

(a) SaSLTa:

MAVAVALGWQGITVACTLAA~~S~~LIVMGFDLVGPDLVFGGLTALYVTSGIISIRDGAAGFANTGVLT~~V~~LVL
YLVAEGVSQTGGLDLAMNFMGRASTVFWAQVRMMIPVMVASAFLNNTPICALMIPILISWGRRCGISPK
KLLIPMSFATVLGGTVTLIGTSTNLVSGLQQEKYGTTPSKVFQFFTITPYGLPYAIWGMAYIILFS**kw**
Llpgedaaddlnygl1vprtsplvgrtakaglaggkltitgiskghrttpdm*i*hegdtlfvtg
svtaveqsvksfalvLLTSDDDVARKSTPGAAVFGAAAADV~~E~~egfdiaasegttnllqvnlkgsqlvgq
svrqigfrgrfgaavivkrskalqpgrigdivlqandvllstgalfastedftknFRGLmyldeala
rqfttavrvvgkrsk~~e~~agktiae~~v~~g~~l~~rginglfeieradgsllkavdhdtvlamgdvwlwfagdldgvay
lqkyttleHMQAdqvaklpsdiiyrrlvqvvvshhdlvgkk~~l~~kevrfrhtygaavlglhrsgqpagnis
evplkagdvlvveagpefatnfknnraf~~SLISEVPNSSPMKRSKMWI~~ALALT~~V~~AMVLTQIIGGAIDKEVI
HLWPCAMLTAGAMLAFKCLSADQARESIEWEVYICIAFAFAVSTAMETKLALAIANV~~F~~VALAQAI~~G~~QT
AALACIYLVTALLSELLTNNAAAIMYPIASAAEKLINPNIMS~~V~~AVMLG**GSAGWILPYSYQCNLMVYA**
AGKYRTKDFVKIGTPYHVWL~~F~~VG~~V~~VLILGSGDRWQIPVIASLVFTGLVILLPAAYEYLLNDSQKLAVDKK
LHALGSSFRRKRSSNSGEEALVEVYGN~~G~~SSKDVS~~A~~ANNGAYNGVVAPASLGHNRSSAGGVA

(b)

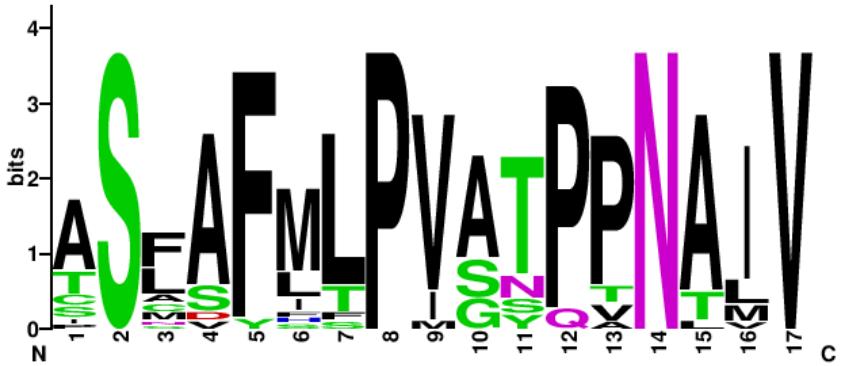
SaSLTb:

FTTDLDGVKYLLKDPRL~~E~~ATQAADAHKLKGRQIYRH**1vqatvspd**salightvremrf~~rty~~yegvvla~~ih~~
rqsgyyvs1rdvcdvelragdvl1leadqsFKKRFKANPAFGLVADVPRSAPIKTRLMWPALGLTAAMVAT
QIISGFTGTSYIDLWPAAILTAAAMLLIGCMTSDQAVEAIDWTYI~~T~~IAFAFGVSSAMERSKVA~~AA~~IASI
FVKISHAIGGRTAALGSMYLVTGLLSEVLTNNAAAALMYPIAANVGDDMGIQP~~K~~LMSVAVMLGASA~~A~~FS
PFGY**QCNLMVFTAGDYKTMDFVRLGVLLQVWQLVA**ACTIFSLPSWWMILCAISLAVVALAVTYAVASSLL
AKRRLKQLKAAASSAGK

