_par1       286 LFLQFVYENEQFNGIAELLEILGSIINGFALPLKEEHKIFLSRVLIPLHKAKSLPLYYPQ
Mo            372 VFFQFTYETERFNGIAELLEILGSIINGFALPLKEEHKLFLTRVLIPLHKVKSLSMYHPQ
Nc            369 VFFQFTYETERFNGIAELLEILGSIINGFALPLKEEHKLFLTR-----------------

At_Btheta     314 LSYCITQFVEKDCKLADTVIRGLLKSWPVTNSSKEVMFLNELEEVLEATQPPEFQRCMVP
Al            317 LSYCITQFVEKDCKLADTVIRGLLKSWPVTNSSKEVMFLNELEEVLEATQPPEFQRCMVP
Cr            317 LSYCITQFVEKDCKLADTVIRGLLKSWPVTNSSKEVMFLNELEEVLEATQPPEFQRCMVP
Es            319 LSYCITQFVEKDCKLADTVIRGLLKSWPVTNSSKEVMFLNELEEILEATQPPEFQRCMVP
At_Beta       335 LSYCITQFVEKDCKLADTVIRGLLKYWPVTNSSKEVMFLNELEEVLEATQPPEFQRCMVP
Csi           331 LSYCITQFVEKDCKLADAVIRGLLKYWPVTNSSKEVMFLNELEEVLEATQLPEFQRCMVP
Pv            326 LSYCITQFVEKDCKLADTIIRGLLKYWPITNSSKEVMFLGELEEVLEATQPPEFQRCMMP
Cs            332 LSYCITQFVEKDCKLADTVIRGLLKYWPVTNSSKEVMFLSELEEVLEATQLPEFQRCMVP
Sl            312 LTYCMTQFVEKDCKLADTVIRGLLKYWPVTNSSKEVMFLGELEEILEATQPPDFQRCMVP
Vv            332 LSYCISQFVEKDCKLADTVIRGLLKYWPITNSSKEVMFLSELEEILEATQPAEFQRCMVP
Os            324 LSYCITQFVEKDCKLADTVIRGLLKYWPITNSSKEVLFLGELEEILEATQPAEFQKCMVP
Zm            318 LSYCITQFVEKDCKLADTVIRGLLKYWPVTNSSKEVMFLGELEEVLEATQLAEFQRCMVP
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At_Bzeta      344 LSYCIVQFVEKDFKLADTVIRGLLKYWPVTNSSKEVMFLGELEEVLEATQAAEFQRCMVP
At_Bgamma     323 LSYCIVQFVEKDFKLADTVIRGLLKYWPVTNSSKEVMFLGELEEVLEATQAAEFQRCMVP
At_Bdelta     302 LSYCVIQFVEKDCKLADTVIRGMLKYWPVTNSAKEIMFLNELEEILEATQLTEFERCMVP
Smo           276 LSYCITQFVEKDCKLADTVIRGLLKYWPVTNSQKEVLFLNELEEVLEATQASEFERCMVP
At_Balpha     313 LSYCIVQFVEKDYKLADTVIRGLLKFWPVTNCTKEVLFLGELEEVLEATQTVEFQRCMVP
At_Bbeta      313 LSYCIVQFVEKDYKLADTVIRGLLKYWPVTNCSKENLFLGELEEVLEATQPVEFQRCMVP
At_Bepsilon   322 LAYCVTQFVEKDYKLADTVIRGLLKFWPLTNCQKEVLFLGELEEVLDATEPSEFQQCVVP
Pp            318 LSYCIIQFVEKDFKLGDVVIRGLLRYWPMTNSQKEVLFLGELEEVLEATQSAEFQKCIVP
M_RCC299      243 LSYCITQFVEKDPRLADTVLRGLLKYWPVTNSQKEVLFLGELEEVLELTQAAEFVKTMLP
Vcfn          310 LAYCVTQFVEKDSKLAEPVLTALLKYWPVTNSQKEVLFLGELEEILELTQAAEFQKVMIP
Cre           311 LAYCVTQFVEKDSKLAEPVLTALLKYWPVTNSQKEVLFLGELEEILELTQAPEFQKVMIP
At_Bkapa      308 LSYCITQFIDKEPKLGSVVIKGLLKFWPITNSQKEVMFLGEVEEIVEAMSVMEFQKIMVP
Hs_PPP2R5C    322 LAYCVVQFLEKDSTLTEPVVMALLKYWPKTHSPKEVMFLNELEEILDVIEPSEFVKIMEP
Dr_gppp2r5cb  320 LAYCVVQFLEKDSTLTEPVVMALLKYWPKTHSPKEVMFLNELEEILDVIEPSEFVKVMEP
Hs_Bdelta     343 LAYCVVQFLEKESSLTEPVIVGLLKFWPKTHSPKEVMFLNELEEILDVIEPSEFSKVMEP
Sc_RTS1       516 LAYCIVQFLEKDPLLTEEVVMGLLRYWPKINSTKEIMFLNEIEDIFEVIEPLEFIKVEVP
