

Table S1: prokaryotes bearing PHY-, LOV- or BLUF-proteins encoding genes

	Bacteria	†Group	PHY	LOV	BLUF
1	† <i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	F		X	
2	† <i>Bacillus amyloliquefaciens</i> FZB42	F		X	
3	† <i>Oceanobacillus iheyensis</i> HTE831	F		X	
4	<i>Bacillus pumilus</i> SAFR-032	F		XX	
5	<i>Bacillus selenitireducens</i> MLS10	F		X	
6	† <i>Listeria monocytogenes</i> EGD-e	F		X	
7	<i>Listeria monocytogenes</i> F6900	F		X	
8	<i>Listeria monocytogenes</i> FSLN3-165	F		X	
9	<i>Listeria monocytogenes</i> 10403S	F		X	
10	<i>Listeria monocytogenes</i> J016	F		X	
11	<i>Listeria monocytogenes</i> J2818	F		X	
12	<i>Listeria monocytogenes</i> HPB2262	F		X	
13	<i>Listeria monocytogenes</i> FSL N1-017	F		X	
14	<i>Listeria monocytogenes</i> F6854	F		X	
15	† <i>Listeria monocytogenes</i> F2365	F		X	
16	<i>Listeria monocytogenes</i> str. 4b H7858	F		X	
17	† <i>Listeria innocua</i> Clip11262	F		X	
18	† <i>Listeria welshimeri</i> serovar 6b str. SLCC5334	F		X	
19	† <i>Rubrobacter xylanophilus</i> DSM 9941	Ac		X	
20	† <i>Kineococcus radiotolerans</i> SRS30216	Ac	X	XXX	
21	† <i>Arthrobacter aureus</i> TC1	Ac		X	
22	† <i>Mycobacterium gilvum</i> PYR-GCK	Ac	X		
23	† <i>Frankia alni</i> ACN14a	Ac	X		
24	† <i>Streptomyces griseus</i> subsp. <i>griseus</i> JCM 4626	Ac	X		
25	† <i>Corynebacterium efficiens</i>	Ac			X
26	† <i>Leifsonia xyli</i> subsp. <i>xyli</i>	Ac			X
27	† <i>Clavibacter michiganensis</i> sub. <i>michiganensis</i> NCPPB 382	Ac			XX
28	† <i>Clavibacter michiganensis</i> sub. <i>sepedonicus</i> ATCC 33113	Ac			X
29	† <i>Rhodobacter sphaeroides</i> ATCC 17023/2.4.1	P(α)	XX	X	XXX
30	† <i>Rhodobacter sphaeroides</i> ATCC 17025	P(α)	X		XX
31	† <i>Rhodobacter sphaeroides</i> ATCC 17029	P(α)		X	XX
32	<i>Rhodobacteriales bacterium</i> HTCC2654	P(α)	X		
33	<i>Sagittula stellata</i> E-37	P(α)	X	X	X
34	<i>Oceanicola granulosus</i>	P(α)	X	X	
35	<i>Oceanicola batsensis</i> HTCC2597	P(α)	X		
36	<i>Oceanibulbus indolifex</i> HEL-45	P(α)		X	
37	† <i>Silicibacter</i> sp. TM1040	P(α)	X		XX
38	<i>Labrenzia aggregata</i> IAM 12614	P(α)	X		X
39	<i>Roseobacter</i> sp. CCS2	P(α)		XX	X
40	<i>Roseobacter</i> sp. SK209-2-6	P(α)			X
41	<i>Roseobacter</i> sp. MED193	P(α)			X
42	<i>Roseobacter</i> sp. AzwK-3b	P(α)			X
43	<i>Roseobacter litoralis</i> Och 149	P(α)		X	X
44	† <i>Roseobacter denitrificans</i> Och 114	P(α)		X	X
45	<i>Roseovarius</i> sp. HTCC2601	P(α)		X	X
46	<i>Roseovarius</i> sp. 217	P(α)			X
47	<i>Roseovarius</i> sp. TM1035	P(α)			X
48	† <i>Dinoroseobacter shibae</i> DFL 12	P(α)		XXX	X
49	† <i>Jannaschia</i> sp. (strain CCS1)	P(α)			XXX
50	† <i>Hyphomonas neptunium</i> ATCC 15444	P(α)			X
51	† <i>Maricaulis maris</i> (strain MCS10)	P(α)			XX
52	<i>Sulfitobacter</i> sp. EE-36	P(α)			X
53	<i>Sulfitobacter</i> sp. NAS-14.1	P(α)			X
54	<i>Loktanella vestfoldensis</i> SKA53	P(α)			X

55	† <i>Caulobacter crescentus</i> CB15	P(α)		X	
56	† <i>Caulobacter</i> sp. K31	P(α)		XXX	
57	<i>Magnetospirillum gryphiswaldense</i>	P(α)	X		XX
58	<i>Magnetospirillum magnetotacticum</i>	P(α)	X	XX	
59	† <i>Granulobacter bethesdensis</i>	P(α)	X	X	
60	<i>Rhodospirillum centenum</i>	P(α)	X		
61	† <i>Rhodospirillum rubrum</i> ATCC 11170	P(α)	X		
62	† <i>Gluconobacter oxydans</i> 621H	P(α)	X		
63	† <i>Erythrobacter litoralis</i> HTCC2594	P(α)		XXXX	
64	<i>Erythrobacter</i> sp. NAP1	P(α)	X	X	
65	<i>Erythrobacter</i> sp. SD-21	P(α)	X	X	
66	<i>Sphingomonas</i> sp. SKA58	P(α)	X	XX	X
67	† <i>Sphingomonas wittichii</i> RW1	P(α)			X
68	† <i>Sphingopyxis alaskensis</i> RB2256	P(α)		X	X
69	† <i>Novosphingobium aromaticivorans</i> DSM 12444	P(α)		XX	
70	† <i>Rhodopseudomonas palustris</i> BisB5	P(α)	XXXXX		
71	† <i>Rhodopseudomonas palustris</i> BisA53	P(α)	XXX		XXXX
72	† <i>Rhodopseudomonas palustris</i> CGA009	P(α)	XXXXXX		XXX
73	† <i>Rhodopseudomonas palustris</i> (strain BisB18)	P(α)	XX		XXX
74	† <i>Rhodopseudomonas palustris</i> (strain HaA2)	P(α)	XXXXXX		X
75	<i>Rhodopseudomonas palustris</i> TIE-1	P(α)	XXXXXXXX		XXX
76	<i>Phaeobacter gallaeciensis</i> 2.10	P(α)	X		
77	<i>Phaeobacter gallaeciensis</i> BS107	P(α)	X		
78	† <i>Bradyrhizobium</i> sp. BTAi1	P(α)	XXXXX	X	
79	† <i>Bradyrhizobium</i> sp. ORS278	P(α)	XX	X	
80	† <i>Rhizobium leguminosarum</i> bv <i>viciae</i> 3841	P(α)	X	X	
81	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325	P(α)		XX	
82	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304	P(α)	XX	X	
83	<i>Rhizobium leguminosarum</i>	P(α)	X		
84	<i>Methylocella silvestris</i> BL2	P(α)	XX		
85	† <i>Azorhizobium caulinodans</i> ORS 571	P(α)	X		
86	<i>Fulvimarina pelagi</i> HTCC2506	P(α)	X	X	XXX
87	† <i>Agrobacterium tumefaciens</i> str. C58	P(α)	XXX		
88	<i>Xanthobacter</i> sp. Py2	P(α)	X		
89	<i>Aurantimonas</i> sp. SI85-9A1	P(α)	X	XX	
90	† <i>Brucella melitensis</i> 16M	P(α)		X	
91	† <i>Brucella abortus</i> biovar 1 str. 9-941	P(α)		X	
92	† <i>Brucella abortus</i> (strain 2308)	P(α)		X	
93	† <i>Brucella suis</i> 1330	P(α)		X	
94	<i>Brucella suis</i> ATCC 23445	P(α)		X	
95	<i>Brucella canis</i> ATCC 23365	P(α)		X	
96	† <i>Brucella ovis</i> (strain ATCC 25840	P(α)		X	
97	† <i>Methylobacterium</i> sp. 4-46	P(α)	XX	XXXX	XX
98	† <i>Methylobacterium extorquens</i> PA1	P(α)	X	XXXXXX	XXX
99	<i>Methylobacterium chloromethanicum</i> CM4	P(α)	X	XXXXXXXX	XXXX
100	† <i>Methylobacterium populi</i> BJ001	P(α)	XX	XXXXXXXX	XX
101	† <i>Methylobacterium radiotolerans</i> ATCC 2732	P(α)	XXX	XXXXXXXX	XXXX
102	<i>Methylobacterium nodulans</i> ORS 2060	P(α)		XXX	X
103	† <i>Ochrobactrum anthropi</i> ATCC 49188	P(α)	X	X	
104	† <i>Parvibaculum lavamentivorans</i> DS-1	P(α)			X
105	<i>Hoeflea phototrophica</i> DFL-43	P(α)			X
106	<i>Parvularcula bermudensis</i> HTCC2503	P(α)	X	XX	
107	<i>alpha proteobacterium</i> HTCC2255	P(α)			X
108	† <i>Methylibium petroleiphilum</i>	P(β)		X	X
109	† <i>Limnobacter</i> sp. MED105	P(β)			XX
110	<i>Burkholderia phytofirmans</i> PsJN	P(β)	X	X	

111	† <i>Burkholderia xenovorans</i> LB400	P(β)		X	
112	† <i>Burkholderia phymatum</i> STM815	P(β)		XX	
113	<i>Ralstonia pickettii</i> 12J	P(β)	X		
114	<i>Ralstonia pickettii</i> 12D	P(β)	X		
115	† <i>Ralstonia solanacearum</i> GMI1000	P(β)		X	
116	† <i>Ralstonia solanacearum</i> UW551	P(β)		X	
117	† <i>Ralstonia metallidurans</i> CH34	P(β)			X
118	† <i>Ralstonia eutropha</i> JMP134	P(β)			X
119	† <i>Ralstonia eutropha</i> H16	P(β)			X
120	† <i>Rhodoferax ferrireducens</i> DSM 15236	P(β)			X
121	† <i>Herminiimonas arsenicoxydans</i>	P(β)		XX	X
122	† <i>Acidovorax</i> sp. JS42	P(β)			X
123	† <i>Acidovorax avenae</i> sub. <i>citrulli</i> AAC00-1	P(β)	X	X	XX
124	† <i>Polaromonas naphthalenivorans</i> CJ2	P(β)		X	XX
125	† <i>Polaromonas</i> sp. strain JS666	P(β)			X
126	† <i>Bordetella avium</i> (strain 197N)	P(β)			X
127	<i>Rubrivivax gelatinosus</i> PM1	P(β)		X	
128	† <i>Nitrospira multififormis</i> ATCC 25196	P(β)		X	
129	† <i>Delftia acidovorans</i> SPH-1	P(β)			X
130	† <i>Verminephrobacter eiseniae</i> strain EF01-2	P(β)			X
131	† <i>Polynucleobacter</i> sp. QLW-P1DMWA-1	P(β)			X
132	<i>Comamonas testosteroni</i> KF-1	P(β)			X
133	† <i>Leptothrix cholodnii</i> SP-6	P(β)			X
134	† <i>Polynucleobacter necessarius</i> STIR1	P(β)			X
135	† <i>Nitrospira multififormis</i> ATCC 25196	P(β)			X
136	† <i>Methylobacillus</i> KT	P(β)		X	
137	† <i>Azoarcus</i> sp. EbN1	P(β)		X	
138	† <i>Chromobacterium violaceum</i>	P(β)		X	
139	† <i>Xanthomonas axonopodis</i> pv. <i>citri</i> str.306	P(γ)	X	X	XX
140	† <i>Xanthomonas campestris</i> pv. <i>campestris</i> ATCC 33913	P(γ)	X	X	
141	† <i>Xanthomonas campestris</i> pv. <i>campestris</i> 8004	P(γ)	X	X	
142	† <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100	P(γ)		X	
143	† <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018	P(γ)	X	X	
144	† <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331	P(γ)	X		
145	† <i>Xanthomonas campestris</i> pv. <i>Vesicatoria</i> 85-10	P(γ)	X	X	
146	<i>Stenotrophomonas maltophilia</i> R551-3	P(γ)	X		XX
147	† <i>Pseudomonas syringae</i> van Hall 1902	P(γ)	X		
148	† <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a	P(γ)	XX	X	
149	† <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000	P(γ)	XX	X	
150	† <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i>	P(γ)	XX	X	
151	† <i>Pseudomonas fluorescens</i> PF0-1	P(γ)	X	X	
152	† <i>Pseudomonas fluorescens</i> PF-5	P(γ)	X	X	
153	† <i>Pseudomonas putida</i> KT2440	P(γ)	XX	XX	
154	† <i>Pseudomonas putida</i> F1	P(γ)	XX	XX	
155	† <i>Pseudomonas putida</i> W619	P(γ)	XX	XX	
156	† <i>Pseudomonas putida</i> GB-1	P(γ)	XX	X	
157	† <i>Pseudomonas stutzeri</i> (strain A1501)	P(γ)	X		
158	† <i>Pseudomonas mendocina</i> ymp	P(γ)		XX	
159	† <i>Pseudomonas entomophila</i> L48	P(γ)	X		
160	† <i>Pseudomonas aeruginosa</i> PAO1	P(γ)	X		
161	<i>Pseudomonas aeruginosa</i> 2192	P(γ)	X		
162	† <i>Pseudomonas aeruginosa</i> UCBPP-PA14	P(γ)	X		
163	<i>Pseudomonas aeruginosa</i> C3719	P(γ)	X		