Figure S1. SaSLTs amino acid sequences and conserved motifs. Predicted TrkA-C domains were highlighted in lowercase italic and bold font, Anion ArsB/NhaD permease domains were highlighted in underlined font, whereas the Prosite pattern PS01271 highlighted in yellow in both SaSLTa **(a)** and SaSLTb **(b)**,

PS01271 / #=22

(a)



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(b)

Bacteria and algal SAC1 proteins

[STACPI]-S-x(2)-[FY]-x(2)-P-[LIVM]-[GSA]-x(3)-N-x-[LIVM]-V

SLT Proteins:

Chlorellales:

[STACPI]-S-x(2)-[FY]-x(2)-**S**-[FLIVM]-[GSA]-x(3)-N-x-[LIVM]-[VAL]

Chlamydomonadales/Volvocales:

[STACPI]-S-x(2)-[FY]-x(2)-P-[FLIVM]-[GSA]-x(3)-N-x-[LIVM]-V

Sphaeropleales:

[GSTACPI]-S-x(2)-[WFY]-x(2)-P-[YLIVM]-[GSA]-x(3)-N-x-[LIVM]-V

Bryophyta:

[STACPI]-S-x(2)-[FY]-x(2)-P-[YLIVM]-[GSA]-x(3)-N-x-[LIVM]-V

Mamiellales:

[STACPI]-S-x(2)-[FY]-x(2)-P-[FLIVM]-[GSA]-x(3)-N-x-[LIVM]-V

Diatoms:

[STACPI]-S-x(2)-[FY]-x(2)-P-[FYLIVM]-[GSA]-x(3)-N-x-[LIVM]-[VI]

Figure S2. Weblogo (a) and Consensus pattern (b) of Sodium:sulfate symporter family signature prosite pattern PS01271. In red were highlight the differences between the sequences belonging to the various algal taxa.

(a)	SaSULP1	-----mglgaasaaaapavsraahrrlvpaglqqhagvcg	35
	CrSulp	mervcshqllassrgpciaqvgqrspirlgtssvahvqvspaglgryq-----rqrlqvva	55
	SaSULP1	caaaaaaaaaagrhirpvpvalqplqasqlqpsrlnppqhqrqqlqt- RQAAAGA -----	87
	CrSulp	SAAAAAA -----AFDPPG-----GVSAGFSQPQQQLPQQHPRQPQAVAEVAVAESVSAPASA	106
	SaSULP1	-----LSAGGSSSEQWPQPPSSSGK--GFRLPRIQLWDLGGPLAWAYMLGYLAVM	135
	CrSulp	APSNDGSPTASMDGGPSGGLSAVPAAATADLFSAARLRLPNLSPPIIT WTMFMSYMAFM	166
	SaSULP1	LILPISALLAKSSLVPLEQFIARATEPVALSAYYVSFSMAIVAGVINAVFGFLLAWVLVK	195
	CrSulp	LIMPITALLQKASLVPLNVFIARATEPVAMHAYYVTFSCSLIAAAAINCVFGFVLAWVLVR	226
	SaSULP1	YEFPGKKWIDAADV LPFALPTSVAGLTLATVYS EEGVLGSLLMKLGVN YNFAGKKILDAAVD LPFALPTSVAGLTLATVYG DEFFIGQFLQAQGVQV	255
	CrSulp	VFTRLGVAVAM	286
	SaSULP1	VFVSFPFVVRTMQPVLOQEMEKEVEEEAAWSLGASPWTTFTQVLLPPLLTPALLTGTALAFSR	315
	CrSulp	IFVSFPFVVRTMQPVMOEIQKEMEEAAWSLGASQWRTFTDVVLPPILLPALLTGTALAFSR	346
	SaSULP1	ALGEFGSIVIVSSNPFKDLIAPVLI FQCLEQYD FVGATVIGTVLLLISLVMMVGVNWLQ	375
	CrSulp	ALGEFGSIVIVSSNFAFKDLIAPVLI FQCLEQYD YVGATVIGTVLLLISLVMMILAVNQLQ	406
	SaSULP1	SYAQRFRK 383	
	CrSulp	KLARK --- 411	
		. *:::	
(b)	SaSULP2	mealssssllqrr-----asgliastrpclccqhtvsspssllrrn---mesrstqr	48
	CrSULP2	---mastllqpalglpsrvgrpsplslnpkirvcthtsapstskycdsssvies-tlgr	56
		. :*:*** . * : * : .. * *. . . :** : *	
	SaSULP2	vqpaaasrravqlqspsnsrrrlvir ASGPAGGMGAHGGGRGE PVDTWQKK TILGVAITY	108
	CrSULP2	qtsvagrpwlaprpaqqsgrdllvs KSGAAGGMGAHGGGLGE PVDNWIKKLLVGVAAY	116
		. *. . . :*. :** *:: ** *****.*****.** ** : :**** : *	
	SaSULP2	ILLTVILPFI NVFIQAFAKGLGPFLEAVMEHDFIHATK LTLM LAAITVPLNTLFGTVA AI	168
	CrSULP2	IGLVLVLPFL NVFVQAFAKGIIPFLEHCADPDFLHALK MTLM LAFTVPLNTVFGTVA AI	176
		* .*. :*:***:*****: **** : * :** : * :***** :*****:*****	
	SaSULP2	LITRNEFPKV LLLSSLDDLPFSISPVVTGIMLMLLY GRAGWFATALADGGLKVVFAFTGM	228
	CrSULP2	NLTRNEFPKV FLMSLLDLPFSISPVVTGIMLTLLY GRTGWFALLRETGINVVFAFTGM	236
		:*****:***:*****:*****:*****:*****: * : * :*****:***	
	SaSULP2	LLATLFTVLPFIV RELIPTLEQMDLAQEEAARSLGANPLQVFWH VTL PNIRWGLLY GVIL	288
	CrSULP2	ALATMFVTLPFVV RELIPILEMDLSQEEAARTLGANDWQVFWN VTL PNIRWGLLY GVIL	296
		:**:***** * :***:*****:***** * :*****:*****:*****	
	SaSULP2	TNARAMGE FGAVSVISGNIIGRTQTLTFLVESAYKEYNSE AAFAAAVLLSCLALGTLWVK	348
	CrSULP2	CNARAMGE FGAVSVISGNIIGRTQTLTFLVESAYKEYNTE AAFAAAVLLSALALGTLWIK	356
		*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*	
	SaSULP2	DKVEQAAAEEAK 361	
	CrSULP2	DKVEEEAAAESRK 369	
		****:*****: *	

