A Chlamydomonas reinhardtii



С

Chara braunii



D



CTN domain GOLD domain WHIM1 domain
Sec14 domain GDAP domain WHIM2 domain
PHD domain DTT domain

Supplemental Figure 1. Phylogenetic analysis and modular structure of the SEC14L-PITP superfamilies in green algae and liver moss.

Left, Phylogenetic trees, generated with full-length amino acid sequences. Right, modular structures of SEC14L-PITPs. (A) *Chlamydomonas reinhardtii*; (B) *Volvox carteri*; (C) *Chara braunii*; (D) *Marchantia polymorha*. Different domains are represented in different color, as indicated. Protein primary structure and relative length of domains are drawn to scale.



В

Solanum lycopersicum



Supplemental Figure 2. Phylogenetic analysis and modular structure of the SEC14L-PITP superfamilies in a lycophyte and eudicot tomato.

Left, Phylogenetic tree, generated with full-length amino acid sequences. Right, modular structures of SEC14L-PITPs. (A) *Selaginella moellendorffii*; (B) *Solanum lycopersicum*. Different domains are represented in different color, as indicated. Protein primary structure and relative length of domains are drawn to scale.

Zea mays



Supplemental Figure 3. Phylogenetic analysis and modular structure of the SEC14L-PITP superfamily in monocot maize (*Zea mays*).

Left, Phylogenetic tree, generated with full-length amino acid sequences. Right, modular structures of SEC14L-PITPs. Different domains are represented in different color, as indicated. Protein primary structure and relative length of domains are drawn to scale.