164	† <i>Pseudomonas aeruginosa</i> PA7	P(γ)	✗		
165	† <i>Acinetobacter</i> sp. (strain ADP1)	P(γ)			XXXX
166	<i>Acinetobacter</i> sp. 93A2	P(γ)			X
167	† <i>Acinetobacter baumannii</i>	P(γ)			X
168	† <i>Psychrobacter cryohalolentis</i> (strain K5)	P(γ)			XXX
169	† <i>Psychrobacter</i> sp. PRwf-1	P(γ)			X
170	† <i>Psychrobacter arcticum</i>	P(γ)			X
171	† <i>Chromohalobacter salexigens</i> DSM 3043	P(γ)		XX	
172	<i>Oceanobacter</i> sp. RED65	P(γ)		X	X
173	† <i>Marinomonas</i> sp. MWYL1	P(γ)			XXX
174	<i>Marinomonas</i> sp. MED121	P(γ)			X
175	† <i>Alkalilimnicola ehrlichei</i> MLHE-1	P(γ)	✗		
176	<i>Thiocapsa roseopersicina</i>	P(γ)	✗		
177	† <i>Nitrosococcus oceani</i> ATCC 19707	P(γ)		X	
178	† <i>Thiomicrospira denitrificans</i> ATCC 33889	P(γ)		X	
179	<i>Beggiatoa</i> sp. PS	P(γ)			X
180	† <i>Escherichia coli</i> .	P(γ)			X
181	† <i>Escherichia coli</i> DH10B	P(γ)			X
182	† <i>Escherichia coli</i> SMS-3-5 / SECEC	P(γ)			X
183	† <i>Escherichia coli</i> ATCC 8739 / DSM 1576 / Crooks	P(γ)			X
184	<i>Escherichia coli</i> O9:H4 / HS	P(γ)			X
185	† <i>Escherichia coli</i> O6	P(γ)			X
186	† <i>Escherichia coli</i> (strain UTI89 / UPEC)	P(γ)			X
187	† <i>Escherichia coli</i> O1:K1 / APEC	P(γ)			X
188	† <i>Escherichia coli</i> O6:K15:H31 536 / UPEC)	P(γ)			X
189	† <i>Escherichia coli</i> (protein YCGF)	P(γ)			X
190	† <i>Escherichia coli</i> E24377A	P(γ)			X
191	† <i>Enterobacter</i> sp. 638	P(γ)			X
192	† <i>Enterobacter sakazakii</i> ATCC BAA-894	P(γ)			XX
193	† <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> ATCC 700721	P(γ)			XX
194	<i>Alteromonas macleodii</i> 'Deep ecotype'	P(γ)	XXX	X	X
195	<i>Alteromonadales bacterium</i> TW-7	P(γ)			X
196	† <i>Pseudoalteromonas atlantica</i> (T6c / BAA-1087)	P(γ)	✗		XX
197	<i>Pseudoalteromonas tunicata</i> D2	P(γ)			XX
198	† <i>Shewanella denitrificans</i> strain OS217	P(γ)	✗		
199	† <i>Shewanella woodyi</i> ATCC 51908	P(γ)			X
200	† <i>Shewanella oneidensis</i>	P(γ)			X
201	† <i>Shewanella</i> sp. ANA-3	P(γ)		X	
202	† <i>Shewanella</i> sp. W3-18-1	P(γ)		X	
203	† <i>Shewanella putrefaciens</i> CN-32	P(γ)		X	
204	<i>Shewanella putrefaciens</i> 200	P(γ)		X	
205	† <i>Shewanella baltica</i> OS195	P(γ)		X	
206	† <i>Shewanella baltica</i> OS185	P(γ)		X	
207	† <i>Shewanella baltica</i> OS223	P(γ)		X	
208	† <i>Shewanella</i> sp. (strain MR-7)	P(γ)		X	
209	† <i>Shewanella</i> sp. (strain MR-4)	P(γ)		X	
210	† <i>Psychromonas ingrahamii</i> (strain 37)	P(γ)			X
211	† <i>Marinobacter aquaeolei</i> VT8	P(γ)			X
212	<i>Marinobacter algicola</i> DG893	P(γ)		X	X
213	<i>Marinobacter</i> sp. ELB17	P(γ)	✗		
214	† <i>Idiomarina baltica</i> OS145	P(γ)	✗		
215	<i>Psychromonas ingrahamii</i> (strain 37)	P(γ)			X
216	<i>Neptuniibacter caesariensis</i>	P(γ)			XX
217	† <i>Methylococcus capsulatus</i> str. Bath	P(γ)		X	

218	<i>Vibrio splendidus</i> 12B01	P(γ)			X
219	<i>Vibrio</i> sp. MED222	P(γ)			X
220	<i>Vibrionales</i> bacterium SWAT-3	P(γ)			X
221	<i>Methylobacterium</i> sp. NI.	P(γ)			X
222	<i>Congregibacter litoralis</i> KT71	P(γ)U			X
223	<i>Reinekea</i> sp. MED297	P(γ)U			XX
224	marine gamma proteobacterium HTCC2080	P(γ)U			XXX
225	<i>Stigmatella aurantiaca</i> DW4/3-1	P(δ)	XX		
226	† <i>Desulfococcus oleovorans</i> Hxd3	P(δ)			X
227	<i>Desulfatibacillum alkenivorans</i> AK-01	P(δ)			X
228	† <i>Myxococcus xanthus</i> DK1622	P(δ)			X
229	† <i>Magnetococcus</i> sp. MC-1 (1)	P(Magn)			XXX
230	uncultured proteobacterium delRiverFos06H03	PUnc			X
231	uncultured proteobacterium.	PUnc			X
232	uncultured bacterium 581	PUnc			X
233	† <i>Chloroflexus aurantiacus</i> J-10-fl	Chl		X	
234	† <i>Herpetosiphon aurantiacus</i> ATCC 23779	Chl		X	
235	<i>Chloroflexus aggregans</i> DSM 9485	Chl		X	
236	† <i>Thermosynechococcus elongatus</i>	Cya	XXXXXX	X	X
237	† <i>Synechococcus</i> sp. PCC 6301	Cya	XXX	XX	
238	† <i>Synechococcus</i> sp. PCC 7942	Cya	XXX	XX	
239	† <i>Synechococcus</i> sp. JA-2-3B'a(2-13)	Cya	XXX		
241	† <i>Synechococcus</i> sp. JA-3-3Ab	Cya	XXXX		
242	† <i>Synechococcus</i> sp. PCC 7002	Cya	X	X	X
243	† <i>Synechocystis</i> sp. PCC 6803	Cya	XXXXXX XXXXX	X	X
244	† <i>Microcystis aeruginosa</i> (strain NIES-843)	Cya	XX		
245	<i>Microcystis aeruginosa</i> PCC 7806	Cya	XX		
246	<i>Cyanothece</i> PCC 8801	Cya	XXX	X	
247	† <i>Cyanothece</i> strain ATCC 51142	Cya	XXX	X	
248	<i>Cyanothece</i> sp. CCY0110	Cya	XXXXXX XXXXX	X	
249	<i>Cyanothece</i> sp. PCC 7424	Cya	XXXXX		
250	<i>Crocospaera watsonii</i>	Cya	XXXXX	X	
251	† <i>Anabaena variabilis</i> ATCC 29413	Cya	XXXXXX XXXXXX XXXXXX	XX	
252	† <i>Nostoc</i> sp. PCC 7120	Cya	XXXXXXXX XXXXXX	XX	
253	† <i>Nostoc punctiforme</i> PCC 73102	Cya	XXXXXXXXXX XXXXXXXXX XXXXXX	XX	
254	<i>Nodularia spumigena</i> CCY9414	Cya	XXXXXXXX		
255	<i>Tolypothrix</i> sp. PCC 7601	Cya	XX		
256	<i>Fremyella diplosiphon</i>	Cya	X		
257	<i>Lyngbya</i> sp. PCC 8106	Cya	XXXXXX XXXXXX XXXXXX	XXXXXX	
258	† <i>Trichodesmium erythraeum</i> (strain IMS101)	Cya	XX		
259	† <i>Acaryochloris marina</i> (strain MBIC 11017)	Cya	XXX	X	
260	† <i>Gloeobacter violaceus</i> PCC 7421	Cya	X		
261	† <i>Deinococcus radiodurans</i> R1	DeTh	X		
262	† <i>Rhodopirellula baltica</i> SH1	PI		X	X
263	<i>Leptospirillum</i> sp. Group II UBA	Nit		X	
264	<i>Pedobacter</i> sp. BAL39	Bact	X	X	X
265	<i>Polaribacter dokdonensis</i> MED152	Bact	X		X
266	<i>Dokdonia donghaensis</i> MED134	Bact	X		X
267	† <i>Gramella forsetii</i> KT0803	Bact	X		X
268	<i>Leeuwenhoekiella blandensis</i> MED217	Bact	X		
269	<i>Blastopirellula marina</i> DSM 3645	Bact	X		

270	† <i>Cytophaga hutchinsonii</i> ATCC 33406	Bact	X		
271	† <i>Flavobacterium johnsoniae</i> UW101	Bact	X		
272	<i>Flavobacterium bacterium</i> BBFL7	Bact			X
273	<i>Psychroflexus torquis</i> ATCC 700755	Bact			X
274	† <i>Bdellovibrio bacteriovorus</i> .	Bact			X
275	<i>Microscilla marina</i> ATCC 23134	Bact			X
276	unidentified eubacterium SCB49	Bact			X
277	<i>Solibacter usitatus</i> Ellin6076	AcidoB			X
278	<i>Lentisphaera araneosa</i> HTCC2155	Lent			X
	Archaea	Group	PHY	LOV	BLUF
1	† <i>Haloarcula marismortui</i> ATCC43049	EuA		XXX	
2	† <i>Natronomonas pharaonis</i> DSM 2160	EuA		XX	
3	† <i>Methanosarcina barkeri</i> str. fusaro	EuA		X	
4	† <i>Methanosarcina acetivorans</i> C2A	EuA		X	
5	† <i>Methanoculleus marisnigri</i> ATCC 35101	EuA		XXX	
6	<i>Halorubrum lacusprofundi</i> ATCC 49239	EuA		XX	

†:fully sequenced (NCBI <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi>).