Figure S3. Alignment between SaSULPs and *C. reinhardtii* SulPs amino acid sequences: conserved motifs and transit peptide. According to Lindberg and Melis (2008) [25], in both SaSULP1 (a) and SaSULP2 (a), in lowercase italic and bold font were highlighted the predicted chloroplast transit peptide; in red font the transmembrane domains; in green font the regions of protein lie in the chloroplast stroma; yellow: regions of protein lie in the intermembrane space.

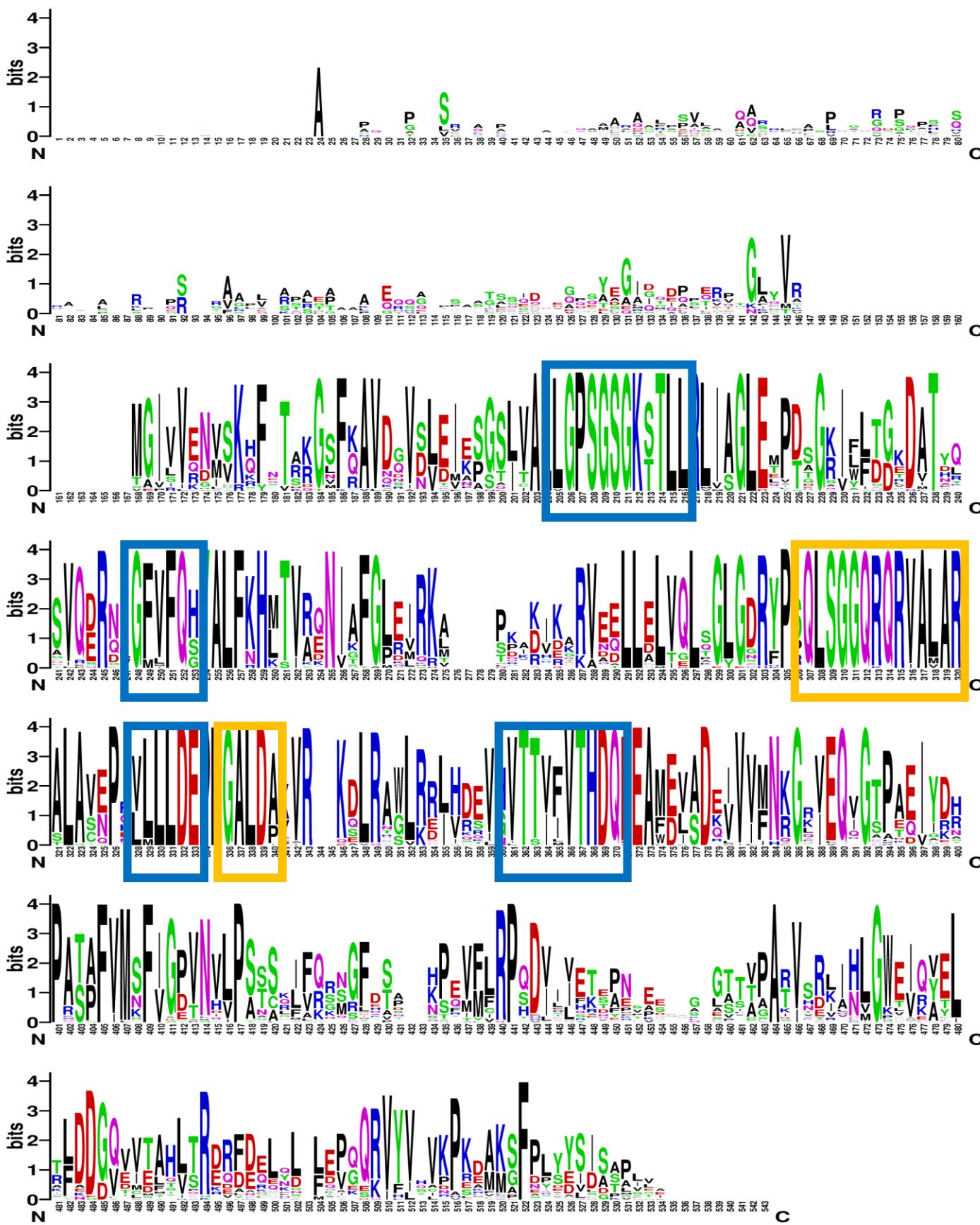


Figure S4. Weblogo of Sabc and CysA amino acid sequences. In the box were highlighted the conserved motifs common to ATP hydrolyzing subunits of ABC transporters: **Blue box**, motifs involved in binding and hydrolysis of ATP; **Orange box** motifs postulated to be involved in ATP hydrolysis and/or interaction with the membrane-spanning subunits.

SaSabc	mlpagraqalrssrdstacaakpgprs----vgsssrrssfprrwwavqaldts ALEEQQQ	56
CrSabc	ma---sllaqttsrlgarpaqaqpvaqmapmasrvqpampsallplharatttsv---- * * :** .: **: ** : .*: : :* : :* * :::	53
SaSabc	QQQAAQLNGNGSSTAHQHRAAAAAGVSRPSGPTATLTDEDVNGMQLDGIQLEQQQQPTGL	116
CrSabc	acrAASIDKPVVYT--PRDSSQQSSNGAGEVSMSISSMDEVGPSYEGIITDAPTRPTGL :***.: * * : . . . : : . * . :** : :****	110
