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Electronic supplementary information (ESI) for:

First molecular characterisation of blue- and red-light photoreceptors from *Methylobacterium radiotolerans*

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Table S1 ***Methylobacteria*** **group: summary of photoreceptors types[a] and number of hits as X in fully sequenced species/strains**

	Methylobacterium	**strain**	**BphP**	**PYP-BphP**	**LOV**	**BLUF**	**Rho**	**BChl enz.**
1	*M. aquaticum*	MA-22A	X	X	XXXXXXXXXX	XXX	X	YES
2	*M. durans*	17SD2-17	XXXX		XXXXXXX	XXX		YES
3	*M. mesophilicum*	SR1.6/6	XX		XXXXXXX	XXX	X	YES
4	*M. nodulans*	ORS 2060			XX	X		NO
5	*M. oryzae*	CBMB20	XX		XXXXXXX	XXXX		YES
6	*M. phyllosphaerae*	CBMB27	X	X	XXXXX	XXX		YES
7	*M. radiotolerans*	JCM 2831	XXX		XXXXXX	XXXX		YES
8	*M.sp.*	17Sr1-1	XX	X	XXXXXXXXXX	XXXX		YES
9	*M. sp.*	17Sr1-43	XX		XXXXXXX	XXXX		YES
10	*M. sp.*	4-46	X	X	XX	XXXXX	X	YES
11	*M. sp.*	AMS5	XXX		XXXXX	XXX		YES
12	*M.sp.*	C1	XX		XXXXXX	XXX		YES
13	*M. sp.*	DM1	XXXX		XXXXXX	XXXX		YES
14	*M. sp.*	XJLW	XX		XXXXXXXXX	XXX		YES
15	*M.terrae*	17Sr1-28	X	X	XXXXXXXXX	XXXX		YES

Methylorubra **group: summary of photoreceptors types[a] and number of hits as X in fully sequenced species/strains**

	Methylorubrum	**strain**	**BphP**	**PYP-BphP**	**LOV**	**BLUF**	**Rho**	**BChl**
1	*M. extorquens*	PSBB040	**X**		**XXXXXX**	**XXXXXX**		YES
2	*M. extorquens*	TK0001	**XX**		**XXXXX**	**XXX**		YES
3	*M. extorquens*	AM1	**X**		**XXXXXX**	**XX**		YES
4	*M. extorquens*	CM4	**X**		**XXXXXX**	**XXXXX**		YES
5	*M. extorquens*	DM4	**X**		**XXXXX**	**XX**		YES
6	*M. extorquens*	PA1	**X**		**XXXXX**	**XXX**		YES
7	*M. populi*	P-1M	**XXX**		**XXXXX**	**XX**		YES
8	*M. populi*	YC-XJ1	**XX**		**XXXXXX**	**XX**		YES
9	*M. populi*	BJ001	**XX**		**XXXXXXXX**	**XX**		YES
10	*M. zatmanii*	PSBB041	**XX**		**XXXXXX**	**XX**		YES

[a] BphP = Bacteriophytochrome; PYP-BphP = hybrid photoreceptors comprising photoactive yellow protein and a BphP; L; LOV = Light, Oxygen and Voltage proteins; BLUF =Blue Light sensing Using Flavins proteins; Rho = Rhodopsin; BChl enz. =enzymes for bacteriochlorophyll synthesis and for photosystems; all listed bacteria but one possess genes for the synthesis of bacteriochlorophylls for photosystems; full sequenced genomes can be found at the NCBI database, https://www.ncbi.nlm.nih.gov/genome/browse#!/prokaryotes/[1].

In the following tables S1.a, S1.b, S1.c, S1.d are reported the protein accession codes (UniProt[2] and NCBI[3]), gene name and domain architecture (InterPro[4,5]) for each photoreceptor. Highlighted in yellow: the two *M. radiotolerans* photoreceptors investigated in this work. The acronym LOV is used in the literature: note that in public databases this domain is named as the more generic PAS.

Domain legenda

BLUF = Blue Light sensing Using Flavin
GAF = cGMP-specific phosphodiesterases, cyanobacterial adenylate cyclases, and formate hydrogen lyase transcription activator FhlA (embedding the chromophore in BphPs)
HWE= Signal transduction histidine kinase, HWE region: defined by the presence of conserved a H residue and a WXE motif
Kinase = His-Kinase of the two component signal transduction system
LOV = Light, Oxygen,Voltage
PAS = Per Arnt Sim domain
PHY = Phytochrome domain
RR = CheY-type Response regulator, receiver domain
Short-LOV or Short-BLUF = standalone LOV and BLUF domains, with flanking regions/no recognizable linked domain

Table S1.a *Methylobacteria* group: BphP proteins, accession codes and domain architecture

	Methylobacterium	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. aquaticum*	MA-22A	A0A0C6F3S7	WP_060848240.1	Maq22A_c21185	855	PYP+PAS+GAF+PHY+Kinase
			A0A0C6FKU5	BAQ49078.1	Maq22A_1p33980	755	PAS+GAF+PHY+Kinase
2	*M. durans*	17SD2-17	A0A2U8W298	WP_109886955.1	DK389_01130	871	PAS$_2$+GAF+PHY+Kinase
			A0A2U8W9H7	WP_109891510.1	DK389_17640	774	PAS+GAF+PHY+Kinase
			A0A2U8W941	WP_109892731.1	DK389_21720	894	PAS+GAF+PHY+HWE-Kinase+RR
			A0A2U8WCF2	WP_109894975.1	DK389_28975	913	PAS+GAF+PHY+Kinase+RR
3	*M. mesophilicum*	SR1.6/6	M7XYB2	QGY04106.1	MmSR116_5310	871	PAS$_2$+GAF+PHY+Kinase
			M7Y016	QGY03396.1	MmSR116_4916	847	PAS+GAF+PHY+HWE-Kinase+RR
4	*M. nodulans*	ORS 2060	----	----	----	----	----
5	*M. oryzae*	CBMB20	A0A089QBR2	AIQ92004.1	MOC_4249	879	PAS$_2$+GAF+PHY+Kinase
			A0A089P3P6	AIQ92678.1	MOC_4923	751	PAS+GAF+PHY+Kinase
6	*M. phyllosphaerae*	CBMB27	----	APT33067.1	MCBMB27_03776	751	PAS+GAF+PHY+Kinase
			----	APT32498.1	MCBMB27_03207	871	PYP+PAS+GAF+PHY+Kinase
7	*M. radiotolerans*	JCM 2831	B1LWZ3	ACB25698.1	Mrad2831_3723	871	PAS$_2$+GAF+PHY+Kinase
			B1M2J7	ACB26237.1	Mrad2831_4270	751	PAS+GAF+PHY+Kinase
			B1M9J3	ACB28168.1	Mrad2831_6244	849	PAS+GAF+PHY+HWE-Kinase+RR
8	*M.sp.*	17Sr1-1	A0A2U8WYI2	WP_109970316.1	DK412_00385	847	PAS+GAF+PHY+HWE-Kinase+RR
			A0A2U8XA43	WP_109975043.1	DK412_03780	862	PYP+PAS+GAF+PHY+HWE-Kinase
			A0A2U8X9M0	WP_109974110.1	DK412_24610	751	PAS+GAF+PHY+Kinase
9	*M. sp.*	17Sr1-43	A0A2U8VST8	WP_109951552.1	DK427_12515	862	PAS$_2$+GAF+PHY+Kinase
			A0A2U8W074	WP_109953861.1	DK427_25725	751	PAS+GAF+PHY+Kinase
10	*M. sp.*	4-46	B0UDE6	WP_012332076.1	M446_2206	762	PAS+GAF+PHY+Kinase
			B0UNZ0	WP_012332998.1	M446_3192	864	PYP+PAS+GAF+PHY+HWE-Kinase
11	*M. sp.*	AMS5	A0A0X1SN35	WP_060771330.1	Y590_20345	875	PAS$_2$+GAF+PHY+Kinase
12	*M.sp.*	C1	----	WP_012321191.1	BKE41_RS19690	871	PAS$_2$+GAF+PHY+Kinase
			----	WP_012321191.1	BKE41_RS22315	751	PAS+GAF+PHY+Kinase
13	*M. sp.*	DM1	A0A2U8HM61	AWI86987.1	C0214_00570	764	PAS+GAF+PHY+Kinase
			A0A2U8HP59	AWI87707.1	C0214_04970	849	PAS+GAF+PHY+HWE-Kinase+RR
			A0A2U8HZE0	AWI90356.1	C0214_20165	849	PAS+GAF+PHY+HWE-Kinase+RR
			A0A2U8HXW5	AWI90731.1	C0214_22420	873	PAS$_2$+GAF+PHY+Kinase
14	*M. sp.*	XJLW	A0A2U9TZ38	AWV15807.1	A3862_10045	751	PAS+GAF+PHY+Kinase
			A0A2U9U7D0	AWV16289.1	A3862_12870	871	PAS$_2$+GAF+PHY+Kinase
15	*M. terrae*	17Sr1-28	A0A2U8WWV6	WP_109962186.1	DK419_07875	862	PYP+PAS+GAF+PHY+Kinase