2+D277.4	VTAEVKVEEKOVESEVVIADAVVDEETVVEED			
ACFAID4 A+DATT.1	MAGEEVOKSA DUA A A DUU-KEKDTEDKEVET DEDVA EKEEVA A DUSDEKAUDEKEVEDEK			
ACPAILI ADDAULO				
AUPATEZ	MAQEEIQAPTASVPVVAEETPAPVAEVEVPVTTEAAVAAPAPEATEEAVVSEVAVPET			
At PATL6				
AtPATL3	MAEEPTTTLVTPEKLPSP			
AtPATL5	MSQDSATTTPPPPLTSDVSMPSGEEDEPKHVTSEEEAPVTSETNLKLPLMPELEES			
AtPATL4	ESKPEGVEKSASFKEESDFFADLKESEKKALSDLKSKLEEAIVDNTLLK-			
AtPATL1	EAPAAEAEKSVSVKEEETVVVAEKVVVLTAEEVQKKALEEFKELVREALNKREFTA-			
AtPATL2	EVTAVKEEEVATGKEI-LQSESFKEEGYLASELQEAEKNALAELKELVREALNKREFTAP			
AtPATL6				
a+pamt.3				
ACPAIDS A+DATIS	NUTA FUNCERUTETMENT FORCT NUAA FORCOTURUTETTAKI FUI NUTAFORCOTU			
ACFAIDS	WHIRE VISENVIPEINIDESEGUNNAREDSEQINE VIPEIEIRNDE VUNNIREDSEQIN-			
A + DAME 4				
ACPATL4	TINKESSPMKERREEVVRPEAEVENREEAAEENVEEERSEAVV			
AtPATL1	PVTPVKEEKTEEKRTEEETKEEEKKEETTTEVKVEEEKPAVP			
AtPATL2	PPPPAPVKEEKVEEKKTEETEEKKEEVKTEEKSLEAETKEEEKSAAPATVETKK			
AtPATL6	MDASLSPFDHQKTQNTEPKKSFI			
AtPATL3	PPETADTTTKPEEETAAEHHPPTVTETETASTEKQEVKDEASQKEV			
AtPATL5	EVTPEKETVKSEFLNHVAEDSEQTHEVTPETETVKSEVLNHAAEDSEQPRGVTPTPET			
AtPATL4	TEEAPKAETVE			
AtPATL1	AAEEEKSSEAA			
a+pamr.2	FFT.33D3TU3F7KKFF7U013D3D0VF7KD32DVU3F7KKFFTT.D33DV77F7KVFFK VV			
A+ DATT.6				
A+DAMI 2				
ACPALLS				
ATPATL5	ETSEADTSLLVTSETEEPNHAAEDISETEPSQKLMLEQRRKYMEVEDWTEPELPDEAVLE			
3+D3m7 4	ANTERTID			
ACPAILS	DUDDYCDDY			
AUPATLI	FVLINSEEN			
AtPATL2	PVETTPAAPVTTETKEEEKAAPVTTETKEEEKAAPGETKKEEKATASTQVKRASKFIKDI			
AtPATL6				
AtPATL3				
AtPATL5	AAASVPEPKOPEPQTPPPPSTTTSTVASR			
a+ pamr.4	ĸ₽₽₩₩₩₩₩₩₩₩₽₽₩₩₽₽₽₩₩₽₽₽₩₩₩₽₽₩₩₩₽₩₩₽₩₩₽₩₽₩			
a+pamr.1				
ACPAILI ADDAME O				
At PATL2	FVSVTTSEKKKEEERPAVVTIEKAFAADQEEETKTVEAVEESIVSITLPETAAY-			
AtPATL6	LSA			
AtPATL3	AEEKKSMIPONLGSFKEESSKLSDLSNSEKKSLDELKHLVRE			
AtPATL5	SLAEMMNREEAEVEEKQKIQIPRSLGSFKEETNKISDLSETELNALQELRHLLQV			
	:*: : . :			
AtPATL4	SVDKDIELWGVPLLPSKGAESTDVILLKFLRARDFKVNEAFEMLKKTLKWRK			
AtPATL1	VAVAEAEPVEPEEVSIWCVPLLODERSDVILTKFLRARDFKVKEALTMLKNTVOWRK			
AtPATL2	VEPEEVSIWGIHLEDERSDVILLKFLRARDFKVKEAFTMLKNTVQWRK			
AtPATL6	SSSKASSMWGVSLLGGDDKADVILLKFLRARDFKVADSLRMLEKCLEWRE			
At PATT.3	ALDNHOFTNTDFFVKTWGTDLLFDDRSDVVLKFLRARFFKVKDSFAMLKNTTKWRK			
At DATT.5	SODSSKTSTWCVDLLKDDRTDVVLLKFLRARDFKDOFAYSMLNKTLOWRT			
11011111100				
AtPATL4	QNKIDSIIGEEFG-EDLA-TAAYMNGVDRESHPVCYNVHSEELYQ-TIGSEKNREK			
