

Figure S1

A

```

At-ABCI10 : -----VSTRQGISVPIIRDSCFRIPSGQLWMLIGPNGCGKSTLLKILAGVVPNSSG-----TVEVE-----KEKNEVFQ : 64
Os-ABCI6 : -----LASSLPPTAIEGQGVLSVITRRGRVLPVLKDCSLRVPPGQLWMLIGPNGCGKSTLLKVLAGFLNPSSG-----TVYIN-----RECSYVFQ : 82
Pp-ABCI10 : AASVRNESETAPNSVAIDARDLGLTVTGDKGEDVVVLKGCSSMOIPEGQLWMLIGPNGCGKSTLLKALTGLLRPNRG-----KLYIV-----GERSFVFQ : 90
Cr-ABCI10 : -----OVRRGSLHMLIGPNGCGKSTLLKVLGGLLVPDSE-----LIDAD-----QESGFVFQ : 47
Syn-ABCI10 : -----MSTPATIAQDLNFQWSADR-----PGIQNCSLAVEQGFVWMLIGTNGSGKSTLLRLLAGLLTPQSG-----LVKIA-----EEMGEVFQ : 74
Glo-ABCI10a1: -----MDSLIEVRGLGFAPPQGER-----QLIHNVQLTLAPGETVLLVAGPTGSGKSTLINAAGVIPAHTGGRLEGEVAFAGRSLLPLSVRERARHICTVLO : 92
Glo-ABCI10a2: -----AGPVVLESRILAYGGYPPLPDLITVRAGETVLLKGDNGCGKTTLLKILCGLLRPTGG-----SFAILGKDALKQNVARARTLGFVLO : 82
    
```

```

At-ABCI10 : NPDHQVVMPTVEADVAFGLGKYHDMNQEEVKSRVIAKALEAVGMRDYMQRPIQTLSSGQKQRIA IAGALAEACKVLLLLDELTTFLESDQMGVIKAVKDLINAKKGDVT : 172
Os-ABCI6 : NPDHQVVMPTVESDVAFGLGKLNLSLDEVRSRVSOSLDAVGMLSYSQRPIQTLSSGQKQRTA IAGALAEASKVLLLLDELTTFLEIDYDQMGVIKAVRKSIVGAG-GEVS : 188
Pp-ABCI10 : NPDHQVVMPTAEADVAFGLGHLDLSEEEVKARVHSSLEAVGMNEYGQRPVQTLSSGQKQRTA IAGALAESSRVLLLLDELTTFLESDQMGVLEAVRNVVGGSG---VT : 194
Cr-ABCI10 : NPDHQVVMPTVAADVAFGLGRYVLAEEEVTAARSSIRLVNMEDEMYRATHLSSGQQRVA IAGALAEADPKLLLLDELTTFLESDQMGVLEAVRNVVGGSG---VT : 153
Syn-ABCI10 : NPDHQLVMPTVGADIAFGIVKEKLSPEQEVQVRVGEALQAVNIAEMARRPIYALSSGQKQRIA IAGATARHCSVLLLLDELTTFLESDQMGVLEAVRNVVGGSG---VT : 179
Glo-ABCI10a1: NVEVQIFTDTRVREEVAFGLIENLN-VPPGRIAEQVGEILAEFGLOSQRDWPFAF LSSGQKQRLV LACVLAMDQEVLLLLDELTTFLESDQMGVLEAVRNVVGGSG---VT : 196
Glo-ABCI10a2: NPNHQLFADSVAGEVAQPGVAPE-----FAEQILLEQLNLLPQREQHPQSLSSGQKRLA LAAVLARRPFCILLDELTTFLESDQMGVLEAVRNVVGGSG---VT : 177
    
```

```

At-ABCI10 : ALWVTHRLEELKYADGAVYMENGRVVRHGDAATISDFIKAKQSSYIDQIGS- : 223
Os-ABCI6 : ALWVTHRLEELRYADGATYMEDGQTIIQGDVSTISKYIKKKQARYFGHFEL- : 239
Pp-ABCI10 : ALWVTHRLEELDYADGAVYMENGRVVLSCAVEEVKRYILKQQEDMSRNGALR : 246
Cr-ABCI10 : ALWVTHRLEELQFADAAAYMENGRVVFVFTGTPDEAKAVMRKLGAPV----- : 198
Syn-ABCI10 : ALWVTHRLEELDYCDGAFLEEGKIVAQGDPKPLKQRMNKTAV----- : 223
Glo-ABCI10a1: LLIVETHRLDLVAAVAHRSYCCADGTLPLGLPQSAVASAVLVRPA----- : 240
Glo-ABCI10a2: ALILLSHDPAASRLGARVVAL----- : 199
    
```

B

	At	Os	Pp	Cr	Syn	GloA1	GloA2
At-ABCI10	100%						
Os-ABCI6	63%	100%					
Pp-ABCI10	55%	60%	100%				
Cr-ABCI10	51%	46%	49%	100%			
Syn-ABCI10	45%	48%	44%	42%	100%		
Glo-ABCI10A1	22%	25%	22%	20%	27%	100%	
Glo-ABCI10A2	21%	23%	22%	24%	23%	25%	100%

FIGURE S1 | ABCI10 is conserved among plants and cyanobacteria. **(A)** Amino acid sequence alignment of ABCI10 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-ABCI10 (*Arabidopsis thaliana*, At4g33460, NP_195072), Os-ABCI6 (*Oryza sativa japonica*, Os01g56400, BAD52721), Pp-ABCI10 (*Physcomitrella patens*, XP_024370958), Cr-ABCI10 (*Chlamydomonas reinhardtii*, XP_001703542), Syn-ABCI10 (*Synechocystis PCC 6803*, gene sll1623, WP_010872403), Glo-ABCI10A1 and A2 (*Gloeobacter violaceus*, NP_925000). The conserved motifs Walker A, Walker B, Q-loop, D-loop, and H-loop (black boxes) form the nucleotide binding sites and the ABC-transporter signature motif LSGGQ is found in the helical subdomain. ABCI10 relatives contain the ECF specific Q-helix motif (X-P-D/E-X-Q-Φ: X is any, Φ a hydrophobic amino acid) indicated by a purple box (compare **Figure 1A**). **(B)** Amino acid identities in % of proteins depicted in **(A)**.