***Methylorubra* group: BphP proteins, accession codes and domain architecture**

	Methylorubrum	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. extorquens*	PSBB040	A0A1P8QPG6	WP_076642174.1	BV511_12120	875	PAS$_2$+GAF+PHY+Kinase
2	*M. extorquens*	TK0001	A0A2N9AXF7	SOR31999.1	TK0001_5433	469	GAF+PHY+Kinase
			A0A2N9AKU2	SOR27981.1	TK0001_1379	875	PAS$_2$+GAF+PHY+Kinase
3	*M. extorquens*	AM1	C5AQ42	ACS42102.1	MexAM1_META1p4471	875	PAS$_2$+GAF+PHY+Kinase
4	*M. extorquens*	CM4	B7KNA8	ACK85225.1	MCHL_4449	875	PAS$_2$+GAF+PHY+Kinase
5	*M. extorquens*	DM4	C7CJI8	WP_017484084.1	METDI5076	875	PAS$_2$+GAF+PHY+Kinase
6	*M. extorquens*	PA1	A9W8V2	ABY32451.1	Mext_4081	895	PAS$_2$+GAF+PHY+Kinase
7	*M. populi*	P-1M	A0A169QFG4	BAU88817.1	MPPM_0212	760	PAS+GAF+PHY+Kinase
			A0A160PCB0	BAU88780.1	MPPM_0175	843	PAS+GAF+PHY+HWE-Kinase+RR
			A0A160PLA1	BAU93051.1	MPPM_4446	874	PAS$_2$+GAF+PHY+Kinase
8	*M.populi*	YC-XJ1	----	QDI79405.1	E8E01_02640	751	PAS+GAF+PHY+Kinase
			----	QDI82714.1	E8E01_20985	874	PAS$_2$+GAF+PHY+Kinase
9	*M.populi*	BJ001	B1ZK65	ACB78717.1	Mpop_0539	751	PAS+GAF+PHY+Kinase
			B1ZGY2	ACB82660.1	Mpop_4562	874	PAS$_2$+GAF+PHY+Kinase
10	*M. zatmanii*	PSBB041	A0A1W6RDZ4	WP_004447074.1	B2G69_02320	875	PAS$_2$+GAF+PHY+Kinase
			A0A1W6RI55	WP_085856811.1	B2G69_10960	751	PAS+GAF+PHY+Kinase

Table S1.b *Methylobacteria* group: LOV proteins, accession codes and domain architecture

	Methylobacterium	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. aquaticum*	MA-22A	A0A0C6F8L7	WP_060846160.1	Maq22A_c06770	813	LOV+PAS+Kinase+RR
			A0A0C6FFC2	WP_060846976.1	Maq22A_c12145	538	LOV+Kinase+RR
			A0A0C6FSQ1	WP_060847120.1	Maq22A_c13200	820	LOV+ PAS$_2$+Kinase+RR
			A0A0C6FBR7	WP_060847150.1	Maq22A_c13440	801	LOV+ PAS$_2$+Kinase+RR
			A0A0C6FEW7	WP_060848127.1	Maq22A_c20420	540	LOV+Kinase+RR
			A0A0C6FMC7	WP_060849616.1	Maq22A_c27090	553	LOV+Kinase+RR
			A0A0C6FMG4	WP_060849092.1	Maq22A_c27510	495	LOV+PAS+HWE-Kinase
			A0A1Y0ZBW9	WP_082742600.1	Maq22A_c28570	854	LOV+PAS+Kinase+RR
			A0A0C6FN59	WP_082742864.1	Maq22A_1p31385	375	LOV+Kinase
			A0A0C6G201	WP_060851125.1	Maq22A_2p41400	801	LOV+ PAS$_2$+Kinase+RR
2	*M. durans*	17SD2-17	A0A2U8W129	WP_012320504.1	DK389_03705	540	LOV+Kinase+RR
			A0A2U8W1K3	WP_109887680.1	DK389_04585	489	LOV+PAS+HWE-Kinase
			A0A2U8W3Y5	WP_109888201.1	DK389_06400	608	LOV+PAS$_2$+GAF
			A0A2U8W4X7	WP_109889038.1	DK389_09260	364	LOV+Kinase
			A0A2U8W806	WP_109891767.1	DK389_18695	364	LOV+Kinase
			A0A2U8WB98	WP_109893174.1	DK389_23370	541	LOV+Kinase+RR
			A0A2U8WD80	WP_109895442.1	DK389_30585	954	LOV+PAS$_3$+Kinase+RR
3	*M. mesophilicum*	SR1.6/6	M7YNE8	QGY02102.1	MmSR116_3087	164	Short-LOV
			M7YQT1	QGY05663.1	MmSR116_2729	492	LOV+PAS+HWE-Kinase
			M7Y7G4	QGY05734.1	MmSR116_2810	538	LOV+Kinase+RR
			M7XRI0	QGY03399.1	MmSR116_4913	1194	LOV+ PAS$_5$+Kinase+RR