AtPATL1	ENKIDELVESGEEVSEFE-KMVFAHGVDKEGHVVIYSSYGEFQNKELFSDKEKLNK			
AtPATL2	ENKIDDLVSEPLEGSEFE-KLVFTHGVDKQGHVVIYSSYGEFQNKEIFSDKEKLSK			
AtPATL6	EFK <mark>#</mark> EKLTEEDLGFKDLEGKVAYMRGYDKEGHPVCYNAYGVFKEKEMYERVFGDEEKLNK			
AtPATL3	EFKIDELVEEDLV-DDLD-KVVFMHGHDREGHPVCYNVYGEFQNKELYNKTFSDEEKRKH			
AtPATL5	DFNIEELIDENLG-DDLD-KVVFMQGQDKENHPVCYNVYGEFQNKDLYQKTFSDEEKRER			
At PATT 4	FT.RWR FOLMEKGTOKINIK-PGGVTSLIOTHDLKNA PGVSRTFTWVGTKKVT PT.ODMVR			
A+PATT.1	FLSWRTQLOFKCVRATDESNPEAKSSEVEVSDERNAPGLGKRALWOFTRRAVKOFEDNYP			
5+ P5T.2	FLEWRIGEOFECURST. DES - DES KSS FURUSDEDNIN DCL.CODALMORTEDATE OF FORMULA			
AUFAILLZ	FINENTIC CENCERTRE - DOCUMENT OUR TANKS			
ACCALDO	T DUDTORT RDSTDET DES-SCCOOMTRONODCT CARRY DOMESTIC STRUCTURES COMPANY			
ACCALDO	TERMINIQUEROINNEDE OGVOTICONNERVOPOLOKKELKSATKQAVELLQDNYP			
ACPATL5	FLEWRIGTERSIENLDFV-AGGVSTICQVNDLENSPGPGETELELATEQALHLLQDNYP			
AtPATL4	EFVSKNIFINVPFWFYAMKAVLSPFLT-QRTKSKFVVARPAKVRETLLKYIPADELPVQY			
ATPATL1	EFAAKELFINVPWWYIPYYKTFGSIITSPRTRSKMVLAGPSKSADTIFKYIAPEQVPVKY			
AtPATL2	EFVAKELFINVPWWYIPYYKTFGSIITSPRTRSKMVLSGPSKSAETIFKYVAPEVVPVKY			
AtPATL6	ELVATKIFINVPWYFSVIYSMFSPFLT-QRTKSKFVMSKEGNAAETLYKFIR‡EDIPVQY —			
AtPATL3	EFVFKQAFINVPWWYLVFYTVIGPFMT-PRSKSKLVFAGPSR <mark>A</mark> ETLFKYISPEQVPVQY			
AtPATL5	EFVSKQIFINVPWWYLAFYRIISPFMS-QRSKSKLVFAGPSRSAETLLKYISPEHVPVQY			
	w			
AtPATL4	GGFKTVDDTEFS-NETVSEVVVKPGSSETIEIPAPETEGTLVWDIAVLGWEVNYKEE			
AtPATL1	GGLSKDTPLT-EETITEAIVKPAANYTIELP-ASEACTLSWELRVLGADVSYGAQ			
AtPATL2	GGLSKDSPFT <mark>V</mark> EDGVTEAVVKSTSKYTIDLP-ATEGSTLSWELRVLGADVSYGAQ			
AtPATL6	GGLSRPTDSQNGPPKPASEFSIKGGEKVNIQIEGIEGGATITWDIVVGGWDLEYSAE			
AtPATL3	GGLSVDPCDCNPDFSLEDSASEITVKPGTKQTVEII-IYEKCELVWEIRVTGWEVSYKAE			
AtPATL5	GGLSVDNCECNSDFTHDDIATEITVKPTTKQTVEII-VYEKCTIVWEIRVVGWEVSYGAE			
	**:			
AtPATL4	FVPTEEGAYTVIVOKVKKMGANEGPI-RNSFKNSOAGKIVI. TVDNVSGKKKKKVI VDVDT			
2+P277.1	FEDDURESSY AVIAS AND			
A-DAMT 2	EEDSNEYSAMAAASUDKACTUDEDALIDEEAJAEYSESTAALIDIOMEKKKKAT			
AUPATLZ A+DAPT C	FEFONEROITVIVONNENVGITUEFVITUOFEASEAGEVVITTUNQTFEEKKEVL-YRSET			
AUPATLO	EVENALLOIALVVLAPAAMAATDEAV-CNSFTTVEAGKLILSVDNTLSRKKKVAAYRYTV			
ATPATL3	FVFEEKDAYTVVIQKPRKMRPSDEPVLTHSFKVNELGKVLLTVDNPTSKKKKLV-YRFNV			
AtPATL5	FVPENKEGYTVIIQKPRKMTAKNELVVSHSFKVGEVGRILLTVDNPTSTKKMLI-YRFKV			
	ww			
AtPATL4	KTESSS-			
AtPATL1	Q			
AtPATL2	QA			
AtPATL6	RKSTTTV			
AtPATL3	KPL			
AtPATL5	KPLACE-			