SaSabc	YVRVRGMVKHFNTAKGVFKAVDGVDIPSSICALL GPGSGKTT LLRLVAGLELPTGG	176
CrSabc	YVRVRNMVKHFSTAKGLFRAVDGVVDIEPSSIVALL GPGSGKTT LLRLIAGLEQPTGG *****.*****.*****:*****:*****:*****:*****:*****:*****:*****:*****	170
SaSabc	KIYFDDLDATDLAVQDRQVG MVFQ SYALFNHMTVSENIKFGLQVRKLPVDHKRAADLLE	236
CrSabc	NIYFDDTDATNLSQLDRQIG FVFQ SYALFNHKTVAENIKFGLVERKLNIDHDKRVAELLA :***** * :*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	230
SaSabc	LVQLTGLGDRYPRQ LGGQRQRVA LARALASNPR LLLLDE PF GALDA VVRKQLRAGLKEI	296
CrSabc	LVQLTGLGDRYPRQ LGGQRQRVA LARALASNPR LLLLDE PF GALDA VVRKQLRTGLREI *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	290
SaSabc	VRSVGVT IIVTHDQ EEAFDLADQVVIFNRGLIEQSGSPNEIIKRPATPFVMGFVGDTNS	356
CrSabc	VRSVGVT IIVTHDQ EEAFDLADKVVVFNRGLVEQQGSPTEIIKRPRTPFIMKFVGETNV *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	350
SaSabc	VPAGCMLVRRSGFNPRLGKARVMFRPSDIRLSKEYVATL-DGQQVVTPATVNEAANMGWT	415
CrSabc	VPATSLLAKRMRFNT--SKTSVMFRPHDIKLFKTVPPESGEALTTVGANVADKANLGWV *** .:.*: * ** .*: ***** :* * : * . . * .: * : ***:***.	408
SaSabc	MKYTLKFDDDVEVEFSVTRAQADKEFKLDVGQRIYVVVPPSAMMEFDETELGSAPII	472
CrSabc	VKYTLRFDDDVECELQLSRDQDEREYNLVVGSRVFVHPHRTMMGFNASDVTPIV :*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	465