			M7Y4Z9	QGY06380.1	MmSR116_2281	334	LOV+Kinase
			M7XWQ9	QGY03759.1	MmSR116_5618	186	Short-LOV
			M7Z8V1	QGY02509.1	MmSR116_1138	370	LOV+Kinase
4	*M. nodulans*	ORS 2060	B8IF91	WP_015927507.1	Mnod_0770	814	LOV+ PAS$_2$+Kinase+RR
			B8IAH5	WP_015932603.1	Mnod_6213	559	LOV+Kinase+RR
5	*M. oryzae*	CBMB20	A0A089NRS9	AIQ88543.1	MOC_0788	348	LOV+Kinase
			A0A089NVZ9	AIQ91572.1	MOC_3817	462	LOV+PAS+HWE-Kinase
			A0A089QB82	AIQ91844.1	MOC_4089	499	LOV+Kinase+RR
			A0A089NYH1	AIQ92422.1	MOC_4667	813	LOV+ PAS$_2$+Kinase+RR
			A0A089NY43	AIQ92927.1	MOC_5101	186	Short-LOV
			A0A089NZW5	AIQ92927.1	MOC_5172	148	Short-LOV
			A0A089P3R8	AIQ93410.1	MOC_5655	461	LOV+PAS+Kinase
6	*M. phyllosphaerae*	CBMB27	----	WP_020093089.1	MCBMB27_02805	462	LOV+PAS+ Kinase
			----	WP_012320504.1	MCBMB27_03052	539	LOV+Kinase+RR
			----	WP_075381089.1	MCBMB27_04019	164	Short-LOV
			----	WP_075381240.1	MCBMB27_04400	495	LOV+PAS+ Kinase
			----	WP_075381708.1	MCBMB27_05465	807	LOV+PAS$_2$+Kinase+RR
7	*M. radiotolerans*	JCM 2831	B1LWD2	ACB22634.1	Mrad2831_0623	334	LOV+Kinase
			B1M4V9	ACB25005.1	Mrad2831_3021	812	LOV+PAS$_2$+Kinase+RR
			B1LSK7	ACB25309.1	Mrad2831_3331	503	LOV+PAS+HWE-Kinase
			B1LUV7	ACB25309.1	Mrad2831_3567	539	LOV+Kinase+RR
			B1M4A2	ACB26397.1	Mrad2831_4431	186	Short-LOV
			B1M516	ACB26477.1	Mrad2831_4511	164	Short-LOV
8	*M.sp.*	17Sr1-1	A0A2U8WWJ1	WP_109970416.1	DK412_01025	538	LOV+Kinase+RR
			A0A2U8WZH9	WP_109970637.1	DK412_02380	540	LOV+Kinase+RR
			A0A2U8WXL4	WP_109970985.1	DK412_04575	1108	LOV+PAS+GAF+PAS$_2$+Kinase+RR
			A0A2U8WY70	WP_109970993.1	DK412_04625	492	LOV+PAS+HWE-Kinase
			A0A2U8X1D7	WP_109971296.1	DK412_06590	559	LOV+Kinase+RR
			A0A2U8X1P7	WP_109971412.1	DK412_07310	810	LOV+PAS$_2$+Kinase+RR
			A0A2U8X098	WP_109971595.1	DK412_08485	493	LOV+PAS+HWE-Kinase
			A0A2U8XCR4	WP_109975163.1	DK412_09505	781	LOV+PAS$_3$+Kinase+RR
			A0A2U8XD68	WP_109975194.1	DK412_11010	504	LOV+Kinase+RR
			A0A2U8XCE2	WP_109974936.1	DK412_29695	382	LOV+Kinase
9	*M. sp.*	17Sr1-43	A0A2U8VZF9	WP_109953906.1	DK427_00790	164	Short-LOV
			A0A2U8VNL5	WP_109950266.1	DK427_04770	410	LOV+PAS$_2$
			A0A2U8VPS9	WP_109950513.1	DK427_06295	363	LOV+Kinase
			A0A2U8VPU1	WP_109950750.1	DK427_07665	540	LOV+Kinase+RR
			A0A2U8VUH2	WP_109952200.1	DK427_16430	804	LOV+PAS$_2$+Kinase+RR
			A0A2U8VZD2	WP_109954309.1	DK427_21670	361	LOV+Kinase
			A0A2U8VZN0	WP_109953855.1	DK427_25685	497	LOV+PAS+HWE-Kinase
10	*M. sp.*	4-46	B0UAI7	WP_012331917.1	M446_2045	812	LOV+PAS$_2$+Kinase+RR
			B0UDT0	WP_012334590.1	M446_4874	544	LOV+Kinase+RR
11	*M. sp.*	AMS5	A0A109QS47	WP_060768604.1	Y590_03300	488	LOV+PAS+HWE-Kinase
			A0A0X1SFS5	AMB44787.1	Y590_07770	541	LOV+Kinase+RR
			A0A0X1SJZ2	WP_060770523.1	Y590_15300	533	LOV+Kinase+RR
			A0A0X1SKE0	WP_060770644.1	Y590_16035	354	LOV+Kinase
			A0A0X1SMN7	WP_060771287.1	Y590_20105	366	LOV+Kinase
12	*M.sp.*	C1	----	WP_059407784.1	BKE41_RS02935	488	LOV+PAS+HWE-Kinase
			----	WP_041372668.1	BKE41_RS16035	810	LOV+PAS+Kinase+RR
			----	WP_024829373.1	BKE41_RS17735	495	LOV+PAS+HWE-Kinase
			----	WP_070999971.1	BKE41_RS18920	539	LOV+Kinase+RR
			----	WP_012321430.1	BKE41_RS23540	164	Short LOV
			----	WP_083374417.1	BKE41_RS25530	907	LOV+PAS$_3$+GAF+Kinase
13	*M. sp.*	DM1	A0A2U8HNC3	WP_108938844.1	C0214_03685	488	LOV+PAS+HWE-Kinase
			A0A2U8HU49	WP_108939664.1	C0214_09580	541	LOV+Kinase+RR
			A0A2U8HV39	WP_108940986.1	C0214_17430	531	LOV+Kinase+RR
			A0A2U8HWM0	WP_108941107.1	C0214_18110	354	LOV+Kinase
			A0A2U8HYZ4	WP_108941304.1	C0214_19325	190	Short LOV
			A0A2Y9CIT5	WP_108943061.1	C0214_22220	366	LOV+Kinase
14	*M. sp.*	XJLW	A0A2U9TQ90	WP_124262936.1	A3862_04950	860	LOV+PAS$_3$+GAF+Kinase
			A0A2U9TTV4	WP_111473376.1	A3862_04960	801	LOV+PAS$_2$+Kinase+RR
			A0A2U9TR90	WP_052083755.1	A3862_07115	495	LOV+PAS+HWE-Kinase
			A0A2U9TS28	WP_043351101.1	A3862_08855	164	Short-LOV
			A0A2U9TW39	WP_043387271.1	A3862_09190	186	Short LOV
			A0A2U9TZA3	WP_043381097.1	A3862_13620	539	LOV+Kinase+RR
			A0A2U9TUF6	WP_043356402.1	A3862_14865	496	LOV+PAS+HWE-Kinase
			A0A2U9TZM6	WP_111473771.1	A3862_15760	791	LOV+PAS+Kinase+RR
			A0A2U9U1C7	WP_051045086.1	A3862_27810	358	LOV+Kinase
15	*M. terrae*	17Sr1-28	A0A2U8WWD0	WP_109962054.1	DK419_01520	778	LOV+PAS$_2$+Kinase+RR
			A0A2U8WIS2	WP_109957826.1	DK419_03285	538	LOV+Kinase+RR
			A0A2U8WKG6	WP_109958164.1	DK419_05290	549	LOV+Kinase+RR
			A0A2U8WNG3	WP_109959390.1	DK419_12660	820	LOV+PAS$_2$+Kinase+RR
			A0A2U8WNK1	WP_109960040.1	DK419_16520	375	LOV+Kinase
			A0A2U8WT64	WP_109960939.1	DK419_21720	496	LOV+PAS+HWE-Kinase
			A0A2U8WXU6	WP_109962446.1	DK419_22485	540	LOV+Kinase+RR
			A0A2U8WUH2	WP_109961378.1	DK419_24350	802	LOV+PAS$_2$+Kinase+RR
			A0A2U8WVC8	WP_109962528.1	DK419_26540	799	LOV+PAS$_2$+Kinase+RR

***Methylorubra* group: LOV proteins, accession codes and domain architecture**

	Methylorubrum	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. extorquens*	PSBB040	A0A1P8QKE8	WP_076640931.1	BV511_03615	488	LOV+PAS+HWE-Kinase
			A0A1P8QPK0	WP_003599658.1	BV511_12335	366	LOV+Kinase
			A0A1P8QRK1	WP_076643086.1	BV511_16105	492	LOV+PAS+HWE-Kinase
			A0A1P8QS50	WP_076643255.1	BV511_17200	354	LOV+Kinase
			A0A1P8QSE4	WP_076643333.1	BV511_17905	533	LOV+Kinase+RR
			A0A1P8QW68	WP_076644147.1	BV511_25115	541	LOV+Kinase+RR
2	*M. extorquens*	TK0001	A0A1P8QPK0	SOR28036.1	TK0001_1434	366	LOV+Kinase
			A0A2N9ANY0	WP_015951675.1	TK0001_2444	354	LOV+Kinase
			A0A2N9APB6	WP_015951576.1	TK0001_2602	533	LOV+Kinase+RR
			A2N9AUC2	WP_085857055.1	TK0001_4342	541	LOV+Kinase+RR
			A0A2N9AX59	WP_003598918.1	TK0001_5339	488	LOV+PAS+HWE-Kinase
3	*M. extorquens*	AM1	C5B055	ACS39405.1	MexAM1_META1p1543	541	LOV+Kinase+RR
			C5AXM1	ACS41089.1	MexAM1_META1p3352	533	LOV+Kinase+RR
			C5B099	ACS39449.1	MexAM1_META1p1590	492	LOV+PAS+HWE-Kinase
			C5AYD0	ACS41229.1	MexAM1_META1p3492	354	LOV+Kinase
			C5AVA5	ACS38573.1	MexAM1_META1p0643	488	LOV+PAS+HWE-Kinase
			C5B328	ACS42058.1	MexAM1_META1p4427	351	LOV+Kinase
4	*M. extorquens*	CM4	B7L0N0	WP_003598918.1	Mchl_0835	488	LOV+PAS+HWE-Kinase
			B7KVX8	WP_012453493.1	Mchl_1931	541	LOV+Kinase+RR
			B7KUQ2	WP_015951576.1	Mchl_3461	533	LOV+Kinase+RR
			B7KW67	WP_015951675.1	Mchl_3604	354	LOV+Kinase
			B7KN66	WP_012255188.1	Mchl_4407	366	LOV+Kinase
			B7KX89	WP_015952969.1	Mchl_5380	890	LOV+PAS+GAF+Kinase+RR
5	*M. extorquens*	DM4	C7CDA8	WP_015821340.1	METDI1014	488	LOV+PAS+HWE-Kinase
			C7CG25	WP_003599902.1	METDI2317	541	LOV+Kinase+RR
			C7CC12	WP_015823367.1	METDI3923	533	LOV+Kinase+RR
			C7CCX6	WP_015823468.1	METDI4072	354	LOV+Kinase
			C7CJE3	WP_012255188.1	METDI5031	351	LOV+Kinase
6	*M. extorquens*	PA1	A9W124	WP_012252593.1	Mext_0875	488	LOV+PAS+HWE-Kinase
			A9W392	WP_003599902.1	Mext_1649	541	LOV+Kinase+RR
			A9VYT5	WP_012254440.1	Mext_3139	533	LOV+Kinase+RR
			A9W705	WP_012254549.1	Mext_3280	354	LOV+Kinase
			A9W8Q8	WP_012255188.1	Mext_4037	366	LOV+Kinase
7	*M. populi*	P-1M	A0A160PC43	WP_096484005.1	MPPM_0898	488	LOV+PAS+HWE-Kinase
			A0A169QVX5	WP_096484658.1	MPPM_1693	501	LOV+Kinase+RR
			A0A160PEM8	WP_096484928.1	MPPM_2008	907	LOV+PAS$_3$+GAF+Kinase
			A0A160PFS2	WP_096486089.1	MPPM_3464	531	LOV+Kinase+RR
			A0A160PJ51	WP_096486812.1	MPPM_4401	366	LOV+Kinase
8	*M.populi*	YC-XJ1	----	WP_141949819.1	E8E01_00790	807	LOV+PAS$_2$+Kinase+RR
			----	WP_141950417.1	E8E01_04015	488	LOV+PAS+HWE-Kinase
			----	WP_141950998.1	E8E01_08060	541	LOV+Kinase+RR
			----	WP_141952096.1	E8E01_15495	531	LOV+Kinase+RR
			----	WP_141952273.1	E8E01_16215	354	LOV+Kinase
			----	WP_141953429.1	E8E01_20770	366	LOV+Kinase
9	*M.populi*	BJ001	B1ZH86	ACB78490.1	Mpop_0309	190	Short-LOV
			B1ZI10	ACB78496.1	Mpop_0315	901	LOV+PAS$_3$+GAF+Kinase
			B1Z812	ACB78979.1	Mpop_0801	488	LOV+PAS+HWE-Kinase
			B1ZG87	ACB79745.1	Mpop_1581	541	LOV+Kinase+RR
			B1ZJK1	ACB81487.1	Mpop_3336	531	LOV+Kinase+RR
			B1ZKQ8	ACB81628.1	Mpop_3478	354	LOV+Kinase
			B1ZCH2	ACB82221.1	Mpop_4105	888	LOV+PAS+GAF+Kinase+RR
			B1ZGT9	ACB82617.1	Mpop_4519	366	LOV+Kinase
10	*M. zatmanii*	PSBB041	A0A1W6RDY7	WP_003599658.1	B2G69_02090	366	LOV+Kinase
			A0A1W6RGV8	WP_085856634.1	B2G69_08090	1072	LOV+PAS$_3$+Kinase+RR
			A0A1W6RIL3	WP_056501423.1	B2G69_11355	488	LOV+PAS+HWE-Kinase
			A0A1W6RKL6	WP_085857055.1	B2G69_15905	541	LOV+Kinase+RR
			A0A1W6RPC0	WP_056499167.1	B2G69_23260	533	LOV+Kinase+RR
			A0A1W6RQ45	WP_056499415.1	B2G69_23955	354	LOV+Kinase