Supplemental Figure 4. Alignment of Arabidopsis PATL protein sequences. The start of different domains is indicated by a box, in blue, CTN, in red, SEC14, in yellow, GOLD domain. The colors of amino acid letters represent red, hydrophobic; green, polar uncharged; pink, basic; blue, acidic amino acids.

AT1G22530 TAP3 TAP1 TAP2	MAQEEIQKPTASVPVVKEETPAPVKEVEVPVTTEKAVAAPAPEATEEKVVSEVAVPETEV			
AT1G22530 TAP3 TAP1 TAP2	TAVKEEEVATGKEILQSESFKEEGYLASELQEAEKNALAELKELVREALNKREFTAPPPP			
AT1G22530 TAP3 TAP1 TAP2	PAPVKEEKVEEKKTEETEEKKEEVKTEEKSLEAETKEEEKSAAPATVETKKEEILAAPAP	180 0 0 0		
AT1G22530 TAP3 TAP1 TAP2	IVAETKKEETPVAPAPVETKPAAPVVAETKKEEILPAAPVTTETKVEEKVVPVETTPAAP	240 0 0 0		
AT1G22530 TAP3 TAP1 TAP2	VTTETKEEEKAAPVTTETKEEEKAAPGETKKEEKATASTQVKRASKFIKDIFVSVTTSEK	300 0 0 0		
AT1G22530 TAP3 TAP1 TAP2	KKEEEKPAVVTIEKAFAADQEEETKTVEAVEESIVSITLPETAAYVEPEEVSIWGIPLLE MSSR-VGDLSPQQQBALARFRENLQDLLPIL MSGR-VGDLSPRQKEALAKFRENVQDVLPAL	360 30 30 0		
AT1G22530 TAP3 TAP1 TAP2	DERSDVILLKFLRARDFKVKEAFTMLKNTVQWRKENKIDDLVSEDLEGSE-FEKLVFTHG PNADDYFLLRWLRARNFDLQKSEDMLRRHMEFRKQQDLDNIVTWQPPEVIQLYDSGGLCG PNPDDYFLLRWLRARSFDLQKSEAMLRKHVEFRKQKDIDNIISWQPPEVIQQYLSGGMCG 	419 90 90 31		
AT1G22530 TAP3 TAP1 TAP2	VDKQGHVVIYSSYGEFQNKEIFSDKEKLSKFLKWRIQFQEKCVRSLDFSPE-AKSSFVFV YDYEGCPVYFNIIGSLDPKGLLLSASKQD-MIRKRIKVCELLLHECELQTQKLGRKIEMA YDLDGCPVWYDIIGPLDAKGLLFSASKQD-LLRTKMRECELLLQECAHQTTKLGRKVETI YDRDGCPVWYDIIGPLDPKGLLFSVTKQD-LLKTKMRDCERILHECDLQTERLGKKIETI * :* * : * : * : * : : * :: * :: *	478 149 149 90		
AT1G22530 TAP3 TAP1 TAP2	SDFRNAPGLGQRALWQFIKRAVKQFEDNYPEFVAKELFINVPWWYIPYYKTFGSII LMVFDMEGLSLKHLWKPAVEVYQQFFSILEANYPETLKNLIVIRAPKLFPVAFNLVKSFM TIIYDCEGLGLKHLWKPAVEAYGEFLCMFEENYPETLKRLFVVKAPKLFPVAYNLIKPFL VMIFDCEGLGLKHFWKPLVEVYQEFFGLLEENYPETLKFMLIVKATKLFPVGYNLMKPFL : ** ::*: :* :**	534 209 209 150		
AT1G22530 TAP3 TAP1 TAP2	TSPRTRSKMVLSGPSKSAETIFKYVAPEVVPVKYGGLSKDSPFTV SEE-TRRKIVILGD-NWKQELTKFISPDQLPVEFGGTMTDPDGNPKCLTKINYGGEVPKS SED-TRKKIMVLGA-NWKEVLLKHISPDQVPVEYGGTMTDPDGNPKCKSKINYGGDIPRK SED-TRRKIIVLGN-NWKEGLLKLISPEELPAQFGGTLTDPDGNPKCLTKINYGGEIPKS : ** *::: * : : * :: * :: * :: * :: *	579 267 267 208		
AT1G22530 TAP3 TAP1 TAP2	EDGVTEAVVKSTSKYTIDLPATEGSTLSWELRVLGADVSYGAQFEPSNEAS YYLCEQVRLQYEHTRSVGRGSSLQVENEILFPGCVLRWQFASDGGDIGFGVFLKTKMGEQ YYVRDQVKQQYEHSVQISRGSSHQVEYEILFPGCVLRWQFMSDGADVGFGIFLKTKMGER MYVRDQVKTQYEHSVQINRGSSHQVEYEILFPGCVLRWQFSSDGADIGFGVFLKTKMGER * * * * * * * * * * * * * * * *	630 327 327 268		
AT1G22530 TAP3 TAP1 TAP2	YTVIVSKNR-KVGLTDEPVITDSFKASEAGKVVITIDNQTFKKKKVLYRSKTQ QSAREMTEVLPSQRYNAHMVPEDGSLTCLQAGVYVLRFDNTYSRMHAKKLSYTVEVL QRAGEMTEVLPNQRYNSHLVPEDGTLTCSDPGIYVLRFDNTYSFIHAKKVNFTVEVL QRAGEMTDVLPSQRYNAHMVPEDGNLTCSEAGVYVLRFDNTYSFVHAKKVSFTVEVL * :: :* : : : : : * *: : : * *: : **	682 384 384 325		
AT1G22530 TAP3 TAP1 TAP2	A 683 LPDKASEETLQSLKAMRPSPTQ 406 LPDKASEEKMKQLGAGTPK 403 LPDEGMQKYDKELTPV 341			