‡:F: Firmicutes, low G+C Gram positives; Ac: Actinobacteria, high G+C Gram-positives; P: Proteobacteria (the class is indicated in parenthesis); **P(α)** = Rhodobacterales; **P(α)**:Rhodospirillales; **P(α)**: Parvularculales; **P(α)**:Sphingomonadales; **P(α)**: Rhizobiales; **P(α)**: Caulobacterales; **P(β)**: Burkholderiales; **P(β)**: Nitrosomonadales; **P(β)**: Neisseriales; **P(β)**:Methylophilales; **P(β)**:Rhodocyclales;**P(γ)**: Xanthomonadales; **P(γ)**: Pseudomonadales; **P(γ)**:Oceanospirillales; **P(γ)**: Chromatiales; **P(γ)**: Thiotrichales; **P(γ)**:Enterobacterales; **P(γ)**:Alteromonadales; **P(γ)**:Vibrionales; **P(γ)**: Methylococcales; U : unclassified; Unc: uncultured; **P(Magn)**: Magnetococcus; Chl: Chloroflexi; Cya: Cyanobacteria; **Cya**: Chroococcales; **Cya**: Oscillatoriales; **Cya**: Nostocales; **Cya**: Acaryochloris; **Cya**: Gloeobacteria; DeTh = Deinococcus-Thermus; Pl: Planctomycetes; Nit: Nitrospirae; Bact: Bacteroidetes; Lent: Lentisphaerae; EuA: Euryarchaeota.

170 sequenced / 665 sequenced = 25.5% of fully sequenced bacteria have one or more bilin or flavin light-sensor.

					B0IPF5 (846) PhyB5	PAS+GAF+PHY+Kinase+RR	47	+	-
					B0IQ06 (731)	PAS+GAF+PHY+PAS	48	+	-
<i>Phaeobacter gallaeciensis</i> 2.10		P(α)	27		A9EIW8 (858)	PAS+GAF+PHY+Kinase+RR	49	+	-
<i>Phaeobacter gallaeciensis</i> BS107		P(α)	28		A9FWA3 (858)	PAS+GAF+PHY+Kinase+RR	50	+	-
† <i>Bradyrhizobium</i> sp. BTAi1		P(α)	29		A5EEA8 (842)	PAS+GAF+PHY+Kinase+RR	51	+	-
					A4YPN9 (853)	PAS+GAF+PHY+Kinase+RR	52	+	-
					A5EQ94 (723)	PAS+GAF+PHY+PAS	54	+	-
					A5EGA4 (783)	PAS+GAF+PHY+Kinase	55	+	-
† <i>Bradyrhizobium</i> sp. ORS278		P(α)	30		Q8VUB6 (724)	PAS+GAF+PHY+PAS	56	+	-
					A4YMN8 (620)	PAS+GAF (+STAS on the genome)	57	-	+
† <i>Rhizobium leguminosarum</i> bv <i>viciae</i> 3841		P(α)	31		Q1MCX7 (855)	PAS+GAF+PHY+Kinase+RR	58	+	-
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304		P(α)	32		B1CE93 (856)	PAS+GAF+PHY+Kinase+RR	59	+	-
					Q0REY5 (420)	PAS+GAF+PHY	60	+	-
<i>Rhizobium leguminosarum</i>		P(α)	33		Q936K0 (855) bphP	PAS+GAF+PHY+Kinase+RR	61	+	-
<i>Methylocella silvestris</i> BL2		P(α)	34		B1TJ66 (771)	PAS+GAF+PHY+Kinase	62	+	-
					B1TU48 (552)	GAF+PHY+Kinase	63	-	-
† <i>Azorhizobium caulinodans</i> ORS 571		P(α)	35		A8HU76 (850)	PAS+GAF+PHY+Kinase+RR	64	+	-
<i>Fulvmarina pelagi</i> HTCC2506		P(α)	36		Q0G229 (888)	PAS+GAF+PHY+Kinase+RR	65	+	-
† <i>Agrobacterium tumefaciens</i> str. C58		P(α)	37		Q7CY45 (745)	PAS+GAF+PHY+Kinase	66	+	-
					A9CI81 (850)	PAS+GAF+PHY+Kinase+RR	67	+	-
† <i>Xanthobacter autotrophicus</i> str. <i>Pv2</i>		P(α)	38		A7II43 (721)	PAS+GAF+PHY+Kinase	68	+	-
<i>Aurantimonas</i> sp. SI85-9A1		P(α)	39		Q1YII9 (726)	PAS+GAF+PHY+Kinase	69	+	-
† <i>Methylobacterium</i> sp. 4-46		P(α)	40		B0UDE6 (762)	PAS+GAF+PHY+Kinase	70	+	-
					B0UNZ0 (864)	PAS ₂ +GAF+PHY+Kinase	71	+	-
† <i>Methylobacterium extorquens</i> PA1		P(α)	41		A9W8V2 (895)	PAS+GAF+PHY+Kinase	72	+	-
<i>Methylobacterium chloromethanicum</i> CM4		P(α)	42		A7W1E9 (895)	PAS+GAF+PHY+Kinase	73	+	-
† <i>Methylobacterium populi</i> B1001		P(α)	43		B1ZK65 (751)	PAS+GAF+PHY+Kinase	74	+	-
					B1ZGY2 (874)	PAS+GAF+PHY+Kinase	75	+	-
† <i>Methylobacterium radiotolerans</i> ATCC 27329		P(α)	44		B1M9J3 (849)	PAS+GAF+PHY+Kinase+RR	76	+	-
					B1M2J7 (751)	PAS+GAF+PHY+Kinase	77	+	-
					B1LWZ3 (871)	PAS+GAF+PHY+Kinase	78	+	-
† <i>Ochrobactrum anthropi</i> ATCC 49188		P(α)	45		A6X7F4 (844)	PAS+GAF+PHY+Kinase+RR	79	+	-
<i>Parvularcula bermudensis</i> HTCC2503		P(α)	46		A3VTF3 (867)	PAS+GAF+PHY+Kinase+RR	80	+	-
† <i>Burkholderia phytofirmans</i> PsJN		P(β)	47		A0GUM8 (791)	PAS+GAF+PHY+Kinase	81	+	-
† <i>Ralstonia pickettii</i> 12J		P(β)	48		A1HAE2 (762)	PAS+GAF+PHY+Kinase	82	-	-
<i>Ralstonia pickettii</i> 12D		P(β)	49		A7CHP2 (763)	PAS+GAF+PHY+Kinase	83	-	-
† <i>Acidovorax avenae</i> sub. <i>citrulli</i> AAC00-1		P(β)			A1TRF7 (567)	PAS+GAF	84	+	-
† <i>Xanthomonas axonopodis</i> pv. <i>citri</i> str.306		P(γ)	50		Q8PEQ2 (634)	PAS+GAF+PHY+PAS	85	+	-
† <i>Xanthomonas campestris</i> pv. <i>campestris</i> ATCC 33913		P(γ)	51		Q8P3C2 (634)	PAS+GAF+PHY+PAS	86	+	-
† <i>Xanthomonas campestris</i> pv. <i>campestris</i> 8004		P(γ)	52		Q4UNL4 (634)	PAS+GAF+PHY+PAS	87	+	-
					B0RZ52 (634)	PAS+GAF+PHY+PAS	88	+	-
† <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018		P(γ)	53		Q2P8V8 (634)	PAS+GAF+PHY+PAS	89	+	-
† <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331		P(γ)	54		Q5H674 (634)	PAS+GAF+PHY+PAS	90	+	-
† <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i>		P(γ)	55		Q3BM90 (634)	PAS+GAF+PHY+PAS	91	+	-
<i>Stenotrophomonas maltophilia</i> K279a		P(γ)	56		B2FRG9 (745)	PAS+GAF+PHY+Kinase	92	+	-
† <i>Pseudomonas syringae</i> van Hall 1902		P(γ)	57		Q8RPQ4 (744)	PAS+GAF+PHY+Kinase	93	+	-

† <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i>	P(γ)	60	Q48G81 (745) Q4LBM8 (797)	PAS+GAF+PHY+Kinase	98	+	-
† <i>Pseudomonas fluorescens</i> PF0-1	P(γ)	61	Q3KEA1 (745)	PAS+GAF+PHY+Kinase	99	+	-
† <i>Pseudomonas fluorescens</i> PF-5	P(γ)	61	Q4K656 (746)	PAS+GAF+PHY+Kinase	100	+	-
† <i>Pseudomonas putida</i> KT2440	P(γ)	62	Q88KD4 (755) Q88HJ2 (847)	PAS+GAF+PHY+Kinase	101	+	-
† <i>Pseudomonas putida</i> F1	P(γ)	63	A5W5Q5 (748) A5W323 (847)	PAS+GAF+PHY+Kinase	102	+	-
† <i>Pseudomonas putida</i> W619	P(γ)	64	B1J6D2 (756) B1J8C3 (844)	PAS+GAF+PHY+Kinase	103	+	-
† <i>Pseudomonas putida</i> GB-1	P(γ)	65	B0KKF3 (748) B0KSG0 (847)	PAS+GAF+PHY+Kinase	104	+	-
† <i>Pseudomonas stutzeri</i> (strain A1501)	P(γ)	66	A4V553 (756)	PAS+GAF+PHY+Kinase	105	+	-
† <i>Pseudomonas entomophila</i> L48	P(γ)	67	Q11877 (746)	PAS+GAF+PHY+Kinase	106	+	-
† <i>Pseudomonas aeruginosa</i> PAO1	P(γ)	68	Q9HWR3 (728)	PAS+GAF+PHY+Kinase	107	+	-
<i>Pseudomonas aeruginosa</i> 2192	P(γ)	69	A3LFL2 (728)	PAS+GAF+PHY+Kinase	108	+	-
† <i>Pseudomonas aeruginosa</i> UCBPP-PA14	P(γ)	70	Q02ST1 (728)	PAS+GAF+PHY+Kinase	109	+	-
† <i>Pseudomonas aeruginosa</i> C3719	P(γ)	71	A3KZ15 (728)	PAS+GAF+PHY+Kinase	110	+	-
† <i>Pseudomonas aeruginosa</i> PA7	P(γ)	72	A6UZX6 (728)	PAS+GAF+PHY+Kinase	111	+	-
† <i>Alkallimnicola ehrlichei</i> MLHE-1	P(γ)	73	Q0A8J1 (689)	PAS+GAF+PHY+Kinase	112	+	-
<i>Thicapsa roseopersicina</i>	P(γ)	74	Q2TJQ7 (729)	PAS+GAF+PHY+Kinase	113	+	-
<i>Alteromonas macleodii</i> 'Deep ecotype'	P(γ)	75	A4B0I5 (884) A4B2B9 (908) A4B0P1 (853)	PAS+GAF+PHY+Kinase	114	+	-
† <i>Pseudoalteromonas atlantica</i> (T6c / BAA-1087)	P(γ)	76	Q15YT5 (799)	PAS+GAF+PHY+Kinase	116	+	-
† <i>Shewanella denitrificans</i> strain OS217	P(γ)	77	Q12SQ8(710)	GAF+PHY+GGDEF+EAL	117	+	-
<i>Marinobacter</i> sp. <i>ELB17</i>	P(γ)	78	A3J9Q2(1020)	PAS+GAF+PHY+GGDEF+EAL	118	+	-
† <i>Idiomarina baltica</i> OS145	P(γ)	79	A3WMD3 (689)	PAS+GAF+PHY+GGDEF	119	+	-
<i>Stigmatella aurantiaca</i> DW4/3-1	P(δ)	80	Q097N3 (760) Q09E27 (747)	PAS+GAF+PHY+Kinase	120	+	-
† <i>Thermosynechococcus elongatus</i>	Cya	81	Q8DHG0(790) Q8DKE8(1240) Q8DLC7 (940) PixJ	RR+GAF+GGDEF+EAL PAS ₃ +GAF+PAS+GGDEF+EAL Hamp+GAF+Hamp+MCP	121	+	-
† <i>Synechococcus</i> sp. PCC 6301	Cya	82	Q8DKG0 (729) Cika Q8DKD5 (773)	GAF+Kinase+RR CBS ₂ + PAS + GAF+GGDEF	122	+	-
† <i>Synechococcus</i> sp. PCC 7942	Cya	83	Q5N3P8 (754) Cika Q5N497 (1406) Q5N1Q4(438)	GAF+Kinase+RR Hamp+GAF ₅ +Hamp+MCP GAF+GGDEF	123	+	-
† <i>Synechococcus</i> sp. JA-2-3B'a(2-13)	Cya	84	Q9KH15 (754) Cika Q31PY1(1406) Q31K55(421)	GAF+Kinase+RR Hamp+GAF ₅ +Hamp+MCP GAF+GGDEF	124	+	-
† <i>Synechococcus</i> sp. JA-3-3Ab	Cya	85	Q2JUZ5 (834) Q2JP01(1526) Q2JKQ1(1247)	GAF+GAF+GAF + Kinase GAF+Chase+PAS ₂ + GAF+Kinase+RR2+Hpt PAS ₃ + GAF+GAF + Kinase	125	+	-
† <i>Synechococcus</i> sp. PCC 7002	Cya	86	Q2JR82 (835) Q2JR31 (1523) Q2JXK5 (1036)	GAF+GAF+GAF + Kinase GAF+Chase+PAS ₂ + GAF+Kinase+RR2+Hpt PAS ₃ + GAF+GAF + Kinase	126	+	-
† <i>Synechocystis</i> sp. PCC 6803	Cya	87	Q2JRS4 (1151) B1XIW2 (760) Cika	PAS ₅ + GAF+GAF + Kinase GAF+ Kinase+RR	127	+	-
			Q55168 (748) Cph1 Q55434 (1276)Cph2	PAS+GAF+PHY+Kinase GAF+GAF+EAL +GAF+GGDEF	128	+	+