Table S1.c *Methylobacteria* group: BLUF proteins, accession codes and domain architecture

	Methylobacterium	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. aquaticum*	MA-22A	A0A0C6EYC5	WP_060846567.1	Maq22A_c09520	150	Short-BLUF
			A0A0C6FG98	BAQ46067.1	Maq22A_c14425	156	Short-BLUF
			A0A0C6FKV3	WP_060848619.1	Maq22A_c23995	165	Short-BLUF
2	*M. durans*	17SD2-17	A0A2U8W8D7	AWN41868.1	DK389_16890	155	Short-BLUF
			A0A2U8W8Y6	AWN41782.1	DK389_16325	158	Short-BLUF
			A0A2U8W305	AWN40447.1	DK389_07765	308	BLUF+Unknown
3	*M. mesophilicum*	SR1.6/6	M7XZR2	QGY00992.1	MmSR116_2001	155	Short-BLUF
			M7XWX4	QGY03645.1	MmSR116_5806	294	Short-BLUF
			M7YN43	QGY02016.1	MmSR116_2990	134	Short-BLUF
4	*M. nodulans*	ORS 2060	B8IB70	WP_015928965.1	Mnod_2309	155	Short-BLUF
5	*M. oryzae*	CBMB20	A0A089NTJ6	AIQ90737.1	MOC_2982	134	Short-BLUF
			A0A089NY66	AIQ92332.1	MOC_4577	134	Short-BLUF
			A0A089P248	AIQ92835.1	MOC_5080	326	BLUF+Unknown
			A0A089QH30	AIQ93878.1	MOC_6124	155	Short-BLUF
6	*M. phyllosphaerae*	CBMB27	----	WP_075380907.1	MCBMB27_03493	134	Short-BLUF

			----	WP_075380932.1	MCBMB27_03588	158	Short-BLUF
			----	WP_075381057.1	MCBMB27_03931	326	BLUF+Unknown
7	*M. radiotolerans*	JCM 2831	B1LTA6	ACB22412.1	Mrad2831_0397	143	Short-BLUF
			B1M108	ACB24558.1	Mrad2831_2569	134	Short-BLUF
			B1M482	ACB26377.1	Mrad2831_4411	309	BLUF+Unknown
			B1M0G5	ACB27487.1	Mrad2831_5542	155	Short-BLUF
8	*M.sp.*	17Sr1-1	A0A2U8X091	AWN52044.1	DK412_10450	150	Short-BLUF
			A0A2U8X872	AWN54755.1	DK412_26675	194	Short-BLUF
			A0A2U8XCY0	AWN55656.1	DK412_15735	270	BLUF+Unknown
			A0A2U8X5G2	AWN53549.1	DK412_19670	156	Short-BLUF
9	*M. sp.*	17Sr1-43	A0A2U8VXJ4	WP_109953153.1	DK427_21505	150	Short-BLUF
			A0A2U8VX32	WP_109953486.1	DK427_23415	155	Short-BLUF
			A0A2U8VRU8	WP_010687537.1	DK427_09910	310	BLUF+Unknown
10	*M. sp.*	4-46	B0U8I2	WP_012331722.1	M446_1828	296	BLUF+Unknown
			B0UJP3	WP_012332391.1	M446_2545	150	Short-BLUF
			B0UIK0	WP_012333772.1	M446_4017	373	BLUF+Unknown
			B0ULI8	WP_012333923.1	M446_4183	155	Short-BLUF
			B0UQT1	WP_012334306.1	M446_4576	162	Short-BLUF
11	*M. sp.*	AMS5	A0A109QSJ5	WP_056200705.1	Y590_03755	155	Short-BLUF
			A0A0X1SLI7	WP_060770931.1	Y590_17880	158	Short-BLUF
			A0A0X1SN06	WP_060771282.1	Y590_20075	148	Short-BLUF
			----	WP_083530896.1	Y590_RS25905	140	Short-BLUF
12	*M.sp.*	C1	----	WP_012317408.1	BKE41_RS02410	143	Short-BLUF
			----	WP_058607382.1	BKE41_RS23015	315	BLUF+Unknown
			----	WP_020092935.1	BKE41_RS29370	155	Short-BLUF
13	*M. sp.*	DM1	A0A2U8HS49	WP_108938908.1	C0214_04065	155	Short-BLUF
			A0A2U8HPZ9	WP_108939204.1	C0214_05920	311	BLUF+Unknown
			A0A2U8HZB6	WP_108941420.1	C0214_20025	150	Short-BLUF
			A0A2U8I2F9	WP_108943058.1	C0214_22190	157	Short-BLUF
14	*M. sp.*	XJLW	A0A2U9U2L3	WP_111473188.1	A3862_02970	155	Short-BLUF
			A0A2U9TWT9	WP_051045092.1	A3862_10910	158	Short-BLUF
			A0A2U9TXI1	WP_043759270.1	A3862_11365	134	Short-BLUF
15	*M. terrae*	17Sr1-28	A0A2U8WHD1	WP_109957997.1	DK419_04285	156	Short-BLUF
			A0A2U8WKG8	WP_109959083.1	DK419_10825	240	BLUF+Unknown
			A0A2U8WKV7	WP_109959101.1	DK419_10950	208	BLUF+Unknown
			A0A2U8WNB0	WP_109959285.1	DK419_12010	150	Short-BLUF

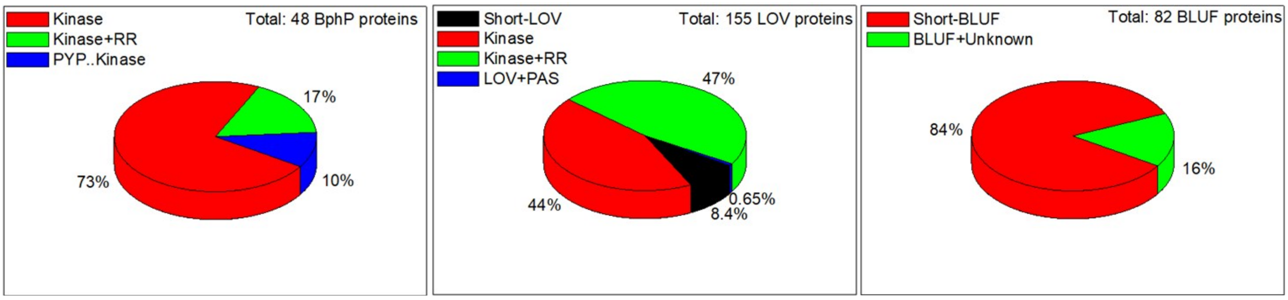
***Methylorubra* group: BLUF proteins, accession codes and domain architecture**