Supplemental Figure 5. Alignment of AtPATL2 with human TAP protein sequences.

The start of the CTN-SEC14-GOLD region is indicated by an arrow. The colors of amino acid letters represented, hydrophobic; green, polar uncharged; pink, basic; blue, acidic amino acids.

Α

Lysophosphatidic Acid (LPA) Lysophosphocoline (LPC) Phosphatidylinositol (PI) Phosphatidylinositol-3-phosphate (PI(3)P) Phosphatidylinositol-4-phosphate (PI(4)P) Phosphatidylinositol-5-phosphate (PI(5)P) Phosphatidylethanolamine (PE) Phosphatidylcholin (PC)

Sphingosine-1-phosphate

Phosphatidylinositol-3,4-bisphosphat (PI(3,4)P₂)

Phosphatidylinositol-3,5-bisphosphat (PI(3,5)P₂)

Phosphatidylinositol-4,5-bisphosphat (PI(4,5)P₂)

Phosphatidylinositol (3,4,5)-trisphosphate (PI(3,4,5)P₃)

Phosphatidic acid (PA)

Phosphatidylserine (PS)

blank



Supplemental Figure 6. Protein-phosphoinositide overlay assay and electrophoretic migration behavior of StrepII-PATL2 and deletion mutants.

(A, B) StrepII-PATL2 and deletion mutant protein–phospholipid overlay assay. PIP binding is quantified in (B). (C) Electrophoretic migration behavior of StrepII-PATL2 and deletion mutant proteins, analyzed by in SDS-PAGE, followed by Coumassie staining. StrepII-PATL2 and deletion mutant protein bands are indicated by an asterisk. The theoretical masses of StrepII-PATL2 and deletion mutants are indicated below. In the presence of the N-terminal domain, migration of proteins is drastically retarded, presumably due to the acidic character of the N-terminal part, as reported before (Peterman et al., 2004; Armstrong and Roman, 1993).