Kl            462 LAYCIVQFLEKEPLLTEEVIMGLLRYWPKINSTKEIMFLNEIEDIFEVIEPLEFIKVEVP
Eg            423 LAYCIVQFLEKEPMLTEEVIMGLLRYWPKVNSTKEIMFLNEIEDIFEVIEPLEFIKVEVP
Sp_par1       346 IAYGIVQFVEKDSSVTEEVVLGLLRYWPKVNSSKEVLFLNEIEDIIEVMEPSEFLKIQVP
Mo            432 LAYCIVQFLEKDASLTEEVVLGLLRYWPKVNSTKEVMFLNEVEDIFEVMDPAEFAKVQEP
Nc            412 ------------------VVLGLLRYWPKVNSTKEVMFLNEVEDIFEVMDPAEFAKVQEP
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At_Btheta     374 LFRQVARCLNSLHFQVAERALFLWNNDHIENLIMQNRKVILPIIFPALERNT--------
Al            377 LFRQVARCLNSLHFQVAERALFLWNNDHIENLIMQNRKVILPIIFPALERNT--------
Cr            377 LFRQVARCLNSLHFQVAERALFLWNNDHIENLIMQNRKVILPIIFPALERNT--------
Es            379 LFRQVARCLNSLHFQVAERALFLWNNDHIESLIMQNRKVILPIIFPALERNT--------
At_Beta       395 LFRQIARCLNSLHFQVAERALFLWNNNHIENLIMQNRKVILPIIFPALERNA--------
Csi           391 LFQQIARCLNSLHFQVAERALFLWNNDHIENLIIQNRKVILPIIFPALEKNA--------
Pv            386 LFRRIARCLNSPHFQVAERALFLWNNDHIVNLIKQNRKVILPIIFPALERNA--------
Cs            392 LFRQIARCLNSSHFQVAERALFLWNNDHIENLIKENRKVILPIIFPALEKNA--------
Sl            372 LFRRIAQCLTSLHFQVAERALFLWNNDHIENLIKQHRKVILPIIFPALERNA--------
Vv            392 LFHQIARCLNSSHFQVAERALFLWNNGHIENLIKQNRGIILPIIFPALEKNA--------
Os            384 LFRQIAHCLNSSHFQVAERALFLWNNDHIENLIKQNSRVILPIIFPALERNA--------
Zm            378 LFRQISRSMNSFHFQVAERALFLWNNDHIETLIKQNYKVLLPIIYPALERNS--------
Gm            393 LFRQISCCLSSSHFQVAERALFLWNNDHIETLIKQNHKIILPIVLPALEHNA--------
Cmsm          391 LFRQIGRCLSSSHFQVAERTLFLWNNNHIENLIKQNRKVILPIIFPALERNS--------
At_Bzeta      404 LSRQIARCLNSSHFQVAERALFLWNNDHIRNLITQNHKVIMPIVFPALERNT--------
At_Bgamma     383 LFRQIARCLNSSHFQVAERALFLWNNDHIRNLITQNHKVIMPIVFPAMERNT--------
At_Bdelta     362 LSRQIAQCLSSSHFQVAERALYLWNNDHVTNLVRQNSRIILPIVFPALEKNG--------
Smo           336 LFRQIARCLNSSHFQVAERALFLWNNDHVVSLVAQNRQTILPLIFSALEMNN--------
At_Balpha     373 LFQQIARCLSSSNFQVAERALFLWNNEHVVGLIAQNRGVILPIIFASLEKNI--------
At_Bbeta      373 LFQQIGRCLTSSHFQVAERALFLWNNEHIVGLIAQNRSVILPIIYPTLEKNI--------
At_Bepsilon   382 LFTQIGKCLNSAHFQVAERALFLWNNEHIVGLIAQNKDVIFPIIFEALERNM--------
Pp            378 LFRQIGRCLNSSHFQVAERALFLWNNDHIVSLVAQNRQVVLPIIFPALERNT--------
M_RCC299      303 LFRQISACINSSHFQVAERALFLWNNDYIVNLVAQNRHVLLPVCFGAFERNA--------
Vcfn          370 LFKQLAKCLNSQHFQVAERSLFLWNNEYIVNLVAQHRHQLLPILFPALEENT--------
Cre           371 LFRQLAKCLNSQHFQVAERSLFLWNNEYIVNLVAQHRHQLLPILFPALEENT--------
At_Bkapa      368 LFLRIACCVTSSHFQVSERALFLWNNDQIVNLIGHNRQAILPIMFTALEKNA--------