	Methylorubrum	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. extorquens*	PSBB040	A0A1S1P3U3	WP_003603713.1	BV511_02980	155	Short-BLUF
			A0A1P8QX67	WP_012251938.1	BV511_06935	150	Short-BLUF
			A0A1S1P5Q9	WP_012251938.1	BV511_10370	150	Short-BLUF
			A0A1P8QPL9	WP_012255183.1	BV511_12365	148	Short-BLUF
			A0A1P8QR36	WP_076642775.1	BV511_15100	307	BLUF+Unknown
			A0A1P8QR02	WP_076642777.1	BV511_15105	150	Short-BLUF
2	*M. extorquens*	TK0001	A0A1S1P0H0	WP_012255183.1	TK0001_1440	148	Short-BLUF
			A0A1S1P3U3	WP_003603713.1	TK0001_5244	155	Short-BLUF
			A0A2N9AYN7	WP_012251938.1	TK0001_5883	150	Short-BLUF
3	*M. extorquens*	AM1	C5AVI4	ACS38652.1	MexAM1_META1p0723	155	Short-BLUF
			C5B322	CAX26640.1	MexAM1_META1p4421	148	Short-BLUF
4	*M. extorquens*	CM4	B7L1R5	WP_012605615.1	Mchl_0527	150	Short-BLUF
			B7L240	WP_003603713.1	Mchl_0912	155	Short-BLUF
			B7KRN3	WP_015951503.1	Mchl_3364	150	Short-BLUF
			B7KN60	WP_015952252.1	Mchl_4401	148	Short-BLUF
			B7KRN3	WP_015951503.1	Mchl_4786	150	Short-BLUF
5	*M. extorquens*	DM4	C7CE09	WP_003603713.1	METDI1095	155	Short-BLUF
			C7CJD7	WP_015824174.1	METDI5025	148	Short-BLUF
6	*M. extorquens*	PA1	A9VWG7	WP_012251938.1	Mext_0114	150	Short-BLUF
			A9W198	WP_003603713.1	Mext_0949	155	Short-BLUF
			A9W8Q2	WP_012255183.1	Mext_4031	148	Short-BLUF
7	*M. populi*	P-1M	A0A160PBB3	WP_017487136.1	MPPM_0981	155	Short-BLUF
			A0A160PM13	WP_096486808.1	MPPM_4395	157	Short-BLUF
8	*M.populi*	YC-XJ1	----	WP_012452822.1	E8E01_04445	155	Short-BLUF
			----	WP_052300129.1	E8E01_20740	158	Short-BLUF
9	*M.populi*	BJ001	B1ZGT3	ACB82611.1	Mpop_4513	162	Short-BLUF
			B1Z908	ACB79066.1	Mpop_0888	155	Short-BLUF
10	*M. zatmanii*	PSBB041	A0A1W6RDU7	WP_052300129.1	B2G69_02060	148	Short-BLUF
			A0A1W6RIT6	WP_085856840.1	B2G69_11735	155	Short-BLUF

Table S1.d *Methylobacteria* group: rhodopsins, accession codes

	Methylobacterium	**strain**	**UniProt**	**NCBI**	**Gene name**	**aa**	**Domain architecture**
1	*M. aquaticum*	MA-22A	A0A0C6F7V1	BAQ48891	Maq22A_1p32955	252	Rhodopsin
2	*M. durans*	17SD2-17	----	----	----	----	----
3	*M. mesophilicum*	SR1.6/6	M7Y840	QGY06042.1	MmSR116_1495	250	Rhodopsin
4	*M. nodulans*	ORS 2060	----	----	----	----	----
5	*M. oryzae*	CBMB20	----	----	----	----	----
6	*M. phyllosphaerae*	CBMB27	----	----	----	----	----
7	*M. radiotolerans*	JCM 2831	----	----	----	----	----

8	*M.sp.*	17Sr1-1	----	----	----	----	----
9	*M. sp.*	17Sr1-43	----	----	----	----	----
10	*M. sp.*	4-46	B0UM74	WP_012330516.1	M446_0537	252	Rhodopsin
11	*M. sp.*	AMS5	A0A0C6F7V1	BAQ48891	Maq22A_1p32955	252	Rhodopsin
12	*M.sp.*	C1	----	----	----	----	----
13	*M. sp.*	DM1	----	----	----	----	----
14	*M. sp.*	XJLW	----	----	----	----	----
15	*M.terrae*	17Sr1-28	----	----	----	----	----
***Methylorubra* group: rhodopsins - none found**							



Relative abundance of domains associated to the photosensing domains/modules in modular, non rhodopsin photoreceptors for the strains analysed in this work. PAS domains are in general not indicated with the exception of PYP in a total of five BphPs and the sole case of a LOV proteins formed by a LOV domain and 2 PAS domains associated (see tables S1a abd S1b). For BLUF proteins in 13 cases there is a quite long region of protein (>150 aa) without any recognizable structure, indicated as “unknown”.

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                      ↓ ↓      ↓                       ↓↓↓ ↓↓
Mr4511         34  MPMIITDPAQHDNPIVFVNDAFLKLTGYTRMEVVGRNCRFLQ-----------
BsYtvA         25  VGVVITDPALEDNPIVYVNQGFVQMTGYETEEILGKNCRFLQ-----------
Asphot1-LOV2  413  KNFVITDPRLPDNPIIFASDSFLQLTEYSREEILGRNCRFLQ-----------
Crphot-Lov1    20  HTFVVADATLPDCPLVYASEGFYAMTGYGPDEVLGHNCRFLQ-----------
NcVVD          71  CALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKST
PstLOVHK       33  MPMIVTDPNRPDNPIIFSNRAFLEMTGYTAEEILGTNCRFLQ-----------
XacLOV         39  MPMTVTDPHLPDNPIVFANRAFLEMTGYAADEVIGNNCRFLQ-----------
VfAureo       217  QNFVITDASLPDNPIVYASRGFLTLTGYSLDQILGRNCRFLQ-----------
DsLOV          36  MSVVFSDPSQPDNPMIYVSDAFLVQTGYTLEEVLGRNCRFLQ-----------
Acvphy3-LOV2  929  KSFVITDPRLPDNPIIFASDRFLELTEYTREEVLGNNCRFLQ-----------
McLOVr         24  NGVTLADPDQPDAPIVYANKAFESMTGYGQEEIIGRNCRFLQ-----------
HjENV1         98  VSLTLCDISLPDAPIVYASPGFYQLTGYSAPEIMGRNCRFLQNSPHMP-----
McPAC         157  VGIVIADARLPDMPLIYVNPAFEEITGYSDAEVLGYNCRFLQ-----------

           Fα             Gβ            Hβ            Iβ
.....HHHHHHHHHHHHH...EEEEEEEEE...EEEEEEEEEEEEEE....EEEEEEEEEEE
        ↓  ↓↓  ↓         ↓ ↓         ↓ ↓ ↓            ↓↓↓ ↓
GPDTEAAAVDRLRAAIRREEDIRVDLLNYRKDGSTFQNALYVGPVRDEAGRVVYFFASQLDV     B1M516
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GDDRDQEGLAPLREAMRTHQHIEVTLRNYRKNGELFFNKLNITPLLDSRGAVIYYLGVQYDV     J7QP72
PPGRVSDAVQEMRRAIRAHQEVQVRIVNYKKNGTPFTNVVTILPLWADPSGHHFAVGLQAEL     G0RUC2
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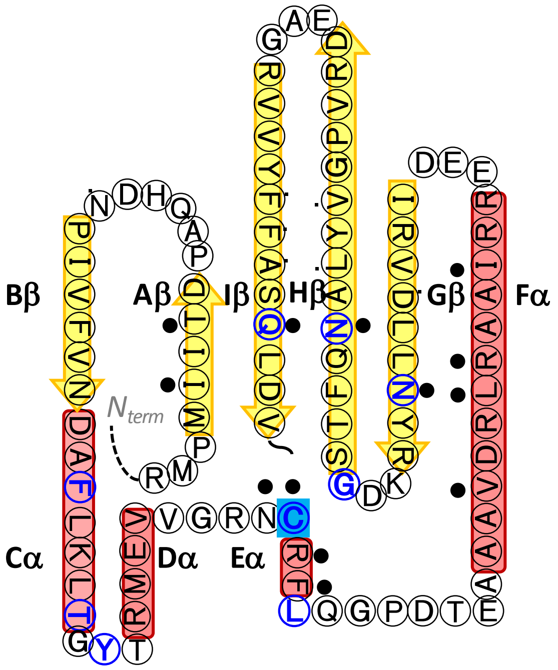


Fig. S1. Top, sequence alignment (performed with the CLUSTAL Omega tool at the European Bioinformatics Institute, EMBL-EBI, using default parameters) of the LOV core of *Mr*4511 with other LOV domains of eukaryotic and prokaryotic origin; the secondary structure elements as derived from the structure of *Bs*YtvA (PDB access code 2pr5) are indicated as E (yellow, β-strands) and H (red, α-helices). Residues interacting with the chromophore are indicated with arrows. UniProt accession code are give at the end of each sequence. Bottom, presumed topology of the LOV core of *Mr*4511 (from Arg33 to Val137) sequence mapped onto the secondary structure elements with one-letter code for amino acids, as derived from the sequence alignment above; marked in blue: the 10 superconserved residues in LOV domains, the reactive Cys71 is further highlighted in cyan; a dot marks aa within 4 Å from FMN.