AGI number	Name	description				
The genes in <i>PATL1-4</i> coexpression module						
At1g72150	PATL1	PATELLIN1				
At1g22530	PATL2	PATELLIN2				
At1g72160	PATL3	PATELLIN3				
At2g17550	TRM26	TON1 RECRUITING MOTIF 26				
At1g61100		disease resistance protein				
At5g40450	RBB1	REGULATOR OF BULB BIOGENESIS1				
At4g33740		MYB-like transcriptoion factor				
At3g27960	KLCR2	KINESIN LIGHT CHAIN-RELATED 2				
At2g01910	MAP65-6	Microtubule-associated protein				
At1g14380	IQD28	IQ-DOMAIN 28				
At4g16563		aspartyl protease				
At2g30930		hypothetical protein				
At4g20260	PCAP1	PLASMA-MEMBRANE ASSOCIATED CATION-BINDING PROTEIN 1				
At2g48030		DNAse-I-like				
At2g36410	DUF662	transcriptional activator				
At1g64390	GH9C2	GLYCOSYL HYDROLASE 9C2				
At1g53730	SRF6	STRUBBELIG RECEPTOR FAMILY6				
At1g30690	PATL4	PATELLIN4				
At3g12110	ACT11	ACTIN11				
At1g03870	FLA9	FASCICLIN-LIKE ARABINOOGALACTAN 9				
At5g16590	LRR1	LEUCINE RICH REPEAT PROTEIN 1				
At1g67750		Pectate lyase				
At4g12730	FLA2	FASCICLIN-LIKE ARABINOGALACTAN 2				
At4g22010	SKS4	SKU5 SIMILAR4				
At1g04680		Pectin lyase-like				
At3g54400		Aspartyl protease				
At5g15350	ENODL17	EARLY NODULIN-LIKE PROTEIN 17				
At4g12420	SKU5	protein of unknown function involved in directed root tip growth				
The genes in PATL6 coexpression module						
At1g27190	BIR3	BAK1-INTERACTING RECEPTOR-LIKE KINASE 3				
At1g70940	PIN3	PIN-FORMED 3				
At2g38120	WAV5 (AUX1)	AUXIN RESISTANT 1				
At3g05100	transferase	SAM methyl transferase				
At1g75500	WAT1	WALLS ARE THIN 1 transporter				
At4g12110	SMO1-1	STEROL-4ALPHA-METHYL OXIDASE 1-1				
At3g51670	PATL6	PATELLING				

Supplemental Table S1. List of genes in coexpression modules

PATL2 deletion mutant	AA position	Predicted molecular weight (kDa)	predicted molecular weight stepII-tagged (kDa)	Molecular running weight stepll- tagged (kDa)
PATL2	1-683	76	79	~ 170
PATL2ΔN	358-683	38	41	~ 40
ΡΑΤL2ΔCTΝ	1-357; 403-683	71	74	~ 170
PATL2DSEC14	1-402; 577-684	56	59	~ 160
PATL2ACTN-SEC14	1-357; 577-685	50	53	~ 160
PATL2AGOLD	1-579	65	68	~ 120
ΡΑΤL2ΔC	1-357	37	40	~ 160

Supplemental Table S2. Information on the generation of PATL2 deletion mutants.

Supplemental Table S3. Primers used in this study.

••	•
Primer	Sequence (5'-3')
PATL2B1F_N	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTATGGCTCAAGAAGAGATACAG
PATL2B2stopR	GGGGACCACTTTGTACAAGAAAGCTGGGTTTATGCTTGGGTTTTGGACC
PATL2∆GOLDstopB2	GGGGACCACTTTGTACAAGAAAGCTGGGTTTAAACGGTGAATGGAC
PATL2∆SEC14_F	ATCGACGACCTAGTCTTCACCGTTGAAGAT
PATL2∆SEC14_R	ATCTTCAACGGTGAAGACTAGGTCGTCGAT
PATL2∆CTN-SEC14_F	ATCTGGGGAATCCCATTCACCGTTGAAGAT
PATL2∆CTN-SEC14_R	ATCTTCAACGGTGAATGGGATTCCCCAGAT
PATL2ΔCTN_F	CAATCTGGGGAATCCCATCAGAAGATCTTGA
PATL2ΔCTN_R	TCAAGATCTTCTGATGGGATTCCCCAGATTG
PATL2∆CstopB2	GGGGACCACTTTGTACAAGAAAGCTGGGTTTATGGGATTCCCCAGATTGAGAC
PATL2ΔNB1_N	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTCTTCTAGAGGACGAAAGATCC
PATL2_F_BamHI	AGGAGTGGATCC T ATGGCTCAAGAAGAGATACAG
PATL2_R_NotI	AGGAGTGCGGCCGC TTA TGCTTGGGTTTTGGACC
PATL2∆GOLD_R_NotI	AGGAGTGCGGCCGC TTA AACGGTGAATGGACTATC
PATL2∆N_F_BamHI	AGGAGTGGATCC T CTTCTAGAGGACGAAAGATCC
PATL2∆C_R_NotI	AGGAGTGCGGCCGC TTA TGGGATTCCCCAGATTG