

Table S1 Cyanobacterial Tvp38/DedA-homologs.

Orthologs search identified by using (Pfam PF09335) and found by BLAST using the database Cyanobase (Nakao *et al.*, 2010).

The identities [in %] of orthologous proteins in relation to Slr0305, Slr0232 or Slr0509 of *Synechocystis* PCC 6803 are indicated. No Tvp38/DedA-homologs were identified for *Thermosynechococcus elongatus* BP-1.

Cyanobacterium	Orthologs	% Identity	Orthologs	% Identity	Orthologs	% Identity
Synechocystis PCC 6803	Slr0305		Slr0232		Slr0509	
	alr2207	78.6	All4799	53.9	all5093	50.5
	alr5186	58.6				
Anabaena PCC 7120	all5119	37.8				
	all7589	33.1				
	---		gll1509	41.2	glr0555	48.5
Gloeobacter violaceus PCC 7421	---		glr0610	32.4		
	MAE22590	77.8	MAE45880	60.8	MAE50240	60.8
	MAE19440	34				
Prochlorococcus marinus SS120	Pro1843	38.1			Pro1785	45.4
	PMM1681	38.6			PMM1624	45.3
	PMM0308	29.1				
Prochlorococcus marinus MED4	PMT2186	47.1			PMT0140	47.8
	PMT0305	28.2				

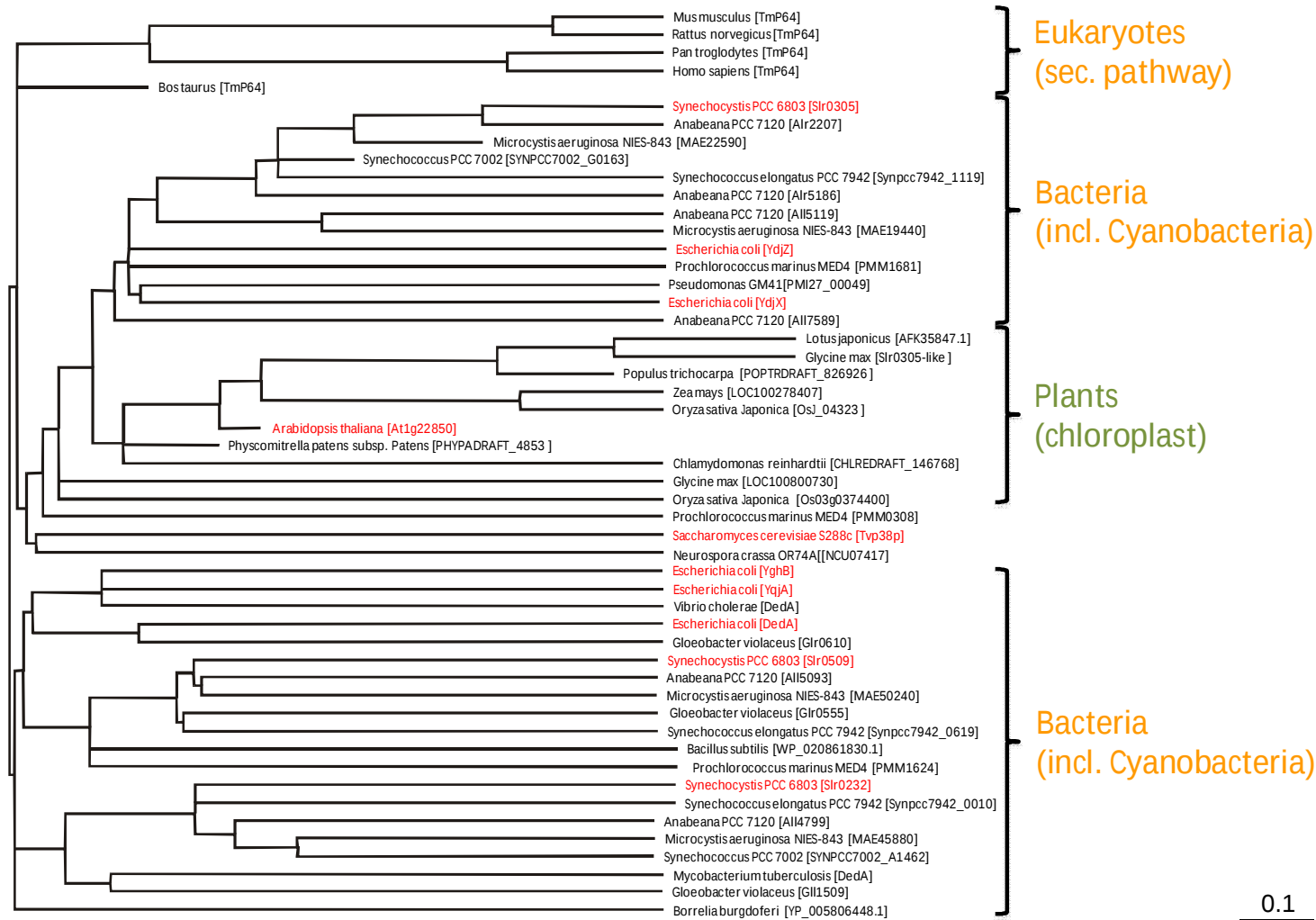
Synechococcus WH8102	SYNW2392	45.1		SYNW0120	50.5
Synechococcus elongatus PCC 6301	syc0430_d	57.1	syc1487_d	61.2	syc0905_c
Synechococcus CC9311	sync_2809	42.3		sync_0109	49
	sync_0876	24.2			
Synechococcus PCC 7002	SYNPCC7002_G0 163	80.4	SYNPCC7002_A 1462	52.1	
Acaryochloris marina MBIC11017	AM1_5085	72.2	AM1_4933	48.6	
	AM1_5086	38.9			
	AM1_3651	31.6			
	AM1_3513	35.2			
	AM1_4639	28.8			
	AM1_5179	28 with Ava2345			
Prochlorococcus marinus NATL2A	PMN2A 1280	37.5		PMN2A_1201	52
	PMN2A_1711	22.1			
Anabaena variabilis ATCC 29413	Ava_2752	76.5	Ava_2069	55.7	Ava_2364
	Ava_2775	59.5			
	Ava_2345	37.1			
Synechococcus CC9902	Syncc9902 _2208	45.3		Syncc9902_0147	53.7
	Syncc9902_1878	27.7			
Synechococcus CC9605	Syncc9605_2554	45.3		Syncc9605_0103	46.8