[illegible]

† <i>Nostoc punctiforme</i> PCC 73102	Cya	97	Q8YPD6 (1036)	GAF ₄ + Kinase	208	-	+			
			Q8YXY7 (1102)	GAF ₄ +Hamp+MCP	209	-	+			
			Q8YSG5 (1286)	CBS ₂ +GAF+PAS+GAF+Kinase +RR	210	-	+			
			Q8YVK9 (879)	GAF+PAS ₇ +GAF+Kinase	211	-	+			
			Q8YQX0 (2021)	Kinase+GAF ₂ +Kinase	212	-	+			
			Q8YYW3 (1645)	RR+GAF+PAS+GAF+PAS+GAF+Kinase+RR	213	-	+			
			Q8YWC5 (676)	CikA	214	-	+			
			B2J2D1 (768)	PAS+GAF+PHY+Kinase	215	-	+			
			B2JWG3 (775)	PAS+GAF+PHY+Kinase	216	-	+			
			B2J4E4 (910)	GAF+GAF+GAF+ Kinase	217	-	+			
			B2J2J0 (706)	GAF+GAF+ Kinase	218	-	+			
			B2JZ18 (1102)	GAF+GAF+GAF ₂ + Kinase	219	-	+			
			B2J3R7 (858)	GAF+GAF ₃	220	-	+			
			B2J0R5 (1042)	GAF ₂ + GAF+GAF+ Kinase	221	-	+			
			B2J1U4 (1102)	GAF ₄ +Hamp+MCP	222	-	+			
			B2J668 (1745)	GAF+ GAF +GAF ₂ + GAF ₃ +MCP	223	-	+			
			<i>Nodularia spumigena</i> CCY9414	Cya	98	B2JAC4 (1204)	GAF+GAF+GAF ₂ + Kinase	224	-	+
B2J1W6 (1504)	RR+ GAF +PAS ₆ +Kinase+RR	225				-	+			
B2IVB0 (742)	EAL+ GAF+GGDEF	226				-	+			
B2J469 (750)	GAF+PAS ₂ +GAF+Kinase	227				-	+			
B2J261 (1005)	GAF ₁ +GAF+ Kinase	228				-	+			
B2J457 (878)	GAF+GAF+PAS ₂ + Kinase+RR	229				-	+			
B2JZ18 (1102)	GAF ₄ +Hamp+MCP	230				-	+			
B2IVK2 (1060)	GAF ₄ + Kinase	231				-	-			
B2JU03 (651)	PAS ₂ +GAF+ Kinase	232				-	+			
B2IV55 (683)	CikA	233				-	+			
B2J4E4 (910)	GAF ₃ + Kinase	234				-	+			
A0ZC04 (752)	PAS+GAF+PHY+Kinase	235				+	-			
A0ZGM2 (765)	PAS+GAF+PHY+Kinase	236				-	+			
A0ZJ29 (472)	PAS+GAF+Kinase	237				-	+			
A0ZGP9 (1613)	GAF+PAS ₈ +GAF+GGDEF	238				-	+			
A0ZB66 (1508)	GAF+CHASE+GAF+GAF+Kinase+RR ₂ +Hpt	239				-	+			
<i>Tolypothrix</i> sp. PCC 7601	Cya	99				A0ZA61 (1045)	CBS ₂ +GAF+PAS+ Kinase +RR	240	-	+
			A0ZEQ4 (850)	GAF+PAS ₂ +GAF+Kinase	241	-	+			
			Q8RTN1 (767)	PAS+GAF+PHY+Kinase	242	-	+			
			Q8RTM9 (765)	PAS+GAF+PHY+Kinase	243	+	-			
			Q47897 (655)	RcaE	244	-	+			
			A0YWS9 (766)	gph1	245	-	+			
			A0YIU6 (816)	PAS+GAF+GGDEF	246	-	+			
			A0YLL7 (872)	GAF+GAF+GGDEF+EAL	247	-	+			
			A0YPG3 (925)	GAF+GAF+GAF+ Kinase	248	-	+			
			A0YVG7 (1016)	PAS+GAF+PHY+Kinase+RR	249	+	-			
			A0YIR3 (1111)	GAF+GAF+GAF+GAF+ Kinase	250	-	+			
			A0YP66 (1781)	CBS ₂ +PAS ₃ +LOV ₁ +GAF+PA S ₁ +Kinase	251	-	+			
			A0YM62 (1008)	CBS+GAF+GAF+GAF+Kinase	252	-	+			
			A0YVN1 (1252)	GAF+LOVH+PAS ₄ +GGDEF	253	-	+			
			A0YM29 (1311)	GAF ₅ +HAMP+MCP	254	-	+			
			<i>Frémyella diplosiphon</i> <i>Lyngbya</i> sp. PCC 8106	Cya	100 101	A0YXJ8 (1027)	GAF+GAF+Kinase+RR	255	-	+
						A0YUF0 (641)	CikA	256	-	+
A0YVU5 (767)	GAF ₂ +GAF+GGDEF	257				-	+			
A0YSU9 (1295)	GAF ₃ +GAF+MCP	258				-	+			
A0YQX7 (799)	CBS ₂ +GAF+ Kinase	259				-	-			
A0YP49 (1291)	GAF ₅ + MCP	260				-	+			
A0YMU5 (1260)	GAF+GAF+GGDEF+EAL+GAF+GGDEF	261				-	+			
A0YPG2 (703)	GAF ₂ + Kinase	262				-	+			
Q118C6 (1313)	GAF ₅ +HAMP+MCP	263				-	+			

† *Trichodesmium erythraeum* (strain IMS101)

† <i>Acaryochloris marina</i> (strain MBIC 11017)				Q115W0 (853) CkA B0CF10 (735) CkA B0C8Z0 (929) B0C1J9 (847)	GAF+Kinase+RR GAF+Kinase+RR GAF ₂ +Kinase+RR PAS+GAF+PHY+Kinase	- - - +	264 265 266 267	- - - +
† <i>Gloeobacter violaceus</i> PCC 7421				Q7NFU2 (566)	PAS+GAF+PHY+Kinase	-	268	+
† <i>Deinococcus radiodurans</i> R1	DeTh			Q9RZA4 (755)	PAS+GAF+PHY+Kinase	+	269	-
<i>Pedobacter</i> sp. BAL39	Bact			A6EDC8 (737) A6EEB3 (509)	PAS+GAF+PHY+Kinase PAS+GAF+PHY	+	270 271	- -
<i>Polaribacter dokdonensis</i> MED152	Bact			A2TX11 (850)	PAS+GAF+PHY+Kinase+RR	+	272	-
<i>Doktonia donghaensis</i> MED134	Bact			A2TTK4 (749)	PAS+GAF+PHY+Kinase	+	273	-
† <i>Gramella forsetii</i> KT0803	Bact			A0M2S9 (737)	PAS+GAF+PHY+Kinase	+	274	-
<i>Leeuwenhoekiella blandensis</i> MED217	Bact			A3XMS7 (737)	PAS+GAF+PHY+Kinase	+	275	-
<i>Blastopirellula marina</i> DSM 3645	Bact			A4A1X6 (754)	PAS+GAF+PHY+Kinase	+	276	-
† <i>Cytophaga hutchinsonii</i> ATCC 33406	Bact			Q11VQ8 (506) Q11YS3 (752)	PAS+GAF+PHY PAS+GAF+PHY+Kinase	+	277 278	- -
† <i>Flavobacterium johnsoniae</i> UW101	Bact			A5FCX0 (757) A5FD80 (755)	PAS+GAF+PHY+Kinase PAS+GAF+PHY+Kinase	+	279 280	- -
<i>Kordia algicida</i> OT-1	Bact			A9E8J4 (753)	PAS+GAF+PHY+Kinase	+	281	-

† : fully sequenced (NCBI <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi>).

‡: Firmicutes, low G+C Gram positives; Ac: Actinobacteria, high G+C Gram-positives; P: Proteobacteria (the class is indicated in parenthesis); **P(α)** = Rhodobacterales; **P(α)**: Rhodospirillales; **P(α)**: Parvularculales; **P(α)**: Sphingomonadales; **P(α)**: Rhizobiales; **P(α)**: Caulobacteriales; **P(β)**: Burkholderiales; **P(β)**: Nitrosomonadales; **P(β)**: Neisseriales; **P(γ)**: Xanthomonadales; **P(γ)**: Pseudomonadales; **P(γ)**: Oceanospirillales; **P(γ)**: Chromatiales; **P(γ)**: Thiotrichales; **P(γ)**: Enterobacteriales; **P(γ)**: Alteromonadales; **P(γ)**: Vibrionales; **P(γ)**: Methyloboccales; **P(γ)**: Nostocales; **Cya**: Acaryochloris; **Cya**: Gloeobacteria; DeTh = Deinococcus-Thermus; Pi: Planctomycetes; Nit: Nitrospirae; Bact: Bacteroidetes; Lent: Lentisphaerae; EuA: Euryarchaeota.

§: classification of domains as in the Interpro database. ¹ **STAS**: Sulphate transporter/antisigma-factor antagonist; SPOIIE: Sporulation stage II, protein E C-terminal/Protein phosphatase 2C-related; GAF: domain first found in cGMP-specific cyclic nucleotide phosphodiesterase, **A**denylyl cyclase, and **F**hIA, when in bold (**GAF**) is recognized as a site for phytochrome chromophore binding; PHY: Phytochrome, central region; GGDEF: named after a conserved sequence, synthesizes cyclic di-GMP; EAL: named after a conserved sequence; cyclic di-GMP phosphodiesterase; Kinase: here always Histidine kinase; PAS: first found in **Per**, **Arnt** and **SimS** proteins, structurally the same as a LOV domain; RR = CheY-type Response regulator, receiver domain; HTH: Helix-turn-Helix regulatory protein, DNA-binding; HAMP: domain for histidine kinases, adenyllyl cyclases, methyl binding proteins and phosphatases; Hpt : subdomain, transphosphorylation; MCP: MCPsignal, bacterial chemotaxis sensory transducer.

