## Figure S11

В

Α		tm1	tm2
At-ABCI12	:ATVDGDGKTGNWVNRLPIPGLGAENVFRLISSATGSPIGQFISSPV	TFLHSVDPRIKLVWLLTLVVLPARANI	VVRLGLVLCTALLSILVLP- : 92
Os-ABCI8	: AASDPSKAAGKGEAGDAVARWAAWIPRAAVGGAGPEQVLRLISGAAATPICQFVDSPF	RTFLHAIDPRVKLVWLLALVVLPARSNI	YLRFGLVAYLTLLSMWVLP- : 104
Pp-ABCI12	:CETQKNEDENVTRARGDQLRSWILNSARKRQESLGERIMRMVAGASSAPIAQYIPFPV	/T <mark>P</mark> LH <mark>T</mark> LDPRVKQAWLLALVVLPARSHN	AIRISMVAFLAVATMCTLP- : 104
Cr-ABCI12	:AAAAASAGGGPGKDGAKPQKTPMQQQILNGVLGISNVPYSSFVPSPV	/TFLHRID <mark>A</mark> RIK <mark>Q</mark> VWLVAL <mark>Y</mark> LM <mark>IAR</mark> ASI	PAIRLAISGSVALVTMANFP- : 93
Syn-ABCI12	:MDLMRSLPIGLYLENPV	/TWLHRLDPRVKLAWLMSFLLAPVLANA	AIWRLGIVIFLILLTFAVRIP : 64

tm3	J	tm4 ch1
At-ABCI12 :RQVWIDQLARVSLLSGILFITLG	GSDGAPPMLQSRTPPSSITSLPNLPMSLSGYSYMLLKLGPLQFTRK	CLSVGSTAACLTFIIFQSASICLA <mark>TI</mark> TPEQLALAL : 197
Os-ABCI8 :NHIWKDQLGRVALLSGIIFIMLG	GSDGAPSLVQTRTPPPSVIGLPNIPTSTNGYSYTIMKLGPLQFTRK	(GLSVASTSACLSFAIFQSASLCLT <mark>IT</mark> PEQLASAL : 209
Pp-ABCI12 :RRIWCDQLGRMAALSGFLFVMLA	GTDGVAPVMQSR <mark>R</mark> PLIASQGLPKLPAALSGYKYVLLKLGPFQLTRK	(GVSLAAAASCLSFTVLQSASLCLT <mark>TTT</mark> PEQLAAAL : 209
Cr-ABCI12 :ERLWCSQLRRLALLCGFIFMTTL	LADSVPPLLQTRAPPLLLESLPAIPATGYQYVLLHVGPITVTHR	R <mark>S</mark> INLAITASSLTFSALQTASLCLV <mark>TT</mark> PGEEMAVAL : 196
Syn-ABCI12 :WRVWKQQMGLLVFFSGLIFLLTT	SPDGFTVLEQPRSPTSEIVVSPTSYQYVLFEWGRLIVTRR	SLEIGIRISTLIFTLVYSTNLYLLITAPEEITAGL : 163

	ch2	x R x	ch3xRx	
At-ABCI12 : RWELF-BLTY	IGVPVSFIILTLLISLRFINLVFDEVRSVSL	GTVSRBVNWOOT.TVLETTDTFASE		GESSSHKTYFFSGSSNK : 303
Os-ABCI8 : WWFMI-PIKH		~~	VRRIFKNIFDHAEOISKAMIARGFR	
Pp-ABCI12 : RWYLA-PFAR	LG <mark>A</mark> PV <mark>E</mark> FLILTLLLSL <b>RFIG</b> IVFDEVRNLAV	GVVARSIEWKSLRLLETADIFFNL	IGRIFKNLFLHADQISQAMVARGYR	GNPVKHRIYFLTKLSIK : 315
Cr-ABCI12 : RWWLA-PLRW	LRVPVEEVAMTLLLSLREMSLVFEEIRNLSL	GLAARGINWEAQGGAGSINMAGRI	CVRLFGNLFQRSEN <mark>I</mark> AQAMLVRGFQ	GPADHHLYQMKVNPTSY : 302
Syn-ABCI12 : EELMA-PLRR	FKLPITEITIIIT <mark>I</mark> AL <u>RET</u> PI <mark>V</mark> MEEIQNLFR	RSIRT <mark>R</mark> AINWKKLGIKRSAQIWILV	VERLLENLLLRAEQMAIAMEVRGFT	T-PNEHQVQ-WHQLRIV : 267

		tm5
At-ABCI12	:	FADFASVLCLIGVISTALLSEYFLV : 328
Os-ABCI8	:	IVDVFSLLCLFALVALASISDKLV : 339
Pp-ABCI12	:	FQDWIAISGLLILTAFSMYLEITLPA- : 341
Cr-ABCI12	:	FANVCALALLIAYSVLIYYFK : 323
Syn-ABCI12	:	RADWLVIGTLILFWGARILNGGMA : 291

	At	Os	Рр	Cr	Syn	
At-ABCI12	100%					
Os-ABCI8	59%	100%				
Pp-ABCI12	46%	48%	100%			
Cr-ABCI12	36%	35%	36%	100%		
Syn-ABCI12	28%	29%	28%	30%	100%	

FIGURE S11 | ABCI12 is conserved among plants and cyanobacteria.

(A) Amino acid sequence alignment of ABCI12 relatives. Different organisms, gene numbers and NCBI Reference Sequences of GenPept entries are given in brackets. Please note that for all plant proteins the predicted mature sequences according to ChloroP (Emanuelsson et al., 1999) are depicted. At-ABCI12 (*Arabidopsis thaliana*, At3g21580, NP\_566688), Os-ABCI8 (*Oryza sativa [japonica]*, Os05g33230, XP\_015639696), Pp-ABCI12 (*Physocomitrella patens*, XP\_024398704), Cr-ABCI12 (*Chlamydomonas reinhardtii*, PNW75614), Syn-CBY (*Synechocystis PCC6803*, gene slr1978, WP\_010872838). The transmembrane helices tm1-5 (blue boxes) and the coupling helices ch1-3 (green boxes) are depicted according to the structural model of At-ABCI12 (Phyre2; Kelley et al., 2015) The two conserved X-R-X motifs at the end of ch2 and ch3, which most likely are responsible for binding to the ATPase AA dimer (compare Figures 1, S10) are indicated by orange arrow heads. The peptide stretch between tm3 and tm4, which is specific for plant and cyanobacterial T proteins (compare Figure S10; Eitinger et al., 2011) is highlighted by a green line.
(B) Amino acid identities in % of proteins depicted in (A).