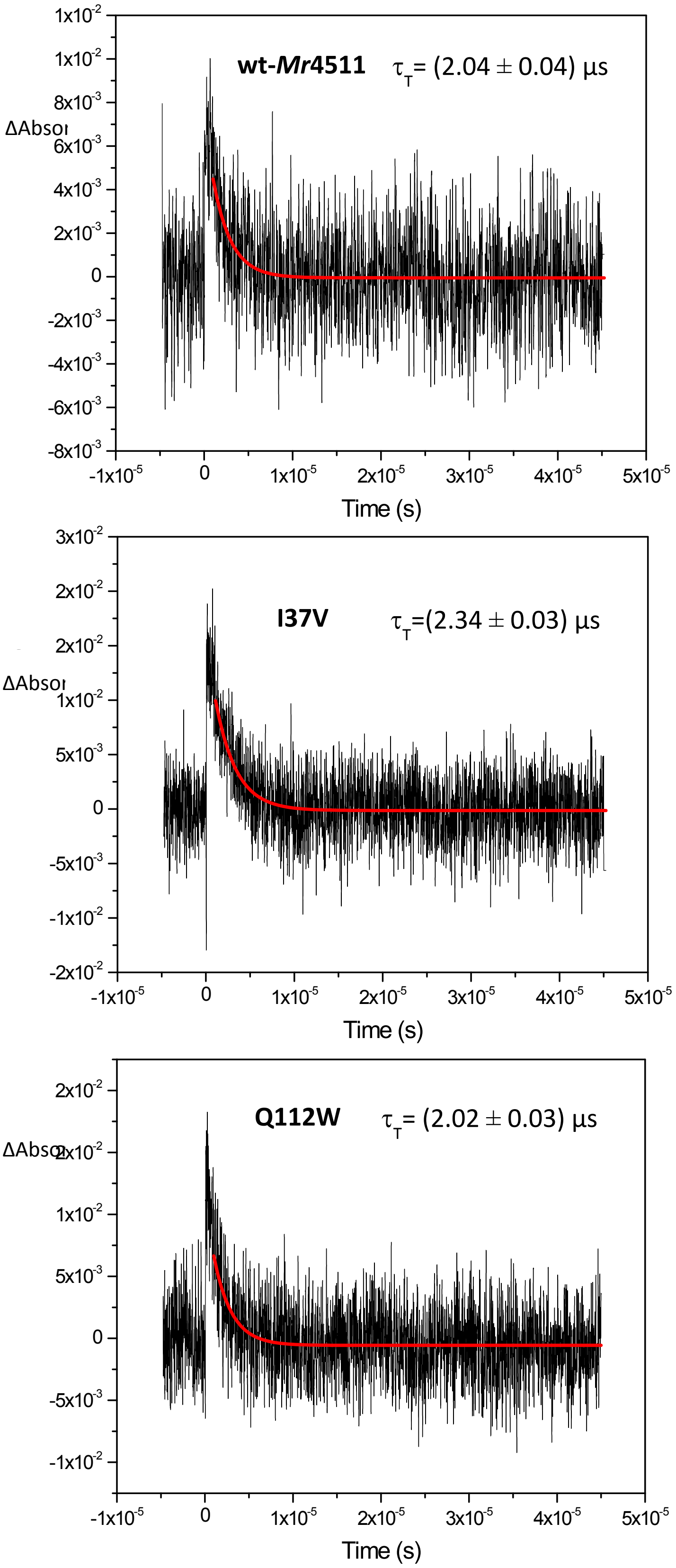


Fig. S2. Triplet-triplet absorption decay for *Mr*4511 obtained by a single-shot transient absorption experiment. The red curve derived from a mono-exponential fitting decay function of the flash photolysis signal (excitation at 475 nm) is overlaid onto the black experimental trace.

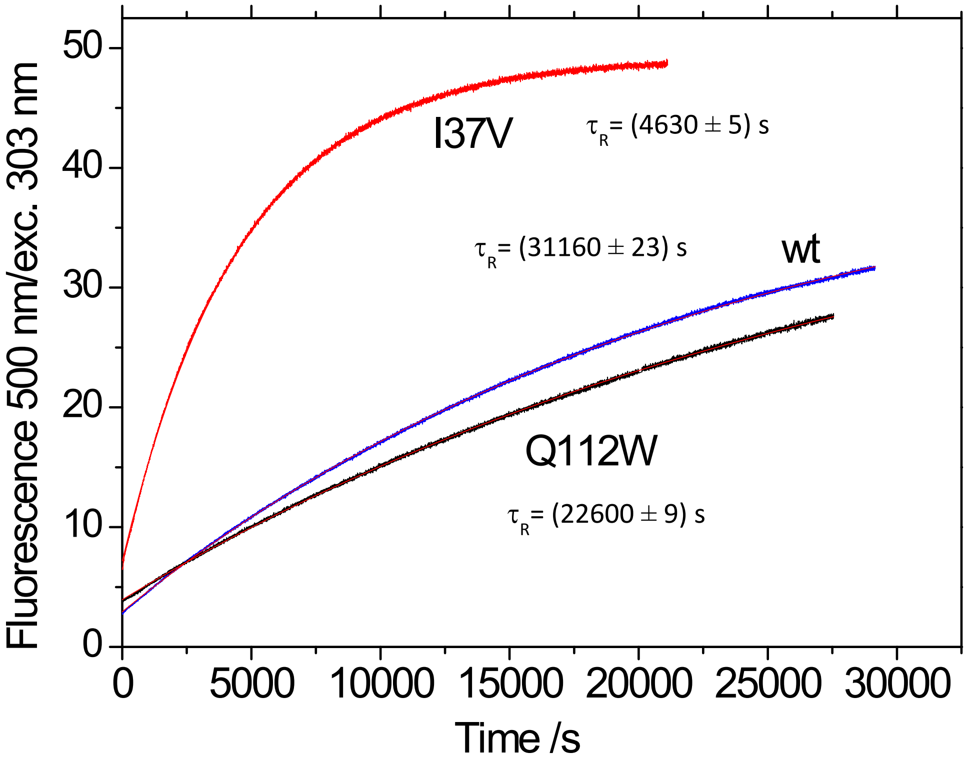
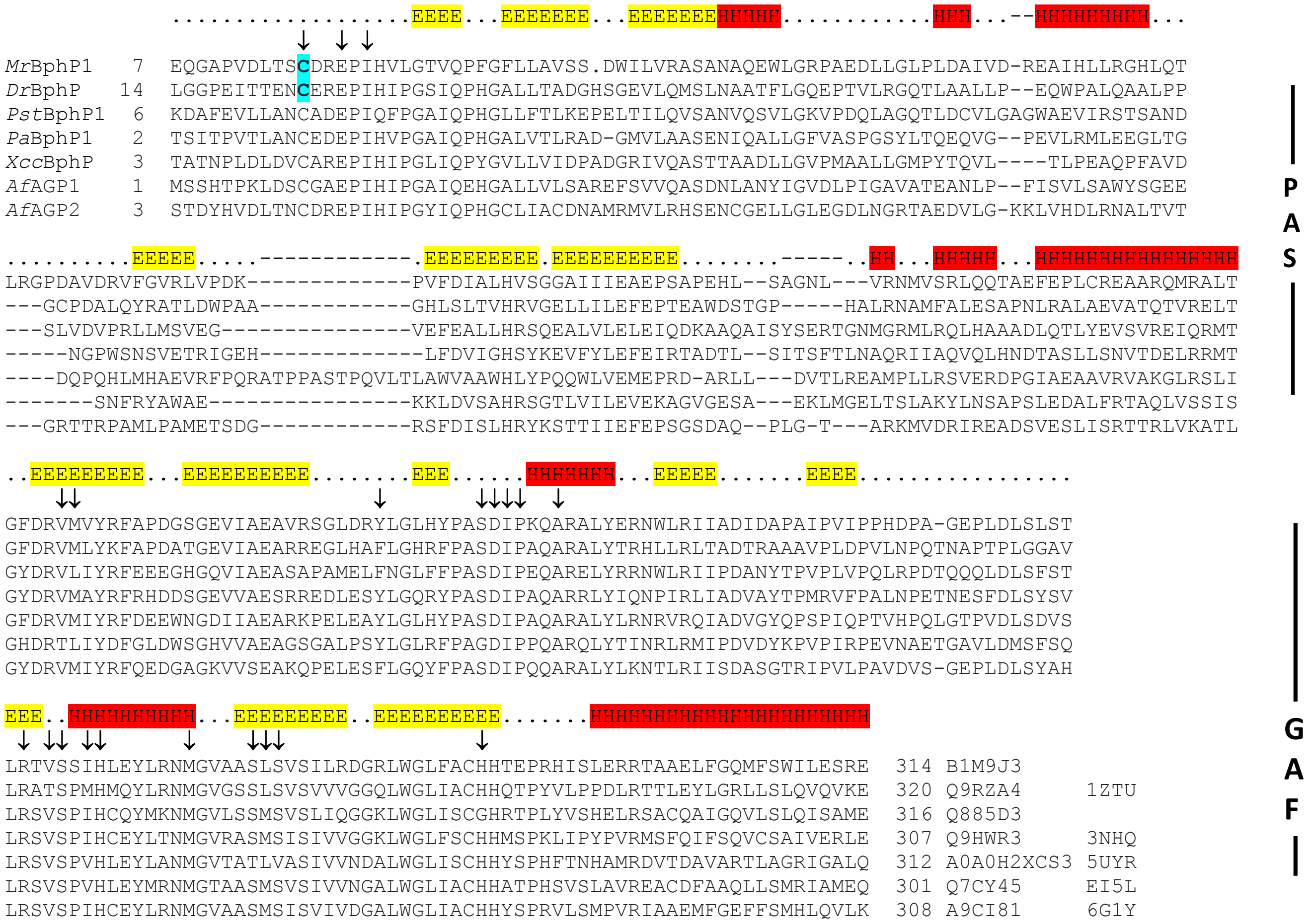


