Table 3. Sequence space analysis of more than 50 BLUF domains identified by PFAM allows identification of three BLUF subfamilies

Subfamily	Class	Members of subfamily/class	
Subfamily I		Egym_pac_alpha_BLUF1	Kq_pac_alpha_BLUF1
BLUF1		Egym_pac_beta_BLUF1	Kq_pac_beta_BLUF1
		Ev_pac_alpha_BLUF1	Eg_pac_alpha_BLUF1
		Ev_pac_beta_BLUF1	Eg_pac_beta_BLUF1
		Cs_pac_alpha_BLUF1	Es_pac_alpha_BLUF1
		Cs_pac_beta_BLUF1	Es_pac_beta_BLUF1
		Al_pac_beta_BLUF1	
Subfamily II		Cs_pac_alpha_BLUF2	Kq_pac_alpha_BLUF2
BLUF2		Cs_pac_beta_BLUF2	Kq_pac_beta_BLUF2
		Egym_pac_alpha_BLUF2	Eg_pac_alpha_BLUF2
		Egym_pac_beta_BLUF2	Eg_pac_beta_BLUF2
		Ev_pac_alpha_BLUF2	Es_pac_alpha_BLUF2
		Ev_pac_beta_BLUF2	Es_pac_beta_BLUF2
		Al_ac_beta_BLUF2	
Subfamily III	Class A	Rs_BlrB	
		Rs_BlrA	
		Ec_YcgF	
	Class B	Rs_AppA	Ce_hp
		Se_TII0078	As_hp
		So_ea	As93A2_hp
		Rp_aop1	Bb_hp
		Rp_aop2	Cv_hp
		Rp_aop3	Rb_hp
		Lx_aop	Xa_XAC3278
		Slr1694	Xa_XAC2120
		uncult	

Subfamily I consists of BLUF I domains originating from diverse putative photoactivated adenylyl-cyclases (PACs), whereas subfamily II encompasses the BLUF II domains of these systems. All non-PAC BLUF-domains, including BlrB_BLUF, AppA_BLUF, and Slr1694_BLUF (marked yellow) belong to subfamily III.

Egym_pac_alpha_BLUF1	*Eutreptiella gymnastica* PAC alpha subunit, BLUF1
Egym_pac_beta_BLUF1	*Eutreptiella gymnastica* PAC beta subunit, BLUF1
Ev_pac_alpha_BLUF1	*Eutreptia viridis* PAC alpha subunit, BLUF1
Ev_pac_beta_BLUF1	*Eutreptia viridis* PAC beta subunit, BLUF1
Cs_pac_alpha_BLUF1	*Colacium sideropus* PAC alpha subunit, BLUF1
Cs_pac_beta_BLUF1	*Colacium sideropus* PAC beta subunit, BLUF1
Al_pac_beta_BLUF1	*Astasia longa* PAC beta subunit, BLUF1
Kq_pac_alpha_BLUF1	*Khawkinea quartana* PAC alpha subunit, BLUF1
Kq_pac_beta_BLUF1	*Khawkinea quartana* PAC beta subunit, BLUF1
Eg_pac_alpha_BLUF1	*Euglena gracilis* PAC alpha subunit, BLUF1
Eg_pac_beta_BLUF1	*Euglena gracilis* PAC beta subunit, BLUF1
Es_pac_alpha_BLUF1	*Euglena stellata* PAC alpha subunit, BLUF1
Es_pac_beta_BLUF1	*Euglena stellata* PAC beta subunit, BLUF1

Egym_pac_alpha_BLUF2	*Eutreptiella gymnastica* PAC alpha subunit, BLUF2
Egym_pac_beta_BLUF2	*Eutreptiella gymnastica* PAC beta subunit, BLUF2
Ev_pac_alpha_BLUF2	*Eutreptia viridis* PAC alpha subunit, BLUF2
Ev_pac_beta_BLUF2	*Eutreptia viridis* PAC beta subunit, BLUF2
Cs_pac_alpha_BLUF2	*Colacium sideropus* PAC alpha subunit, BLUF2
Cs_pac_beta_BLUF2	*Colacium sideropus* PAC beta subunit, BLUF2
Al_pac_beta_BLUF2	*Astasia longa* PAC beta subunit, BLUF2
Kq_pac_alpha_BLUF2	*Khawkinea quartana* PAC alpha subunit, BLUF2
Kq_pac_beta_BLUF2	*Khawkinea quartana* PAC beta subunit, BLUF2
Eg_pac_alpha_BLUF2	*Euglena gracilis* PAC alpha subunit, BLUF2
Eg_pac_beta_BLUF2	*Euglena gracilis* PAC beta subunit, BLUF2

Es_pac_alpha_BLUF2	*Euglena stellata* PAC alpha subunit, BLUF2
Es_pac_beta_BLUF2	*Euglena stellata* PAC beta subunit, BLUF2

Rs_BlrB	*Rhodobacter sphaeroides* BlrB
Rs_BlrA	*Rhodobacter sphaeroides* BlrA
Ec_YcgF	*E. coli* YcgF
Rs_AppA	*Rhodobacter sphaeroides* AppA
Se_TII0078	*Synechococcus elongatus* protein
So_ea	*Shewanella oneidensis* expression activator
Rp_aop	*Rhodopseudomonas palustris* activator of puc exp
Rp_aop2	
Rp_aop3	
Lx_aop	*Leifsonia xyli* activator of puc expression
Slr1694	*Synechocystis sp*. 1694
uncult	*Uncultured proteobacterium* hypothetical protein
Ce_hp	*Corynebacterium efficiens* hypothetical protein
As_hp	*Acinetobacter sp*. hypothetical protein
As93A2_hp	*Acinetobacter sp*. 93A2 hypothetical protein
Bb_hp	*Bdellovibrio bacteriovorus* hypothetical protein
Cv_hp	*Chromobacterium violaceum* hypothetical protein
Rb_hp	*Rhodopirellula baltica* hypothetical protein
Xa_XAC3278	*Xanthomonas axonopodis* protein XAC3278
Xa_XAC2120	*Xanthomonas axonopodis* protein XAC2120
Mx_USC2	*Myxococcus xanthus* protein USC2-2p
St_ABC	*Symbiobacterium thermophilum* glycine/betaine/carnitine ABC transporter substrate-binding protein
uncult_581_FADBD	*uncultured bacterium* 581 putative FAD binding domain