Hs_PPP2R5C    382 LFRQLAKCVSSPHFQVAERALYYWNNEYIMSLISDNAAKILPIMFPSLYRNS--------
Dr_gppp2r5cb  380 LFRQLAKCVSSPHFQVAERALYYWNNEYIMSLISDNAAKILPIMFPSLYRNS--------
Hs_Bdelta     403 LFRQLAKCVSSPHFQVAERALYYWNNEYIMSLISDNAARVLPIMFPALYRNS--------
Sc_RTS1       576 LFVQLAKCISSPHFQVAEKVLSYWNNEYFLNLCIENAEVILPIIFPALYELTSQLELD--
Kl            522 LFVQLAKCISSPHFQVAEKVLSYWNNEYFLNLCIENAEVILPIIFPPLYKLTSQLDKNDP
Eg            483 LFVQLAKCISSPHFQVAEKVLSYWNNEYFLNLCIENAEVILPIIFPALYELTSQLDLDS-
Sp_par1       406 LFHKLATSISSQNFQVAERALYFFNNDYFVHLVEENVDIILPIIYPALFEIS--------
Mo            492 LFHQLAKSVASPHFQVAERALYFWNNEYFCNLVSDNVEIILPIMFAPLYENS--------
Nc            454 LFHQLAKSVASPHFQVAERALYFWNNEYFCNLVSDNVEIILPIMFAPLYENS--------

At_Btheta     426 ---------------------QKHWNQAVHSLTLNVQKIFNDIDAELFKDCLAKFREDES
Al            429 ---------------------QKHWNQAVHSLTLNVQKIFNDIDAELFKECLAKFREDES
Cr            429 ---------------------QKHWNQAVHSLTLNVQKIFNDIDAELFKDCLGKFREDES
Es            431 ---------------------QKHWNQAVHSLTLNVQKIFNDIDPEFFKECLAKFRENEA
At_Beta       447 ---------------------QKHWNQAVHSLTLNVRKIFHDLDPELFKECLAKFKEDES
Csi           443 ---------------------RNHWNQAVHSLTLNVRKIFFDLDPELFKECLAKFREYES
Pv            438 ---------------------RSHWNQAVHSLTLNVRKIFNDVDADLSKECLQKFEEDES
Cs            444 ---------------------RSHWNQAVHSLTLNVRKIFYDLDPDLLKECLVKFQEDEL
Sl            424 ---------------------RNHWNQAVHSLSLNIRKIFYDLDPELFKECLHNFQEDEL
Vv            444 ---------------------RNHWNQAVHGLTLNVRKIFFDLDPELYKECLLKFQEDES
Os            436 ---------------------NGHWNQAVQSLTLNVRKLFSDHDVGVYDECQRKYEDEKA
Zm            430 ---------------------RDHWNQAVRSLTLNVRKIFSDHDSTFFGECVQRFSDEEL
Gm            445 ---------------------RNHWNQAVQSLTINVRKIFVDTDPEFYEECMIKVRENEA
Cmsm          443 ---------------------RNHWNQAVQNLTQNVRKIFSDADPELFDECLLKFQEEET
At_Bzeta      456 ---------------------RGHWNQAVQSLTINVRKVLCEIDQVLFDECLAKFQVEEV
At_Bgamma     435 ---------------------RGHWNQAVQSLTLNVRKVMAETDQILFDECLAKFQEDEA
At_Bdelta     414 ---------------------SSHWNQAVKNLTENVLKVLSDTNPDLFEECLHKFQEDQQ
Smo           388 ---------------------RNHWNQAVHGLTCNVRKMFSEMDPELFQECQRKFQEDEE
At_Balpha     425 ---------------------ESHWNQAVHGLSANIKRMFMEMDPELFEECQQQYEEKQA
At_Bbeta      425 ---------------------QSHWNQAVHGLTTNIKKMFMEMDPELFEECQRQYEEKQA
At_Bepsilon   434 ---------------------KGHWNQAVHGLSENVRRMFLEMDTELFEECEKQYLENEA
Pp            430 ---------------------RSHWNQAVHGLTLNVRKMFVEMDQELFQECQRKYEEDEA