Prochlorococcus marinus MIT 9312	PMT9312_1774	37		PMT9312_1717	43.9
	PMT9312_0310	29.1			
Synechococcus elongatus PCC 7942	Synpcc7942_1119	57.1	Synpcc7942 0010	61.2	Synpcc7942_0619 53.3
Synechococcus JA-2-3B'a(2-13)	CYB_0557	60.1	---		---
	CYB_2273	24.3			
Synechococcus JA-3-3Ab	CYA 2613	24.3	---		---
Prochlorococcus marinus AS9601	A9601 18911	36.7		A9601_18341	43.6
	A9601_03321	28.2			
Prochlorococcus marinus MIT 9515	P9515 18721	38.6		P9515_18131	42.3
	P9515_04161	22			
	P9515_03421	29.5			
Prochlorococcus marinus MIT 9303	P9303 29081	46.5		P9303_01771	46
	P9303_20551	24.6			
	P9303_20181	28.2			
Prochlorococcus marinus NATL1A	NATL1 21521	38.1		NATL1_20761	50.3
	NATL1_04261	26.3			
	NATL1_03931	28.2			
Prochlorococcus marinus MIT 9301	P9301 18721	36.2		P9301_18161	44.7
	P9301_03331	29.1			
Synechococcus RCC307	SynRCC307_2414	43.4		SynRCC307_0107	49.2

Synechococcus WH 7803	SynWH7803_2431	46.9			SynWH7803_0170	46.5
	SynWH7803_0603	28				
Prochlorococcus marinus MIT 9215	P9215_19541	39.1			P9215_18981	43.2
	P9215_03331	28.2				
	P9215_4121	22				
Prochlorococcus marinus MIT 9211	P9211_18091	41.1			P9211_17501	52.6
	P9211_03691	27.7				
	cce_4297	57.6	cce_1755	63	cce_3254	46.5
Cyanothece ATCC 51142	cce_3995	36.2				
	cce_2348	37.8				
	cce_3820	26.4				
Nostoc punctiforme ATCC 29133	Npun_R3471	77.3	Npun_F5562	52.2	Npun_R4473	53
	Npun_R3472	58	Npun_F4627	28.8		
Cyanothece PCC 7424	PCC7424_2229	62.8	PCC7424_0186	60.8	PCC7424_1977	63.5
	PCC7424_2230	36.4				
	PCC7424_0620	34.6				
Cyanothece PCC 7425	Cyan7425_1944	38.5	Cyan74254907	54.2	Cyan7425_2737	57
	Cyan7425_2175	40.3				

Cyanothece PCC 8801	PCC8801_4073 (ok)	59.2	PCC8801_1260	65.6
	PCC8801_4094	37.1		
	PC8801_0962			
Arthrospira platensis NIES-39	NIES39_O01540	68.1	NIES39_A00840	61.4
Trichodesmium erythraeum IMS101	Tery_1993	66.8		

Figure S1 Phylogenetic tree of selected pro- and eukaryotic DedA-like proteins. The tree is midpoint rooted. The tree is based on a constrain-based multiple sequence alignment (Papadopoulos *et al.*, 2007). For further details see figure 2 and the text.



Reference

Nakao. M., Okamoto. S., Kohara. M., Fujishiro. T., Fujisawa. T., Sato. S., Tabata. S., Kaneko. T., and Nakamura. Y. (2010). CyanoBase: the cyanobacteria genome database update 2010. *Nucleic Acids Res.* 38 (Database issue). D379-381.

Papadopoulos. J. S., and Agarwala R. (2007) COBALT: constraint-based alignment tool for multiple protein sequences. *Bioinformatics* 23.1073-1079.