Fig. S3. Recovery kinetics of *Mr*4511 proteins, measured at 22 °C as increase in fluorescence at 500 nm starting from the light state. λ_{ex}=303 nm. Fitting mono-exponential solid lines are superimposed.



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             ...................EEEE...EEEEEEE...EEEEEEEHHHHH............HHH...--HHHHHHHHH...
                       ↓  ↓ ↓
MrBphP1    7  EQGAPVDLTSCDREPIHVLGTVQPFGFLLAVSS.DWILVRASANAQEWLGRPAEDLLGLPLDAIVD-REAIHLLRGHLQT
DrBphP    14  LGGPEITTENCEREPIHIPGSIQPHGALLTADGHSGEVLQMSLNAATFLGQEPTVLRGQTLAALLP--EQWPALQAALPP
PstBphP1   6  KDAFEVLLANCADEPIQFPGAIQPHGLLFTLKEPELTILQVSANVQSVLGKVPDQLAGQTLDCVLGAGWAEVIRSTSAND
PaBphP1    2  TSITPVTLANCEDEPIHVPGAIQPHGALVTLRAD-GMVLAASENIQALLGFVASPGSYLTQEQVG--PEVLRMLEEGLTG
XccBphP    3  TATNPLDLDVCAREPIHIPGLIQPYGVLLVIDPADGRIVQASTTAADLLGVPMAALLGMPYTQVL----TLPEAQPFAVD
AfAGP1     1  MSSHTPKLDSCGAEPIHIPGAIQEHGALLVLSAREFSVVQASDNLANYIGVDLPIGAVATEANLP--FISVLSAWYSGEE
AfAGP2     3  STDYHVDLTNCDREPIHIPGYIQPHGCLIACDNAMRMVLRHSENCGELLGLEGDLNGRTAEDVLG-KKLVHDLRNALTVT

..........EEEEE.....------------.EEEEEEEEE.EEEEEEEEEE........-----..HH...HHHHH...HHHHHHHHHHHHHHHH
LRGPDAVDRVFGVRLVPDK-------------PVFDIALHVSGGAIIIEAEPSAPEHL--SAGNL---VRNMVSRLQQTAEFEPLCREAARQMRALT
---GCPDALQYRATLDWPAA------------GHLSLTVHRVGELLILEFEPTEAWDSTGP-----HALRNAMFALESAPNLRALAEVATQTVRELT
---SLVDVPRLLMSVEG---------------VEFEALLHRSQEALVLELEIQDKAAQAISYSERTGNMGRMLRQLHAAADLQTLYEVSVREIQRMT
-----NGPWSNSVETRIGEH-------------LFDVIGHSYKEVFYLEFEIRTADTL--SITSFTLNAQRIIAQVQLHNDTASLLSNVTDELRRMT
----DQPQHLMHAEVRFPQRATPPASTPQVLTLAWVAAWHLYPQQWLVEMEPRD-ARLL---DVTLREAMPLLRSVERDPGIAEAAVRVAKGLRSLI
-------SNFRYAWAE----------------KKLDVSAHRSGTLVILEVEKAGVGESA---EKLMGELTSLAKYLNSAPSLEDALFRTAQLVSSIS
---GRTTRPAMLPAMETSDG------------RSFDISLHRYKSTTIIEFEPSGSDAQ--PLG-T---ARKMVDRIREADSVESLISRTTRLVKATL

..EEEEEEEEE...EEEEEEEEEE........EEE......HHHHHHH...EEEEE.......EEEE.................
    ↓↓                       ↓       ↓↓↓↓  ↓
GFDRVMVYRFAPDGSGEVIAEAVRSGLDRYLGLHYPASDIPKQARALYERNWLRIIADIDAPAIPVIPPHDPA-GEPLDLSLST
GFDRVMLYKFAPDATGEVIAEARREGLHAFLGHRFPASDIPAQARALYTRHLLRLTADTRAAAVPLDPVLNPQTNAPTPLGGAV
GYDRVLIYRFEEEGHGQVIAEASAPAMELFNGLFFPASDIPEQARELYRRNWLRIIPDANYTPVPLVPQLRPDTQQQLDLSFST
GYDRVMAYRFRHDDSGEVVAESRREDLESYLGQRYPASDIPAQARRLYIQNPIRLIADVAYTPMRVFPALNPETNESFDLSYSV
GFDRVMIYRFDEEWNGDIIAEARKPELEAYLGLHYPASDIPAQARALYLRNRVRQIADVGYQPSPIQPTVHPQLGTPVDLSDVS
GHDRTLIYDFGLDWSGHVVAEAGSGALPSYLGLRFPAGDIPPQARQLYTINRLRMIPDVDYKPVPIRPEVNAETGAVLDMSFSQ
GYDRVMIYRFQEDGAGKVVSEAKQPELESFLGQYFPASDIPQQARALYLKNTLRIISDASGTRIPVLPAVDVS-GEPLDLSYAH

EEE..HHHHHHHHHH...EEEEEEEEE..EEEEEEEEEE.......HHHHHHHHHHHHHHHHHHHHHH
 ↓ ↓↓ ↓↓      ↓    ↓↓↓               ↓
LRTVSSIHLEYLRNMGVAASLSVSILRDGRLWGLFACHHTEPRHISLERRTAAELFGQMFSWILESRE  314 B1M9J3
LRATSPMHMQYLRNMGVGSSLSVSVVVGGQLWGLIACHHQTPYVLPPDLRTTLEYLGRLLSLQVQVKE  320 Q9RZA4     1ZTU
LRSVSPIHCQYMKNMGVLSSMSVSLIQGGKLWGLISCGHRTPLYVSHELRSACQAIGQVLSLQISAME  316 Q885D3
LRSVSPIHCEYLTNMGVRASMSISIVVGGKLWGLFSCHHMSPKLIPYPVRMSFQIFSQVCSAIVERLE  307 Q9HWR3     3NHQ
LRSVSPVHLEYLANMGVTATLVASIVVNDALWGLISCHHYSPHFTNHAMRDVTDAVARTLAGRIGALQ  312 A0A0H2XCS3 5UYR
LRSVSPVHLEYMRNMGTAASMSVSIVVNGALWGLIACHHATPHSVSLAVREACDFAAQLLSMRIAMEQ  301 Q7CY45     EI5L
LRSVSPIHCEYLRNMGVAASMSISVIVDGALWGLIACHHYSPRVLSMPVRIAAEMFGEFFSMHLQVLK  308 A9CI81     6G1Y
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Fig. S4. sequence alignment of the PAS-GAF module from *Mr*BphP1 and other bacterial phytochromes. After application of the CLUSTAL Omega tool (see fig. S1) the alignment was adjusted for the PAS domain, that bears a larger variability than the GAF domain, according to secondary structure elements as derived from published bacteriophytochrome structures. ; the secondary structure elements as derived from the structure of *DrBphP* (*Dr* = Deinococcus radiodurans; PDB access code 1ZTU) are indicated as E (yellow, β-strands) and H (red, α-helices). Residues interacting with the chromophore are indicated with arrows. UNIPROT protein codes are given at the end for the sequences considered as well as the PDB access codes used to improve the alignment of the PAS domains.