Figure S5. Alignment between SaSabc and *C. reinhardtii* Sabc amino acid sequences: conserved motifs. Lowercase **bold** predicted transit peptide. **Bold fonts** conserved motifs common to ATP hydrolyzing subunits of ABC transporters: **Blue bold**, motifs involved in binding and hydrolysis of ATP; **Orange bold**, motifs postulated to be involved in ATP hydrolysis and/or interaction with the membrane-spanning subunits, according to Lindberg and Melis (2008) [25].

SaSBP	-----	0
CrSBP	MSFLAPSLGVARGILEPASAARPPAHAAGHAPVLTSRTGGPAANHDRPAGAPSPHAASL	60
SaSBP	-----	0
CrSBP	TPSSSGQASQQGDPQRSQHQQAQRQDQQQSQRSLQSHLITAATLLPALPPPPGGNGDG	120
SaSBP	----NPGPQPLALLAANKEPLV LTVASFAVTKLAYVRLTKLFREKYLQEKGVDVRFR LT	56
CrSBP	DGGEAAGPQPLADVAA-QFPEV VLTASFAVTKLAYVRVTRAFREWYERTKGVDVRFR LT ***** : * : : * : ***** : * : *** * : : * : *****	179
SaSBP	FAGSGVQARAVIDGLPADMVALALPLDVQKIADAGLLSANWQKGFPLGSVVCE TTVALVV	116
CrSBP	FAASGVQARAVIDGLPADIVALALPLLDKIVSAGLIRPDWRSAYPAASVVCE TTVAFVV ** . ***** : ***** : * . *** : : * : . ***** : **	239
SaSBP	RPGNPKNIQSWEDLTOPGLQVIVANPKTAGVARWIFLALWGSKMKKGAAAKEYITKVFD	176
CrSBP	RQGNPKNIRTWEDLTTRAGVEVVLANPKTAGVARWIFLALWGAKMKKGNAALAYVQRVFE * ***** : ***** : * : * : ***** : ***** : ***** : **** * * : : * :	299
SaSBP	NVLVQPRDAREASDVFYRQLGDVLLTYENEVLTNQVYGP EKA LPEKALPYVVPSNVRIEC PM	236
CrSBP	NVVVQPRDAREASDVFYKQKVGDVLLTYENEVILTNEVYGD-KALPYLVPSYNIRIEC P *** : ***** : * : : ***** : * : *** * : *** : *** * : * : ***** :	358
SaSBP	ALVDKVLDARPAAREAHHAFGKFCFTPEAQVEFG RVGFRTNRKLC KTPPAHLAGQ PQIK	296
CrSBP	ALVDKVVDARGPEVREAASEFCRF LFPTAAQHEFARLGFRVN PRTCKEVA AQQTGLPPAN ***** : *** . **** * : * *** * * . * : *** . * : ** * : * : * : *	418
SaSBP	MWTVDKE LGWGSAQRRFFDAGEILD QI QADVGARKAEARKAGKK---- 341	
CrSBP	LWQVDKE LGWAAAQKKFFDAGAILDD IQS AVGKL RVEQRKAAQAAARR 467 : * ***** : * : : ***** * : * : * : . * *** .	