- 1 N. J. Mulder, R. Apweiler, T. K. Attwood, A. Bairoch, D. Barrell, A. Bateman, M. Biswas, P. Bucher, R. R. Copley, E. Courcelle, U. Das, R. Durbin, L. Falquet, W. Fleischmann, S. Griffiths-Jones, D. Haft, N. Harte, N. Hulo, D. Kahn, A. Kanapin, M. Krestyaninova, R. Lopez, I. Letunic, D. Lonsdale, V. Silventoinen, S. E. Orchard, M. Pagni, D. Peyruc, C. P. Ponting, J. Selengut, F. Servant, C. J. Sigrist, R. Vaughan and E. M. Zdobnov, The InterPro Database, 2003 brings increased coverage and new features., *Nucl. Acids Res.*, 2003, **31**, 315-318.

73 fully sequenced /665 bacteria = 10.9%

Table S3: LOV proteins in prokaryotes.

Bacteria				Proteins			
Species/strain	*Group	Nr.	Accession (aa)	[§] Domain structure	Nr.		
† <i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	F	1	O34627-YtvA (261)	LOV+STAS	1		
† <i>Bacillus amyloliquefaciens</i> FZB42	F	2	A7Z7V9 (261)	LOV+STAS	2		
† <i>Oceanobacillus iheyensis</i> HTE831	F	3	Q8ESN8 (264)	LOV+STAS	3		
† <i>Bacillus pumilus</i> SAFR-032	F	4	A8FGG2 (267)	LOV+STAS	4		
			A8FI66 (262)	LOV+STAS	5		
<i>Bacillus selenitireducens</i> MLS10		5	A8W065 (265)	LOV+STAS	6		
† <i>Listeria monocytogenes</i> EGD-e	F	6	P58724 (253)	LOV+STAS	7		
<i>Listeria monocytogenes</i> F6900	F	7	A4DSW3 (253)	LOV+STAS	8		
<i>Listeria monocytogenes</i> FSLN3-165	F	8	A4DK24 (253)	LOV+STAS	9		
<i>Listeria monocytogenes</i> 10403S	F	9	A3G852 (253)	LOV+STAS	10		
<i>Listeria monocytogenes</i> J016	F	10	A3FT85 (253)	LOV+STAS	11		
<i>Listeria monocytogenes</i> J2818	F	11	A3G0P2 (253)	LOV+STAS	12		
<i>Listeria monocytogenes</i> HPB2262	F	12	A4E0Q0 (253)	LOV+STAS	13		
<i>Listeria monocytogenes</i> FSL N1-017	F	13	A4DCD4 (253)	LOV+STAS	14		
<i>Listeria monocytogenes</i> F6854	F	14	Q4EN15 (253)	LOV+STAS	15		
† <i>Listeria monocytogenes</i> F2365	F	15	Q722B8 (253)	LOV+STAS	16		
† <i>Listeria monocytogenes</i> str. 4b H7858	F	16	Q4EEF6 (253)	LOV+STAS	17		
† <i>Listeria innocua</i> Clip11262	F	17	Q92DM1 (253)	LOV+STAS	18		
† <i>Listeria welshimeri</i> serovar 6b str. SLCC5334	F	18	A0AGP3 (253)	LOV+STAS	19		
† <i>Rubrobacter xylanophilus</i> DSM 9941	Ac	19	Q1ARZ9 (581)	LOV+GAF+SpolIE	20		
† <i>Kineococcus radiotolerans</i> SRS30216	Ac	20	A6WG47 (743)	GGDEF+LOV+EAL	21		
			A6W4U8 (723)	LOV+GAF+SpolIE	22		
			A6W4X7 (408)	LOV+SpolIE	23		
† <i>Arthrobacter aureus</i> TC1	Ac	21	A1RDS2 (727)	LOV+ GGDEF+EAL	24		
† <i>Rhodobacter sphaeroides</i> ATCC 17023	P(α)	22	Q3J4A0 (176)	Short LOV	25		
† <i>Rhodobacter sphaeroides</i> ATCC 17029	P(α)	23	A3PI49 (176)	Short LOV	26		
<i>Roseobacter</i> sp. CCS2	P(α)	24	A4EHF4 (175)	Short LOV	27		
			A4EIJ8 (181)	Short LOV	28		
<i>Roseobacter litoralis</i> Och 149	P(α)	25	A9HBJ6 (350)	LOV+ Kinase	29		
† <i>Roseobacter denitrificans</i> Och 114	P(α)	26	Q167W8 (350)	LOV+ Kinase	30		
<i>Roseovarius</i> sp. HTCC2601	P(α)	27	Q0FR10 (182)	Short LOV	31		
† <i>Dinoroseobacter shibae</i> DFL 12	P(α)	28	A8LHT0 (338)	LOV+ Kinase	32		
			A8LNC2 (920)	LOV+PAS+PAS+Kinase+RR	33		
			A8LP63 (139)	Short LOV	34		
<i>Sagittula stellata</i> E-37	P(α)	29	A3K7J8 (169)	Short LOV	35		
<i>Oceanicola granulosus</i>	P(α)	30	Q2CIF5 (341)	LOV+ Kinase	36		
<i>Oceanibulbus indolifex</i> HEL-45	P(α)	31	A9DXF0 (354)	LOV+ Kinase	37		
† <i>Caulobacter crescentus</i> CB15	P(α)	32	Q9ABE3 (449)	LOV+ Kinase	38		

† <i>Caulobacter</i> sp. K31	P(α)	33	BOT3W0 (360)	LOV+ Kinase	39
			BOT127 (369)	LOV+ Kinase	40
			BOT3W1 (922)	LOV+PAS ₃ +Kinase+RR	41
<i>Granulobacter bethesdensis</i>	P(α)	34	Q0BT22 (185)	Short LOV	42
<i>Magnetospirillum magnetotacticum</i>	P(α)	35	ZP_00051334 (425)	LOV+ Kinase	43
			ZP_00052303 (358)	LOV+ Kinase	44
† <i>Erythrobacter litoralis</i> HTCC2594	P(α)	36	Q2NB98 (225)	LOV+HTH	45
			Q2NB77 (346)	LOV+ Kinase	46
			Q2N9L9 (362)	LOV+ Kinase	47
			Q2NCA3 (360)	LOV+ Kinase	48
			A5PBU7 (359)	LOV+ Kinase	49
<i>Erythrobacter</i> sp. SD-21	P(α)	37			
<i>Erythrobacter</i> sp. NAP1	P(α)	38	A3WAQ8 (358)	LOV+ Kinase	50
† <i>Sphingopyxis alaskensis</i> RB2256	P(α)	39	Q1GUF5 (195)	LOV+HTH	51
<i>Sphingomonas</i> sp. SKA58	P(α)	40	Q1N7J1 (238)	LOV+HTH	52
† <i>Novosphingobium aromaticivorans</i> DSM 12444	P(α)	41	Q1NI33 (570)	LOV+Kinase+RR	53
			Q2G5U0 (364)	LOV+ Kinase	54
			Q2G8Z7 (223)	LOV+HTH	55
† <i>Bradyrhizobium</i> sp. BTA1	P(α)	42	A5EAE7 (534)	LOV+Kinase+RR	56
† <i>Bradyrhizobium</i> sp. ORS278	P(α)	43	A4Z279 (534)	LOV+Kinase+RR	57
† <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325	P(α)	44	Q1M667 (345)	LOV+ Kinase	58
<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841	P(α)	45	B0JC21 (342)	LOV+ Kinase	59
			B0JAE2 (281)	LOV+ Kinase	60
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304	P(α)	46	B1CL99 (306)	LOV+ Kinase	61
<i>Fulvimarina pelagi</i> HTCC2506	P(α)	47	Q0G496 (420)	LOV+ Kinase	63
<i>Aurantimonas</i> sp. SI85-9A1	P(α)	48	Q1YFS4 (389)	LOV+ Kinase	64
			Q1YEU2 (415)	LOV+ Kinase	65
† <i>Brucella melitensis</i> 16M	P(α)	49	Q8YC53 (489)	LOV+PAS+ Kinase	66
† <i>Brucella abortus</i> biovar 1 str. 9-941	P(α)	50	Q577Y7 (458)	LOV+PAS+ Kinase	68
† <i>Brucella abortus</i> (strain 2308)	P(α)	51	Q2YKK7 (463)	LOV+PAS+ Kinase	69
† <i>Brucella suis</i> 1330	P(α)	52	Q8FW73 (463)	LOV+PAS+ Kinase	70
<i>Brucella suis</i> ATCC 23445	P(α)	53	A9WYQ7 (463)	LOV+PAS+ Kinase	71
<i>Brucella canis</i> ATCC 23365	P(α)	54	A9MBM8 (463)	LOV+PAS+ Kinase	72
† <i>Brucella ovis</i> (strain ATCC 25840	P(α)	55	A5VUS1 (463)	LOV+PAS+ Kinase	73
† <i>Methylobacterium</i> sp. 4-46)	P(α)	56	B0UAI7 (812)	LOV+PAS ₂ +Kinase+RR	74
			B0UDT0 (544)	LOV+Kinase+RR	75
			B0UC38 (368)	LOV+Kinase	76
			A9VYT5 (533)	LOV+Kinase+RR	77
			A9W705 (354)	LOV+Kinase	78
† <i>Methylobacterium extorquens</i> PA1	P(α)	57	A9W8Q8 (366)	LOV+Kinase	79
			A9W392 (541)	LOV+Kinase+RR	80
			A9W124 (488)	LOV+Kinase	81
			A7WBJ1 (533)	LOV+Kinase+RR	82
			A7W6D6 (354)	LOV+Kinase	83
<i>Methylobacterium chloromethanicum</i> CM4	P(α)	58	A7W1J2 (366)	LOV+Kinase	84
			A7WC15 (890)	LOV+PAS+GAF+Kinase+RR	85
			A7W014 (541)	LOV+Kinase+RR	86