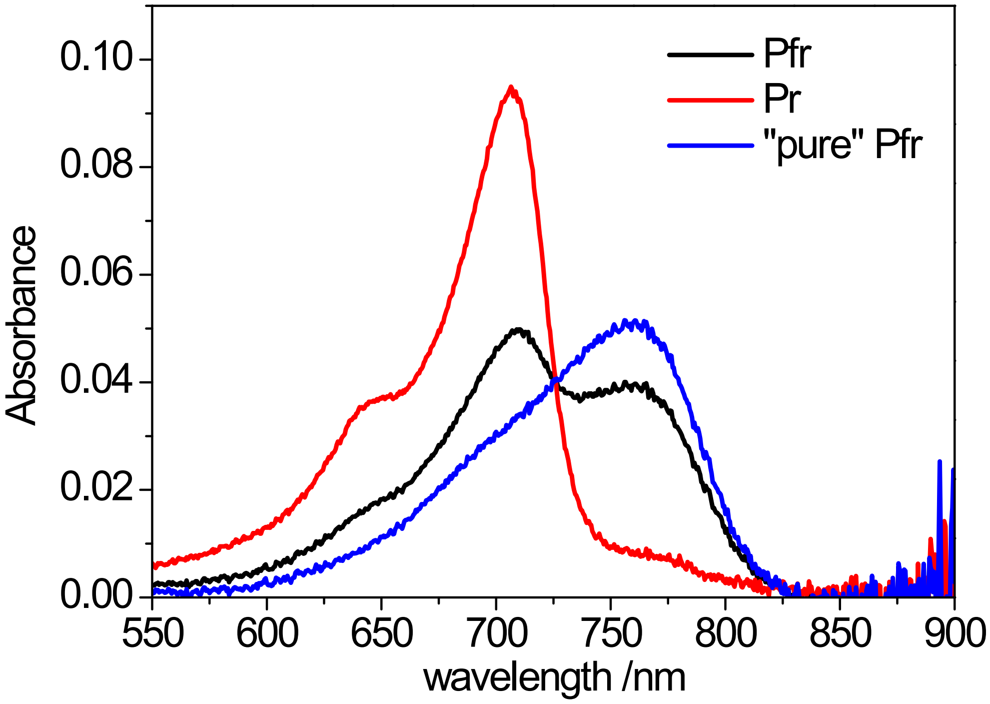

Fig. S5. Absorption spectra of *Mr*BphP1$_{\mathrm{PGP}}$. Starting from the Pr form (red), the maximally obtainable amount of Pfr is shown (black, steady state irradiation, λ = 650 nm). The spectrum of the calculated pure Pfr form (blue line) was obtained by assuming a linear combination of Pr and Pfr fractions summing up to 1. $A_{pure\,Pfr} = \frac{A_{Pfr} - f \times A_{Pr}}{1 - f}$ where $f = \frac{Pr}{Pfr}$ is the photoconverted fraction, here we obtained the spectrum with $f = 0.27$.

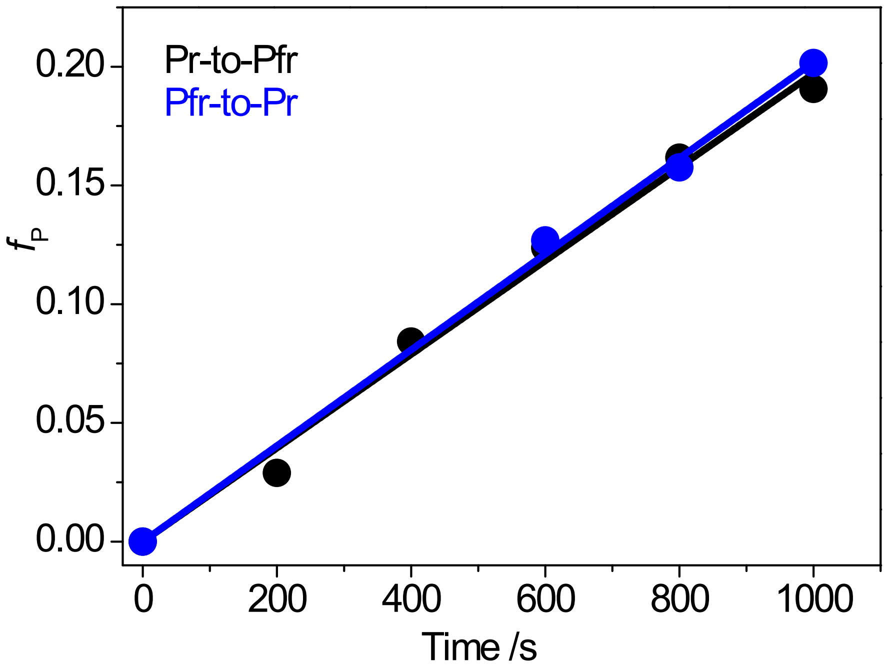

Fig. S6. Kinetics of the Pfr-to-Pr route of photoconversion for *Mr*BphP1$_{504}$ (blue circles) compared to the Pr-to-Pfr photoconversion. (see also figure 7 in the main text). In this case photoconversion was achieved by illuminating with light coming form the excitation lamp of the steady-state fluorimeter (660 nm for the Pr state and 760 nm for the Pfr state), absorbance was recorded using the spectrophotometer in the kinetic mode and recording absorbances for 5 s under illumination with a 670 nm laser light.

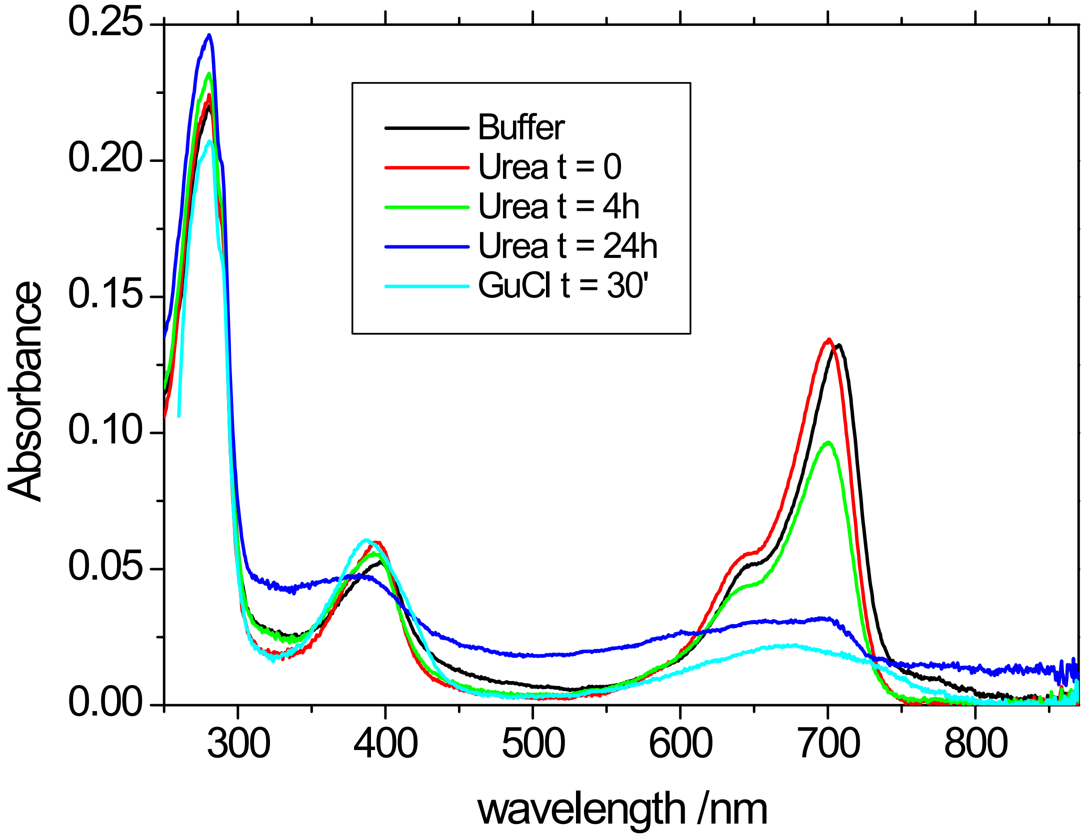

Fig. S7. Absorption spectra of *Mr*BphP1 in buffer compared to spectra taken in urea 7.6 M (pH=2) at several times, and in GuCl 7.8 M after half and hour.