M_RCC299      355 ---------------------RSHWNAAVGGLTVNVRKMLMEMDQQLYEECQRNWEEEEL
Vcfn          422 ---------------------NSHWNPAVHGLTCNVRKMFQELDEQLYEECKRKYEEEQA
Cre           423 ---------------------NSHWNPAVHGLTCNVRKMFQELDEALYEECKRKYEEEQT
At_Bkapa      420 ---------------------QNHWNQSVLNLTLNVRKMFCEMDEALFMSCHARFKEDEA
Hs_PPP2R5C    434 ---------------------KTHWNKTIHGLIYNALKLFMEMNQKLFDDCTQQFKAEKL
Dr_gppp2r5cb  432 ---------------------KTHWNKTIHGLIYNALKLFMEMNQKLFDDCTQQFRAEKN
Hs_Bdelta     455 ---------------------KSHWNKTIHGLIYNALKLFMEMNQKLFDDCTQQYKAEKQ
Sc_RTS1       634 -TANGEDSISDPYMLVEQAINSGSWNRAIHAMAFKALKIFLETNPVLYENCNALYLSSVK
Kl            582 LSLEDGDNGEDPYLMVEQAINSGSWNRAIHAMAFKALKIFLETNNVLYENCNALYISSLK
Eg            542 QTDEEGNPNQDPYMLVEQAINSGSWNRAIHAMAFKALKIFLETNPVLYENCNSLYLSSLK
Sp_par1       458 ---------------------KSHWNRVIHSMVCNVLKLFMDINPSLFDEVDAEYSESRR
Mo            544 ---------------------KGHWNRTIHGMVYNAMKLFMEINPQLFDDCSHEYTEQQN
Nc            506 ---------------------KGHWNRTIHGMVYNAMKLFMEINPQLFDDCSHEYTENQS
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At_Btheta     465 KEAEIGAKREATWKRLEEIGN---------------------------------------
Al            468 KEAEIDAKRESTWKRLEEIGN---------------------------------------
Cr            468 KEAEIGAKREATWKRLEEIGN---------------------------------------
Es            470 KEAEVEAKREATWKRLEEIGM---------------------------------------
At_Beta       486 KAAETEAKREATWKRLEELGV---------------------------------------
Csi           482 KEGEIEARREATWKRLEELAEGNV------------------------------PINKLV
Pv            477 KESEVKAGREATWKRLEELAMKKA------------------------------ASGEAV
Cs            483 KENELKARREATWNRLEELAAKKA------------------------------ASNEAV
Sl            463 KEDEIKSKREATWKRLEELAAKNT------------------------------TSNEAV
Vv            483 KEDEIKAKREAAWKLLEEMAAKRV------------------------------ASNEAV
Os            475 KEKETKLKQEVAWKRLEEMASAKA------------------------------TSGAAV
Zm            469 KQAESDSKRDAMWKRLEEMGASKP------------------------------GGNHPL
Gm            484 QEKDMKSKREARWKRLEEMGGMKA------------------------------TTNEAV
Cmsm          482 QEKDMKSKREAKWKRLEEIAARKA------------------------------ASIEAV
At_Bzeta      495 NKTEVKAKRERTWQRLEDLATSKTV-----------------------------VTNEAV
At_Bgamma     474 NETEVVAKREATWKLLEELAASKS------------------------------VSNEAV
At_Bdelta     453 KAEDTKKKNGETWRQLEEIVASMAK-----------------------------------
Smo           427 KSKGIEEKREITWKRLEAAAATKA------------------------------VSSEAV