Figure S6 Alignment between SaSBP and *C. reinhardtii* SBP amino acid sequences: conserved motifs. Lowercase bold predicted transit peptide. Bold fonts conserved region homologous to sulfate- and thiosulfate-binding proteins in cyanobacteria and other organisms according to Lindberg and Melis (2008) [25].

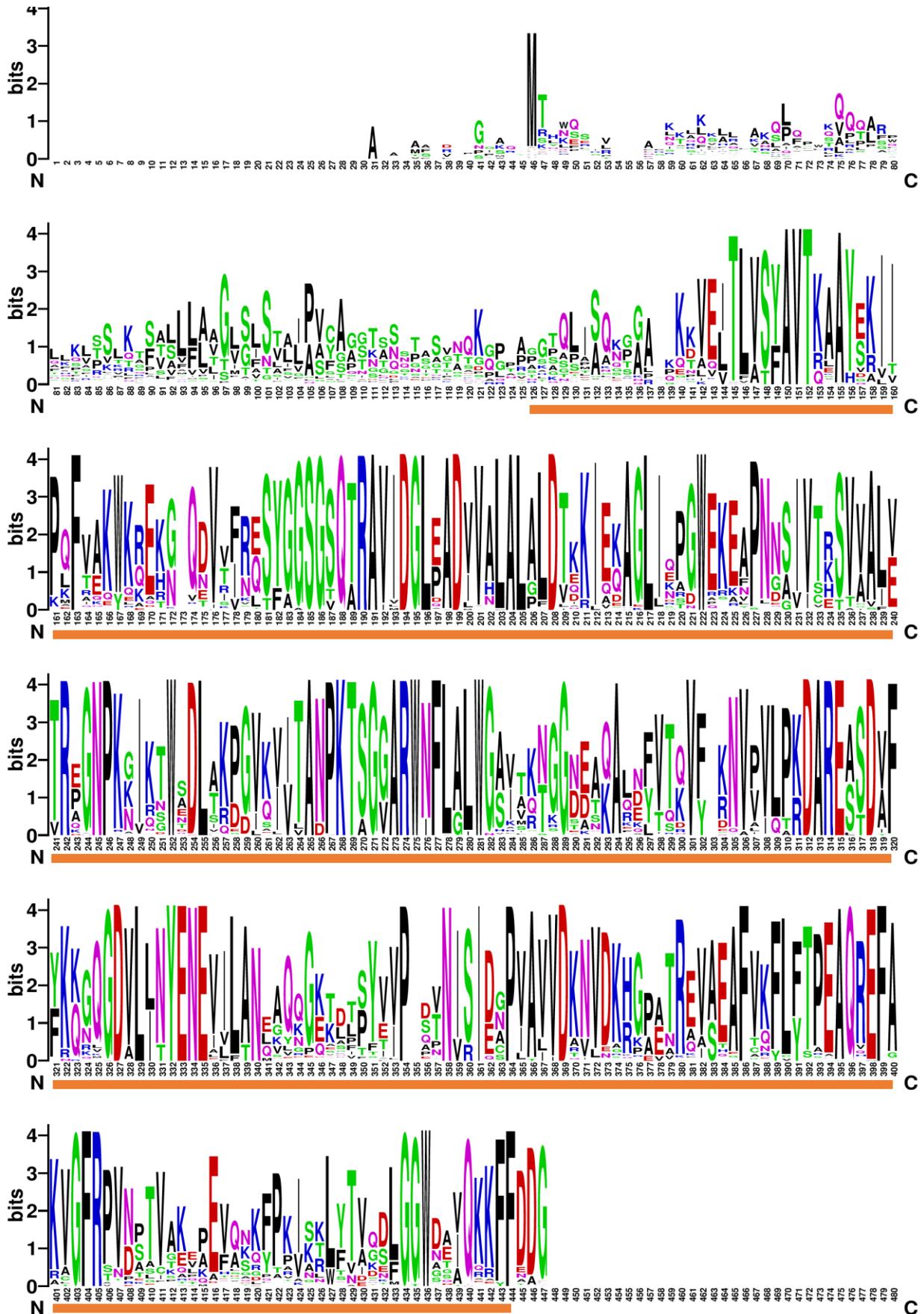


Figure S7. Weblogo of SBP and CysA amino acid sequences. Conserved region homologous to sulfate- and thiosulfate-binding (CysA) proteins and to SBP of eukaryotic organisms. Orange line denotes the position of SaSBP in the alignment.