† Methylobacterium populi BJ001	P(α)	59	A7W7Z9 (488) B1Z812 (488) B1ZJK1 (531) B1ZCH2 (888) B1ZG87 (541) B1ZKQ8 (354) B1ZGT9 (366) B1ZHH6 (190) B1Z110 (901)	LOV+PAS+ Kinase LOV+PAS+ Kinase LOV+Kinase+RR LOV+PAS+GAF+Kinase+RR LOV+Kinase+RR LOV+Kinase Short LOV LOV+PAS ₃ +GAF+Kinase	87 88 89 90 91 92 93 94 95
† Methylobacterium radiotolerans ATCC 27329	P(α)	60	B1M4A2 (186) B1LWD2 (334) B1LUV7 (539) B1M516 (164) B1LSK7 (503) B1M4V9 (812) A9FG42 (357) A9G4X2 (559) A9HHIP8 (814) A6X554 (491) A3VPU8 (367) A3VTS2 (361)	Short LOV LOV+ Kinase LOV+Kinase+RR Short LOV LOV+PAS+Kinase LOV+PAS ₂ +Kinase+RR Short LOV LOV+Kinase+RR LOV+PAS ₂ +Kinase+RR LOV+PAS+ Kinase LOV+ Kinase LOV+ Kinase	96 97 98 99 100 101 102 103 104 105 106 107
Methylobacterium nodulans ORS 2060	P(α)	61	A2SIR0 (1317) A0GKF8 (1036) B1FWL0 (1036) Q145M2 (1036) A0FWN5 (533) A0FQ81 (1040) Q8XT61 (1178) A3RWI2 (1234) A4G7R2 (313) A4G3M6 (818) A1TT27 (544)	GAF+PAS ₃ +LOV+PAS ₂ +Kinase+ RR PAS+PAS+LOV+ GGDEF+EAL PAS+PAS+LOV+ GGDEF+EAL PAS+PAS+LOV+ GGDEF+EAL LOV+Kinase+RR PAS ₂ +LOV+GGDEF+EAL HAMP+PAS ₂ +LOV+GGDEF+EAL HAMP+PAS ₂ +LOV+GGDEF+EAL LOV+GGDEF RR+PAS+LOV+GGDEF+EAL LOV+Kinase+RR	108 109 110 111 112 113 114 115 116 117 118
† Ochrobactrum anthropi ATCC 49188	P(α)	62	A1VS30 (389)	LOV+ Kinase	119
† Parvularcula bermudensis HTCC2503	P(α)	63	ZP_00244844 (1317) Q2Y837 (152)	GAF+PAS ₃ +LOV+PAS ₂ +Kinase+ RR Short-LOV	120 121
† Methylilbium petroleiphilum PM1	P(β)	64	Q1GXZ6 (1238) Q8P4K8 (698) Q8PJH6 (540) Q8P827 (540) Q4UW16 (540) BORRL1 (540) Q2P134 (540) Q3BRX8 (540) Q4ZSY3 (534)	NMT1+LOV+GAF+PAS+ GGDEF+EAL Globin+LOV+GGDEF+EAL LOV+Kinase+RR LOV+Kinase+RR LOV+Kinase+RR LOV+Kinase+RR LOV+Kinase+RR LOV+Kinase+RR LOV+Kinase+RR	122 123 124 125 126 127 128 129 130
† Burkholderia phytofirmans PsJN	P(β)	65			
Burkholderia graminis C4D1M	P(β)	66			
† Burkholderia xenovorans LB400	P(β)	67			
† Burkholderia phymatum STM815	P(β)	68			
† Ralstonia solanacearum GM1000	P(β)	69			
† Ralstonia solanacearum UW551	P(β)	70			
† Hermiinilimonas arsenicoxydans	P(β)				
† Acidovorax avenae sub. citrulli AAC00-1	P(β)	71			
† Polaromonas naphthalenivorans CJ2	P(β)	72			
Rubrivivax gelatinosus PM1	P(β)	73			
† Nitrosospora multiformis ATCC 25196	P(β)	74			
† Methylobacillus KT	P(β)	75			
† Azoarcus sp. EbN1	P(β)	76			
† Xanthomonas axonopodis pv. citri str. 306	P(γ)	77			
† Xanthomonas campestris pv campestris ATCC 33913	P(γ)	78			
† Xanthomonas campestris pv campestris 8004	P(γ)	79			
† Xanthomonas campestris pv. campestris B100	P(γ)	80			
† Xanthomonas oryzae pv. oryzae MAFF 311018	P(γ)	81			
† Xanthomonas campestris pv. vesicatoria 85-10	P(γ)	82			
† Pseudomonas syringae pv. syringae B728a	P(γ)	83			

† <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000	P(y)	84	Q881J7 (534)	LOV+Kinase+RR	131
† <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A	P(y)	85	Q48IV1 (507)	LOV+Kinase+RR	132
† <i>Pseudomonas stutzeri</i> (strain A1501)	P(y)	86	A4VKZ3 (146)	Short-LOV	133
† <i>Pseudomonas fluorescens</i> PF0-1	P(y)	87	Q3KHW7 (158)	Short LOV	134
† <i>Pseudomonas fluorescens</i> PF-5	P(y)	88	Q4KI48 (152)	Short LOV	135
† <i>Pseudomonas putida</i> KT2440	P(y)	89	Q88E39 (142)	Short LOV	136
			Q88JB0 (151)	Short LOV	137
† <i>Pseudomonas putida</i> F1	P(y)	90	A5W8Z9 (142)	Short LOV	138
			A5W4T2 (148)	Short LOV	139
† <i>Pseudomonas putida</i> W619	P(y)	91	B1JAC4 (148)	Short LOV	140
			B1J385 (152)	Short LOV	141
† <i>Pseudomonas putida</i> GB-1	P(y)	92	B0KGV4 (142)	Short LOV	142
† <i>Pseudomonas mendocina</i> ymp	P(y)	93	A4XP68 (1254)	MASE1+LOV+PAS ₂ + GGDEF+EAL	143
			A4XXH1 (148)	Short LOV	144
† <i>Chromohalobacter salexigens</i> DSM 3043	P(y)	94	Q1QUF0 (836)	LOV+PAS ₂ + GGDEF+EAL	145
			Q1QU87 (144)	Short LOV	146
<i>Oceanobacter</i> sp. <i>RED65</i>	P(y)	95	Q1N482 (938)	LOV+ Kinase+ RR+RR	147
† <i>Nitrosococcus oceanus</i> ATCC 19707	P(y)	96	Q3J6W8 (150)	Short LOV	148
† <i>Thiomicrospira denitrificans</i> ATCC 33889	P(y)	97	Q30NS0 (240)	HTH+ LOV	149
<i>Alteromonas macleodii</i> 'Deep ecotype'	P(y)	98	A4AZT0(959)	PAS+LOV+ Kinase+ RR	150
† <i>Shewanella</i> sp. <i>ANA-3</i>	P(y)	99	AOL2H7 (1228)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	151
† <i>Shewanella</i> sp. <i>W3-18-1</i>	P(y)	100	A1RE55 (1216)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	152
† <i>Shewanella putrefaciens</i> CN-32	P(y)	101	A4YC79 (1216)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	153
<i>Shewanella putrefaciens</i> 200	P(y)	102	A2V2K2 (740)	PAS+LOV+GGDEF+EAL	154
† <i>Shewanella baltica</i> OS195	P(y)	103	A9KV07 (1215)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	155
† <i>Shewanella baltica</i> OS185	P(y)	104	A6WU43 (1215)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	156
† <i>Shewanella baltica</i> OS223	P(y)	105	A5NDX2 (1215)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	157
† <i>Shewanella</i> sp. (strain <i>MR-7</i>)	P(y)	106	Q0HPR6 (1209)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	158
† <i>Shewanella</i> sp. (strain <i>MR-4</i>)	P(y)	107	Q0HDI3 (1209)	MASE1+CHASE+PAS+LOV+GGDEF+EAL	159
<i>Marinobacter algicola</i> DG893	P(y)	108	A6EZIP7 (858)	GAF+PAS+LOV+ GGDEF+EAL	160
† <i>Methylococcus capsulatus</i> str. Bath	P(y)	109	Q607S2 (853)	PAS+LOV+PAS ₁ PAS+PAS+SpolIE	161
† <i>Chloroflexus aurantiacus</i> J-10-fl	Chl	110	A9WHI1 (915)	LOV +PAS ₂ +Kinase+RR+Hpt	162
† <i>Herpetosiphon aurantiacus</i> ATCC 23779	Chl	111	A9B110 (1877)	HAMP+GAF+LOV+PAS ₄ +GAF+Kinase	164
<i>Chloroflexus aggregans</i> DSM 9485	Chl	112	A0H5C8 (913)	LOV+PAS+PAS+Kinase+RR	165
† <i>Thermosynechococcus elongatus</i> BP-1	Cya	113	Q8DJE3 (1353)	GAF+PAS+LOV+GAF ₂ +Kinase+ RR	166
† <i>Synechocystis</i> sp. <i>PCC 6803</i>	Cya	114	Q55576 (1244)	GAF+LOV+PAS ₃ +GGDEF+EAL	167
† <i>Synechococcus</i> sp. <i>PCC 6301</i>	Cya	115	Q5N2F7(578)	LOV+GGDEF+EAL	168
			Q5N5M8 (929)	RR+PAS+PAS+LOV+ GGDEF+EAL	169
† <i>Synechococcus</i> sp. <i>PCC 7942</i>	Cya	116	Q3IRU9 (578)	LOV+GGDEF+EAL	170
			Q31NI4 (929)	RR+PAS+PAS+LOV+ GGDEF+EAL	171
† <i>Synechococcus</i> sp. <i>PCC 7002</i>	Cya	117	B1XLQ8 (780)	GAF+LOV+PAS+GGDEF	172
<i>Cyanothece</i> sp. <i>CCY0110</i>	Cya	118	A3IMW4 (483)	RR+LOV+GGDEF	173

† <i>Cyanothece</i> ATCC 51142	Cya	119	B1WPX1 (483)	RR+LOV+GGDEF	173
<i>Cyanothece</i> PCC 8801/ <i>Synechococcus</i> sp. PCC 8801	Cya	120	B1U402 (481)	RR+LOV+GGDEF	174
<i>Crocospaera watsonii</i>	Cya	121	Q4BW45 (297)	RR + LOV	175
† <i>Acaryochloris marina</i> MBIC 11017	Cya	122	B0C6M6 (935)	PAS+LOV+PAS ₂ +GGDEF+EAL	176
† <i>Anabaena variabilis</i> ATCC 29413	Cya	123	Q3MBB3 (1021)	LOV+PAS ₂ +GGDEF+EAL	177
			Q3MED3 (1820)	PAS+LOV+PAS ₃ +GAF+Kinase+ RR ₂ +Hpt	178
† <i>Nostoc punctiforme</i> PCC 73102	Cya	124	B2JAQ5 (1043)	LOV+PAS ₂ +GGDEF+EAL	179
			B2J8F4 (1403)	PAS+LOV+PAS+GAF+Kinase+RR ₂ +Hpt	180
† <i>Nostoc</i> sp. PCC 7120	Cya	125	Q8YSB9 (1021)	LOV+PAS ₂ +GGDEF+EAL	181
			Q8YT51 (1817)	PAS+LOV+PAS ₃ +GAF+Kinase+ RR ₂ +Hpt	182
<i>Lyngbya</i> sp. PCC 8106	Cya	126	A0YV17 (477)	RR + LOV+ GGDEF	183
			A0YYE1 (1090)	PAS+LOV+PAS+GGDEF+EAL	184
			A0YS28 (1261)	RR+RR+LOV+PAS+GAF+Kinase+RR	185
			A0Y113 (1006)	PAS+LOV+PAS ₃ +GAF+GGDEF	186
			A0YJV6 (1211)	GAF+PAS+LOV+PAS+GAF+Kinase	187
			A0YYE8 (990)	PAS+GAF+LOV+GGDEF+EAL	188
† <i>Rhodospirella baltica</i> SH1	PI	127	Q7USG5 (1637)	CHEB+CHER+PAS+LOV+PAS+Kinase+ RR	189
<i>Leptospirillum</i> sp. Group II UBA	Nit	128	A3ERH5 (1036)	GAF+LOV+PAS+GGDEF+EAL	190
<i>Pedobacter</i> sp. BAL39	Bact	129	A6E9H1 (512)	LOV+PAS+Kinase	191
Archaea					
† <i>Haloarcula marismortui</i> ATCC43049	EuA	1	Q5UW17 (2306)	PAS+GAF+PAS ₄ +GAF+PAS ₄ +LOV+PAS ₃ +Kinase	1
			Q5V5P7 (726)	RR+PAS+LOV+PAS+ Kinase	2
			Q5V3S3 (748)	RR+PAS+LOV+GAF+ Kinase	3
† <i>Natronomonas pharaonis</i> DSM 2160	EuA	2	Q31TW5 (681)	RR+LOV+GAF+HtH	4
			Q3IM51 (596)	PAS+LOV+PAS+ Kinase	5
† <i>Methanosarcina barkeri</i> str. <i>fusaro</i>	EuA	3	Q468V8 (886)	LOV+(PAS) ₃ + Kinase	6
† <i>Methanosarcina acetivorans</i> C2A	EuA	4	Q8TQA5 (886)	LOV+(PAS) ₃ + Kinase	7
† <i>Methanoculleus marisnigri</i> ATCC 35101	EuA	5	A3CUN9 (753)	PAS ₂ +LOV+H-DimKinase	8
			A3CV78 (888)	PAS ₃ +LOV+H-DimKinase	9
			A3CS54 (630)	PAS ₂ +GAF+LOV+H-DimKinase	10
<i>Halorubrum lacusprofundi</i> ATCC 49239	EuA	6	A7D0X3 (447)	LOV+kinase	11
			A7D6B2 (501)	LOV+kinase	12

† : fully sequenced (NCBI <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi>).
‡: Firmicutes, low G+C Gram positives; Ac: Actinobacteria, high G+C Gram-positives; P: Proteobacteria (the class is indicated in parenthesis); **P(α)** = Rhodobacterales; **P(α)**: Rhodospirillales; **P(α)**: Parvularculales; **P(α)**: Sphingomonadales; **P(α)**: Rhizobiales; **P(α)**: Caulobacterales; **P(β)**: Burkholderiales; **P(β)**: Nitrosomonadales; **P(β)**: Neisseriales; **P(β)**: Methylophilales; **P(β)**: Rhodocyclales; **P(γ)**: Xanthomonadales; **P(γ)**: Pseudomonadales; **P(γ)**: Oceanospirillales; **P(γ)**: Chromatiales; **P(γ)**: Thiotrichales; **P(γ)**: Enterobacterales; **P(γ)**: Alteromonadales; **P(γ)**: Vibrionales; **P(γ)**: Methylococcales; U : unclassified; Unc: uncultured. Chl: Chloroflexi; Cya: Cyanobacteria; **Cya**: Chroococcales; **Cya**: Acaryochloris; **Cya**: Oscillatoriales; **Cya**: Nostocales; **Cya**: Gloeobacteria; DeTh = Deinococcus-Thermus; PI: Planctomycetes; Nit: Nitrospirae; Bact: Bacteroidetes; Lent: Lentisphaerae; EuA: Euryarchaeota.