At_Balpha     464 KSKQVEEQRQNRWRRLDEAVEERE------------------------------------
At_Bbeta      464 KSKEVEEQRQYTWKRLAEAAAERDG-----------------------------------
At_Bepsilon   473 KACELLEQRELTWKRLEEAASLAAN-----------------------------------
Pp            469 KAKGVGEMRDLTWKRLEIAGNPRSNVGS----------------------QHTFASSHDV
M_RCC299      394 RSQETEENRKQRWKQVEALAAKSI------------------------------------
Vcfn          461 SERQAMENRDRKWEYLQKLALQKS------------------------------------
Cre           462 SERAAMETRDRKWEYLQKLAVQKS------------------------------------
At_Bkapa      459 KQCSAAEKRKEVWARLENAASMKP-----------------------------ITGKTAV
Hs_PPP2R5C    473 KEKLKMKEREEAWVKIENLAKANP------------------------------------
Dr_gppp2r5cb  471 KEKAKWKEREEAWIKIENLAKSNPQFLMYIDANSLCSPMDMETDGPMLEDVLMLKKTVEE
Hs_Bdelta     494 KGRFRMKEREEMWQKIEELARLNPQYPMFRAPPPLPPVYSMETETPTAEDIQLLKRTVET
Sc_RTS1       693 ETQQRKVQREENWSKLEEYVKNLRINN---------------------------DKDQYT
Kl            642 ENNRRQKEREMNWKQLEDYVSKLKIAE---------------------------S-----
Eg            602 ESQKRREKREENWNKLQEYVRNLHISS---------------------------VDNPVA
Sp_par1       497 KKEDEEIIREERWTILENIAKEN------------------------------AMKLKSQ
Mo            583 SAAAREAMRERKWAAIAEQANKRKANG--------------------SGEPSGPPTRLTQ
Nc            545 NAPAREAHRQSKWARLEELAKQRKVESG------------------TSNGTSSIPARTTV


At_Btheta     486 ---QKQKSSL----------------------------------------
Al            489 ---QKQKSSL----------------------------------------
Cr            489 ---QKQKSSL----------------------------------------
Es            491 ---QKQKSSS----------------------------------------
At_Beta       507 ---RKAS-------------------------------------------
Csi           512 PVPQKVQPSPSSG-------------------------------------
Pv            507 LIGNKAPTRPSAG-------------------------------------
Cs            513 LVSHKLPTRTASV-------------------------------------
Sl            493 LVPSTGHSRT----------------------------------------
Vv            513 LVP-----------------------------------------------
Os            505 LVSRTLPRQSSAV-------------------------------------
Zm            499 GAPNGKPSHAAG--------------------------------------
Gm            514 LVSPRTASHTPSGKASRAQLE-----------------------------
Cmsm          512 LVAPKVALRAPSG-------------------------------------
At_Bzeta      526 LVPRFVSSVNLTTSSSESTGS-----------------------------
At_Bgamma     504 LVPRFSSSVTLATG--KTSGS-----------------------------
