

$\alpha N1$ $\alpha N2$ $\alpha N3$
00000000 00000000 00000000 00000000000000000000 00000000000000000000 0000

SRP54 N domain

SRP54 G domain

β_6 α_6 β_7 β_8 α_7

	320	*	340	*	360	*	380	*	400	*	
Ara_tha	GLILTKLDGSARGGC	VVS	VDELGLIPVKFIGVGE	AVEDLP	OP	DPE		AFVNA	IF	S	: 325
Zea_may	GLILTKLDGTARGGC	VVS	VDELGLIPVKFIGVGE	AMEDLP	OP	DAE		AFVEA	IF	P	: 325
Sel_moe	GFVLTKLDGTARGGC	VAS	VDELGLIPVKFVGVE	GLEDLP	OP	DAE		AFVNA	IF	P	: 326
Phy_pat	GLILTKLDGTARGGC	VVS	VDELGLIPVKFVGVE	GIDLP	OP	DAQ		SEVDAL	IF	P	: 325
Chl_rei	GLILTKLDGTARGGA	VVS	VDELGLIPVKFIGVGET	AEEDLP	OP	DPE		AFAEA	IF	PKVKEPATATGK	: 334
Ost_tau	GLILTKLDGTARGGA	VVS	VDELGLIPVKFIGVGE	AMEDLP	OP	SEAE		SEVDAL	IF	PEEA	: 330
Cya_mer	GLVLTKLDGTARAG	FLVS	VDELGLIPVKFVGVE	KLNDRD	DPV			AYDGL	LLSDTPAAARRA	---AP	: 355
Gal_sul	GLILVTKLDGT	GRACYLVS	INDEKLPVKLIGVGE	GLEDLRS	DPQ			LYQLF	IF	D	: 327
Pha_tri	GLILTKLDGSARGCS	VAS	ISRDILPVKLIGVGE	GIEDLR	DVSCRRSETKLNIAAWSSPVVYFAGADN	FSLNQASLTVS		MSVRLVVDRRRAKES			: 387
Con_woo	GLVLTKLDGTAKGGIA	AARELE	IPVKMIGIGE	QLEDLR	RP	DPD		DFARAL	IF	S	: 305
Esc_col	GLILTKLDGTAKGGV	IFS	ADFGIPRIYIGVGER	IEDLR	RP	KAD		DFEAL	IF	ARED	: 309
Ths_aqu	GVIVTKLDGTAKGGV	LIPHVRTLKVP	IRFIRIGVGE	GPDDLP	OP	DPE		AFVEAIL	IF	EE	: 304
Tha_mar	GLILTKLDGTAKGGIT	AARELGL	IPKIFIGVGE	KAEEDLP	OP	DPE		AFVEVIL	IF	SE	: 294
Vic_vad	GLVLTKLDGT	GKGGMYVA	HOEFELPTFFIGVGE	QPEDLP	OP	SAE		YVAGAL	IF	GEESK	: 309
Thm_ros	DLALTKLDGTAKGGIA	AARELGLIPTAYVGT	GEKPTFAE	EDLP	OP	DPE		AYVDAL	IF	FFGDEED	: 320
Bac_cla	GLVLTKLDGTAKGGI	VIAHQELD	LPVKFIGLGE	QKDDLP	OP	DPE		QFVYGL	IF	QDAIDAE	---KE : 327
Fla_bac	SLAVTKLDGTAKGGV	VIGSDFOH	PVRYIGVGE	KMDHOVN	NKT			EFVDSFF	IF	N	: 317
Gra_fro	SLAVTKLDGTAKGGV	VIGSDFKL	IPVKYIGVGE	GIEDLOVN	NKY			EFVDSFF	IF	K	: 317
Pvr_lun	---	---	---	---	---	---		EYVN	IF		: 70

Fig. S7. MAFFT alignment of FtsY proteins and the translated ORF from the *Pyrocystis lunula* AF490367 minicircle. Unalignable N-terminal ends of some sequences were truncated. Graphical elements above the alignment concern the homolog from *Arabidopsis thaliana*, while those under the alignment refer to the *Pyrocystis* sequence. Particular secondary structure elements in the *Arabidopsis* sequence according to Chandrasekar et al. (2008) are denoted as follows: kN1-4 (k helices of the N domain), k1-7 (k helices of the GTPase G domain), and r1-8 (r strands of the G domain). The ranges of k-helices shown in the *Pyrocystis* sequence were predicted by more than 50% of eight applied algorithms (see Materials and methods in Supplementary Material online). The predicted SRP54 N helical bundle domain and SRP54 G domain with GTPase activity found in Pfam database are shown as red and blue rectangles, respectively. Name abbreviations: Ara_tha – *Arabidopsis thaliana*, Zea_may – *Zea mays*, Sel_moe – *Selaginella moellendorffii*, Phy_pat – *Physcomitrella patens*, Chl_rei – *Chlamydomonas reinhardtii*, Ost_tau – *Ostreococcus tauri*, Cya_mer – *Cyanidioschyzon merolae*, Gal_sul – *Galdieria sulphuraria*, Pha_tri – *Phaeodactylum tricorutum*, Con_woe – *Conexibacter woesei* DSM 14684, Esc_col – *Escherichia coli* E24377A, Ths_aqu – *Thermus aquaticus* Y51MC23, Tha_mar – *Thermotoga maritime* MSB8, Vic_vad – *Victivallis vadensis* ATCC BAA-548, Thm_ros – *Thermomicrobium roseum* DSM 5159, Bac_cla – *Bacillus clausii* KSM-K16, Fla_bac – *Flavobacterium bacterium* BBFL7, Gra_for – *Gramella forsetii* KT0803, Pyr_lun – *Pyrocystis lunula*.