§: classification of domains as in the Interpro database¹ **STAS**: Sulphate transporter/antisigma-factor antagonist; SPOIIE: Sporulation stage II, protein E C-terminal/Protein phosphatase 2C-related; GAF: domain first found in cGMP-specific cyclic nucleotide phosphodiesterase, **A**denylyl cyclase, and **F**hIA; GGDEF: named after a conserved sequence, synthesizes cyclic di-GMP; EAL: named after a conserved sequence, cyclic di-GMP phosphodiesterase; Kinase: here always

Histidine kinase; PAS: first found in Per, Arnt and SimS proteins, structurally the same as a LOV domain; RR = CheY-type Response regulator, receiver domain; HTH: Helix-turn-Helix regulatory protein, DNA-binding; MASE1: Predicted integral membrane sensory domain found bacterial signaling proteins; CHASE=Cyclases/Histidine kinases Associated Sensory Extracellular; HAMP: domain for histidine kinases, adenylyl cyclases, methyl binding proteins and phosphatases; Hpt : subdomain, transphosphorylation; CHEB : CHEB-type response regulator; CHER: CHER-type S-adenosylmethionine-dependent methyltransferase; NMT1: domain found in NMT1 and THI5 protein, proposed to be required for the biosynthesis of the pyrimidine moiety of thiamine.

- 1 N. J. Mulder, R. Apweiler, T. K. Attwood, A. Bairoch, D. Barrell, A. Bateman, M. Biswas, P. Bradley, P. Bucher, R. R. Copley, E. Courcelle, U. Das, R. Durbin, L. Falquet, W. Fleischmann, S. Griffiths-Jones, D. Haft, N. Harte, N. Hulo, D. Kahn, A. Kanapin, M. Kreszanyanova, R. Lopez, I. Letunic, D. Lonsdale, V. Silventoinen, S. E. Orchard, M. Pagni, D. Peyruc, C. P. Ponting, J. Selengut, F. Servant, C. J. Sigrist, R. Vaughan and E. M. Zdobnov, The InterPro Database, 2003 brings increased coverage and new features., *Nucl. Acids Res.*, 2003, **31**, 315-318.

89/665 sequenced bacteria (13.4 %)
5/52 sequenced Archaea (9.6 %)

Table S4: BLUF proteins in prokaryotes.

Bacteria				Proteins			
Species/strain	†Group	Nr.	Accession (aa)	§Domain structure	Nr.		
†Corynebacterium efficiens	Ac	1	Q8FMY2 (158)	BLUF	1		
†Leifsonia xyli subsp. xyli	Ac	2	Q6AGS2 (145)	BLUF	2		
†Clavibacter michiganensis subsp. michiganensis NCPPB 382)	Ac	3	A5CNT4 (142)	BLUF	3		
			A5CM94 (148)	BLUF	4		
†Clavibacter michiganensis subsp. sepedonicus ATCC 33113	Ac	4	B0RBP8 (126)	BLUF	5		
†Rhodobacter sphaeroides ATCC 17023/2.4.1	P(α)	5	Q3J677 (450)	BLUF+SCHICH ^{II}	6		
			Q3IV98 (134)	BLUF	7		
			Q3IYE4 (140)	BLUF	8		
†Rhodobacter sphaeroides ATCC 17029	P(α)	6	A3PG69 (450)	BLUF+SCHICH	9		
			A3PNV7 (140)	BLUF	10		
†Rhodobacter sphaeroides ATCC 17025	P(α)	7	A4WX15 (448)	BLUF+SCHICH	11		
			A4WZZ2 (135)	BLUF	12		
Roseobacter sp. CCS2	P(α)	8	A4EDL7 (158)	BLUF	13		
			A4EKD4 (95)	BLUF	14		
Roseobacter sp. SK209-2-6	P(α)	9	A4EP54 (143)	BLUF	15		
Roseobacter sp. MED193	P(α)	10	A3X3E5 (146)	BLUF	16		
Roseobacter sp. AzwK-3b	P(α)	11	A6FLZ7 (138)	BLUF	17		
Roseobacter litoralis Och 149	P(α)	12	A9HGK3 (131)	BLUF	18		
†Roseobacter denitrificans Och 114	P(α)	13	Q169R5 (131)	BLUF	19		
Roseovarius sp. HTCC2601	P(α)	14	Q0FHM9 (131)	BLUF	20		
Roseovarius sp. 217	P(α)	15	A3W442 (137)	BLUF	21		
Roseovarius sp. TM1035	P(α)	16	A6E0Y7 (137)	BLUF	22		
†Dinoroseobacter shibae DFL 12	P(α)	17	A8LL23 (135)	BLUF	23		
Sagittula stellata E-37	P(α)	18	A3JX11 (157)	BLUF	24		
†Jannaschia sp. (strain CCS1)	P(α)	19	Q28NL5 (164)	BLUF	25		
			Q28QR5 (150)	BLUF	26		
			Q28M24 (135)	BLUF	27		
†Silicibacter sp. TM1040	P(α)	20	Q1GF07 (144)	BLUF	28		
			Q1GF09 (169)	BLUF	29		
†Hyphomonas neptunium ATCC 15444	P(α)	21	Q0C3J3 (152)	BLUF	30		
Labrenzia aggregata IAM 12614	P(α)	22	A0NTY6 (152)	BLUF	31		
†Maricaulis maris (strain MCS10)	P(α)	23	Q0AMF1 (152)	BLUF	32		
			Q0ALH8 (141)	BLUF	33		
Sulfitobacter sp. EE-36	P(α)	24	A3S970 (110)	BLUF	34		
Sulfitobacter sp. NAS-14.1	P(α)	25	A3SU32 (110)	BLUF	35		
Loktanella vestfoldensis SKA53	P(α)	26	A3V3H6 (136)	BLUF	36		
Magnetospirillum gryphiswaldense	P(α)	27	A4U007 (156)	BLUF	37		
			A4U445 (151)	BLUF	38		
†Sphingopyxis alaskensis	P(α)	28	Q1GWG4 141)	BLUF	39		
Spingomonas sp. SKA58	P(α)	29	Q1NAZ4 (133)	BLUF	40		
†Sphingomonas wittichii RW1	P(α)	30	A5VFD3 (164)	BLUF	41		

† <i>Rhodopseudomonas palustris</i> BisA53	P(α)	31	Q07KQ3 (202)	BLUF	42
			Q07NU1 (172)	BLUF	43
			Q07V95 (146)	BLUF	44
			Q07LL8 (134)	BLUF	45
			Q06NCF0 (147)	BLUF	46
† <i>Rhodopseudomonas palustris</i> CGA009	P(α)	32	Q6N1X0 (157)	BLUF	47
			Q6N4H0 (156)	BLUF	48
			Q211J0 (225)	BLUF	49
			Q21C17 (147)	BLUF	50
			Q214S4 (131)	BLUF	51
† <i>Rhodopseudomonas palustris</i> (strain BisB18)	P(α)	33	Q2J2T2 (141)	BLUF	52
			B0IGJ4 (148)	BLUF	53
			B0IK64 (147)	BLUF	54
			B0IMC0 (157)	BLUF	55
			B0UJP3 (150)	BLUF	56
† <i>Rhodopseudomonas palustris</i> (strain HaA2) <i>Rhodopseudomonas palustris</i> TIE-1	P(α)	34	B0ULI8 (155)	BLUF	57
			B0UJ82 (296)	BLUF	58
			B0UQT1 (162)	BLUF	59
			B0UIK0 (373)	BLUF	60
			A9VWG7 (150)	BLUF	61
† <i>Methylobacterium sp. 4-4</i>	P(α)	35	A9W8Q2 (148)	BLUF	62
			A9W198 (155)	BLUF	63
			A7WDB1 (150)	BLUF	64
			A7W2G3 (165)	BLUF	65
			A7W7S5 (155)	BLUF	66
† <i>Methylobacterium extorquens</i> PA1	P(α)	36	A7W1J8 (148)	BLUF	67
			B1ZGT3 (162)	BLUF	68
			B1Z908 (155)	BLUF	69
			B1M482 (309)	BLUF	70
			B1M108 (139)	BLUF	71
<i>Methylobacterium chloromethanicum</i> CM4	P(α)	37	B1LTA6 (143)	BLUF	72
			B1M0G5 (155)	BLUF	73
			A9FZZ4 (155)	BLUF	74
			Q0G5H1 (144)	BLUF	75
			Q0G0Q7 (145)	BLUF	76
† <i>Methylobacterium populi</i> BJ001	P(α)	38	Q0G114 (122)	BLUF	77
			A7HQ46 (153)	BLUF	78
			A9DDP2 (130)	BLUF	79
			Q0FFK4 (142)	BLUF	80
			A2SEP7 (142)	BLUF	81
† <i>Methylobacterium radiotolerans</i> ATCC 27329	P(β)	39	A2SHW7 (97)	BLUF	82
			A6GT96 (157)	BLUF	83
			A6GT66 (134)	BLUF	84
			Q1LG69 (147)	BLUF	85
			Q46V06 (147)	BLUF	86
<i>Methylobacterium nodulans</i> ORS 2060 <i>Fulvimarina pelagi</i> HTCC2506	P(α)	40	Q0JZS4 (147)	BLUF	87
			Q21YW7 (140)	BLUF	88
† <i>Parvibaculum lavamentivorans</i> DS-1	P(α)	41			
<i>Hoeflea phototrophica</i> DFL-43 <i>alpha proteobacterium</i> HTCC2255	P(α)	42			
† <i>Methylobium petroleiphilum</i> (strain PM1)	P(β)	43			
† <i>Limnobacter sp. MED105</i>	P(β)	44			
† <i>Ralstonia metallidurans</i> CH34	P(β)	45			
† <i>Ralstonia eutropha</i> JMP134	P(β)	46			
† <i>Ralstonia eutropha</i> H16	P(β)	47			
† <i>Rhodoferris ferrireducens</i> DSM 15236	P(β)	48			