At_Bdelta         --------------------------------------------------
Smo           457 LVMGMAPSFNQQRTMVGV--------------------------------
At_Balpha     488 ---REDPMITS---------------------------------------
At_Bbeta      489 GGGEEDHMITS---------------------------------------
At_Bepsilon       --------------------------------------------------
Pp            507 PNSTTVPKNAAAGTRASVAA------------------------------
M_RCC299      418 -AS-----------------------------------------------
Vcfn          485 -NGRPLPEVKPLSALLRV--------------------------------
Cre           486 -NGRPLPEVKPLSALLRV--------------------------------
At_Bkapa      490 LVTPRATSIAC---------------------------------------
Hs_PPP2R5C    497 ---QAQKDPKKDRPLARRKSELPQDPHTKKALEAHCRADELA-SQDGR--
Dr_gppp2r5cb  531 EATPLHREQRKERPLMRRKSELPQDTSTVKALETHRRAEDMIGTQDGH--
Hs_Bdelta     554 EAVQMLKDIKKEKVLLRRKSELPQDVYTIKALEAHKRAEEFLTASQEAL-
Sc_RTS1       726 IKNPELRNSFNTASENNTLNEENENDCDSEIQ------------------
Kl                --------------------------------------------------
Eg            635 VDRIGTGDLH----------------------------------------
Sp_par1       527 NPTT----VHSTTERLKKLS-LDYTNG-----------------------
Mo            623 NPMPRLDEVDHSDDNQKRLDSLKLQDGERR--RPGMHDRQNSVGSNRSQR
Nc            587 HPLPRLEEVDGTEDNQKRLDSLKLQDGDRRERRPGMHERQSSVGSSRSR-
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Supplemental Figure S7. PP2A B’θ homolog sequences alignment. Sequences of full-length protein homologs were identified by BLAST, aligned by ClustalW/MEGA6 (Tamura et al., 2013), and conserved residues were shaded by BoxShade (http://www.ch.embnet.org/software/BOX_form.html). For phylogenetic analysis and PTS1 conservation, see also Figure 5. The species abbreviations are as follows: At, *Arabidopsis thaliana*; Al, *Arabidopsis lyrata*; Cr, *Capsella rubella*; Es , *Eutrema salsugineum*; Csi, *Citrus sinensis*; Pv , *Phaseolus vulgaris*; Cs , *Cucumis sativus*; Sl, *Solanum lycopersicum*; Vv , *Vitis vinifera*; Os , *Oryza sativa*; Zm, *Zea mays*; Gm, *Glycine Max*; Cmsm, *Cucumis melo subsp. melo*; Smo , *Selaginella moellendorffii*; Pp , *Physcomitrella patens*; M. RCC299, *Micromonas.sp.RCC299*;Vcfn , *Volvox carteri f. nagariensis*; cre, *Chlamydomonas reinhardtii*; Hs , *Homo sapiens*; Dr , *Danio rerio*; Sc, *Saccharomyces cerevisiae*; Kl , *Kluyveromyces lactis*; Eg, *Eremothecium gossypii*; Sp, *Schizosaccharomyces pombe*; Mo, *Magnaporthe oryzae*; Nc, *Neurospora crassa*.

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