† <i>Hermiiniimonas arsenicoxydans</i>	P(β)	52	A4G7R3 (116)	BLUF	89
† <i>Acidovorax</i> sp. JS42	P(β)	53	A1W4E7 (140)	BLUF	90
† <i>Acidovorax avenae</i> sub. <i>citrullii</i> AAC00-1	P(β)	54	A1TT92 (140)	BLUF	91
		55	A1TUE4 (137)	BLUF	92
† <i>Polaromonas naphthalenivorans</i>	P(β)	56	A1VKQ2 (140)	BLUF	93
			A1VJM4 (134)	BLUF	94
† <i>Polaromonas</i> sp. strain JS666	P(β)	57	Q12F66 (140)	BLUF	95
† <i>Bordetella avium</i> (strain 197N)	P(β)	58	Q2L1Z3 (421)	BLUF-EAL	96
† <i>Delftia acidovorans</i> SPH-1	P(β)	59	A9BX41 (133)	BLUF	97
† <i>Verminephrobacter eiseniae</i> strain EF01-2	P(β)	60	A1WMH3 (133)	BLUF	98
† <i>Polynucleobacter</i> sp. QLW-P1DMWA-1	P(β)	61	A4SVS3 (135)	BLUF	99
<i>Comamonas testosteroni</i> KF-1	P(β)	62	A0HJ47 (131)	BLUF	100
† <i>Leptothrix cholodnii</i> SP-6	P(β)	63	B1XZW9 (141)	BLUF	101
† <i>Polynucleobacter necessarius</i> STIR1	P(β)	64	B1XTH8 (135)	BLUF	102
† <i>Chromobacterium violaceum</i>	P(β)	65	Q7NSR1 (141)	BLUF	103
† <i>Xanthomonas axonopodis</i> pv. <i>citri</i> str.306	P(γ)	66	Q8PHH6 (147)	BLUF	104
<i>Stenotrophomonas maltophilia</i> R551-3	P(γ)	67	Q8PKP9 (158)	BLUF	105
			A1FT77 (142)	BLUF	106
			A1FSW1 (144)	BLUF	107
† <i>Acinetobacter</i> sp. (strain ADP1)	P(γ)	68	Q6FAI1 (149)	BLUF	108
			Q6FAJ5 (155)	BLUF	109
<i>Acinetobacter</i> sp. 93A2	P(γ)	69	Q6FAH9 (163)	BLUF	110
† <i>Acinetobacter baumannii</i>	P(γ)	70	Q7BC36 (149)	BLUF	111
			Q933L6 (149)	BLUF	112
† <i>Psychrobacter cryohalolentis</i> (strain K5)	P(γ)	71	B0V7Y7 (156)	BLUF	113
			Q1QDR2 (210)	BLUF	114
			Q1Q9K9 (196)	BLUF	115
			Q1QAA1 (169)	BLUF	116
† <i>Psychrobacter</i> sp. PRwf-1	P(γ)	72	A5WCY1 (209)	BLUF	117
			A5WEX6 (216)	BLUF	118
† <i>Psychrobacter arcticum</i>	P(γ)	73	Q4FUS2 (210)	BLUF	119
<i>Beggiatoa</i> sp. PS	P(γ)	74	A7BT71(350)	BLUF+Cyclase	120
<i>Oceanobacter</i> sp. RED65	P(γ)	75	Q1N3J0 (163)	BLUF	121
† <i>Marinomonas</i> sp. MWYL1	P(γ)	76	A6VYY7 (142)	BLUF	122
<i>Marinomonas</i> sp. MED121	P(γ)	77	A3YED7 (140)	BLUF	123
			A3YFN4 (152)	BLUF	124
			A3YFL0 (154)	BLUF	125
† <i>Escherichia coli</i> .	P(γ)	78	P75990 (403)	BLUF+ EAL	126
† <i>Escherichia coli</i> DH10B	P(γ)	79	B1XA50 (403)	BLUF+ EAL	127
† <i>Escherichia coli</i> SMS-3-5 / SECEC	P(γ)	80	B1L104 (403)	BLUF+ EAL	128
† <i>Escherichia coli</i> ATCC 8739 / DSM 1576 / Crooks	P(γ)	81	B1IUC7 (403)	BLUF+ EAL	129
<i>Escherichia coli</i> O9:H4 / HS	P(γ)	82	A7ZZ94 (403)	BLUF+ EAL	130
† <i>Escherichia coli</i> O6	P(γ)	83	Q8FI42 (429)	BLUF+ EAL	131
† <i>Escherichia coli</i> (strain UT189 / UPEC)	P(γ)	84	Q1RCT6 (429)	BLUF+ EAL	132

† <i>Escherichia coli</i> O1:K1 / APEC	P(γ)	85	A1AA89 (403)	BLUF+ EAL	133
† <i>Escherichia coli</i> O6:K15:H31 536 / UPEC)	P(γ)	86	Q0TIL8 (403)	BLUF+ EAL	134
† <i>Escherichia coli</i> (protein YCGF)	P(γ)	87	Q2LD83 (403)	BLUF+ EAL	135
† <i>Escherichia coli</i> E24377A	P(γ)	88	A7ZKT0 (403)	BLUF+ EAL	136
† <i>Enterobacter</i> sp. 638	P(γ)	89	A4WAH8 (406)	BLUF+ EAL	137
			A4W9Q6 (418)	BLUF+ EAL	138
† <i>Enterobacter sakazakii</i> ATCC BAA-894	P(γ)	90	A7MRH4 (406)	BLUF+ EAL	139
			A7MJM6 (403)	BLUF+ EAL	140
† <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> ATCC 700721	P(γ)	91	A6T8V8 (405)	BLUF+ EAL	141
			A6T6J7 (403)	BLUF+ EAL	142
<i>Alteromonas macleodii</i> 'Deep ecotype'	P(γ)	92	A4AX64 (390)	BLUF+ EAL	143
<i>Alteromonadales bacterium</i> TW-7	P(γ)	93	A0XX52 (141)	BLUF	144
† <i>Pseudoalteromonas atlantica</i> (T6c / BAA-1087)	P(γ)	94	Q15XU6 (138)	BLUF	145
			Q15W34 (133)	BLUF	146
<i>Pseudoalteromonas tunicata</i> D2	P(γ)	95	A4C8E2(140)	BLUF	147
			A4CA03 (133)	BLUF	148
† <i>Psychromonas ingrahamii</i> (strain 37)	P(γ)	96	A1SZ77 (157)	BLUF	149
† <i>Shewanella woodyi</i> ATCC 51908	P(γ)	97	B1KH49 (156)	BLUF	150
† <i>Shewanella oneidensis</i>	P(γ)	98	Q8EBA3 (140)	BLUF	151
† <i>Marinobacter aquaeolei</i> VT8	P(γ)	99	A1U4G7 (189)	BLUF	152
<i>Marinobacter algicola</i> DG893	P(γ)	100	A6F2F1 (188)	BLUF	153
<i>Neptuniibacter caesariensis</i>	P(γ)	101	Q2BIC6 (142)	BLUF	154
			Q2BP57 (147)	BLUF	155
<i>Vibrio splendidus</i> 12B01	P(γ)	102	A3UYZ3 (141)	BLUF	156
<i>Vibrio</i> sp. MED222	P(γ)	103	A3Y2H2 (142)	BLUF	157
<i>Vibrionales bacterium</i> SWAT-3	P(γ)	104	A5L553 (139)	BLUF	158
<i>Methylobacterium</i> sp. NI.	P(γ)	105	Q25BV7 (141)	BLUF	159
<i>Congregibacter litoralis</i> KT71	P(γ)U	106	A4A4X0 (160)	BLUF	160
			A4ACN4(120)	BLUF	161
<i>Reinekea</i> sp. MED297	P(γ)U	107	A4A4X0 (160)	BLUF	162
<i>marine gamma proteobacterium</i> HTCC2080	P(γ)U	108	A4BGV1 (172)	BLUF	163
			A0Z2D8 (150)	BLUF	164
			A0Z4F4 (159)	BLUF	165
			A0Z3A0 (152)	BLUF	166
† <i>Desulfococcus oleovorans</i> Hxd3	P(δ)	109	A9A0H4 (148)	BLUF	167
<i>Desulfatibacillum alkenivorans</i> AK-01	P(δ)	110	A9JC98 (144)	BLUF	168
† <i>Myxococcus xanthus</i> DK1622	P(δ)	111	Q93SK7(253)	BLUF	169
† <i>Magnetococcus</i> sp. MC-1	P(Magn)	112	A0LAZ4 (1118)	PAS+GGDEF+EAL+BLUF	170
			A0L5S5 (139)	BLUF	171
			A0LAQ1 (160)	BLUF	172
<i>uncultured proteobacterium delRiverFos06H03</i>	PUnc	113	Q58PP1 (147)	BLUF	173
<i>uncultured proteobacterium.</i>	PUnc	114	Q8KZ47 (146)	BLUF	174
<i>uncultured bacterium</i> 581	Unc	115	Q6SFE3 (159)	BLUF	175
† <i>Thermosynechococcus elongatus</i>	Cya	116	Q8DMN3 (143)	BLUF	176
† <i>Synechocystis</i> sp. PCC 6803	Cya	117	P74295 (150)	BLUF	177

† <i>Synechococcus</i> sp. PCC 7002	Cya	118	B1XJZ3 (145)	BLUF	178
† <i>Rhodopirellula baltica</i>	PI	119	Q7UXU1 (141)	BLUF	179
<i>Flavobacterium bacterium BBFL7</i>	Bact	120	Q26D86 (139)	BLUF	180
<i>Polaribacter dokdonensis MED152</i>	Bact	121	A2TY78 (481)	HTH-BLUF	181
<i>Psychroflexus torquus ATCC 700755</i>	Bact	122	Q1VYM2 (142)	BLUF	182
† <i>Bdellovibrio bacteriovorus</i>	Bact	123	Q6MPS8 (142)	BLUF	183
<i>Dokdonia donghaensis MED134</i>	Bact	124	A2TPW0 (135)	BLUF	184
† <i>Gramella forsetii KT0803</i>	Bact	125	A0LYB8 (133)	BLUF	185
<i>Microscilla marina ATCC 23134</i>	Bact	126	A1ZRF7 (137)	BLUF	186
<i>unidentified eubacterium SCB49</i>	Bact	127	A6ENE1 (133)	BLUF	187
<i>Pedobacter</i> sp. BAL39	Bact	128	A6E9F4 (152)	BLUF	188
† <i>Solibacter usitatus Ellin6076</i>	AcidoB	129	Q0TS10 (141)	BLUF	189
<i>Lentisphaera araneosa HTCC2155</i>	Lent	130	A6DQ35 (132)	BLUF	190

† : fully sequenced (NCBI <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi>).

‡: Firmicutes, low G+C Gram positives; Ac: Actinobacteria, high G+C Gram-positives; P: Proteobacteria (the class is indicated in parenthesis); **P(α)** = Rhodobacterales; **P(α)**: Rhodospirillales; **P(α)**: Parvularculales; **P(α)**: Sphingomonadales; **P(α)**: Rhizobiales; **P(β)**: Caulobacterales; **P(β)**: Burkholderiales; **P(β)**: Nitrosomonadales; **P(β)**: Neisseriales; **P(γ)**: Xanthomonadales; **P(γ)**: Pseudomonadales; **P(γ)**: Oceanospirillales; **P(γ)**: Chromatiales; **P(γ)**: Thiotrichales; **P(γ)**: Enterobacteriales; **P(γ)**: Vibrionales; **P(γ)**: Alteromonadales; **P(γ)**: Methylococcales; **P(Magn)**: Magnetococcus; U : unclassified; Unc: uncultured. Chl: Chloroflexi; Cya: Cyanobacteria; **Cya**: Chroococcales; **Cya**: Oscillatoriales; **Cya**: Nostocales; **Cya**: Gloeobacteria; DeTh = Deinococcus-Thermus; Pl: Planctomycetes; Nit: Nitrospirae; Bact: Bacteroidetes; Lent: Lentisphaerae; EuA: Euryarchaeota.

§: classification of domains as in the Interpro database.¹ GGDEF: named after a conserved sequence, synthesizes cyclic di-GMP; EAL: named after a conserved sequence, cyclic di-GMP phosphodiesterase; HTH: Helix-turn-Helix regulatory protein, DNA-binding
†SCHICH: sensor containing heme instead of cobalamin.²

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76 sequenced/665 = 11.4%