

<i>M. loti</i>	<i>S. meliloti</i>	<i>P. aeruginosa</i>	<i>A. tumefaciens</i>	<i>C. crescentus</i>	Regulatory motif
9	25	1	3	0	Adenylate and Guanylate cyclase catalytic domain
0	0	1	0	0	Adenylate cyclase, class-I
22	15	9	14	8	AsnC (Irp) family
4	1	2	1	0	Autoinducer synthetase
43	38	63	36	13	Bacterial regulatory helix-turn-helix proteins, araC family
85	95	122	75	12	Bacterial regulatory helix-turn-helix proteins, lysR family
24	17	5	14	7	Bacterial regulatory proteins, arsR family
18	12	8	13	5	Bacterial regulatory proteins, crp family
14	8	4	7	2	Bacterial regulatory proteins, deoR family
12	9	21	8	7	Bacterial regulatory proteins, Fis family
55	56	29	48	12	Bacterial regulatory proteins, gntR family
18	29	6	22	13	Bacterial regulatory proteins, lacl family
29	24	32	23	5	Bacterial regulatory proteins, luxR family
6	7	8	7	3	Bacterial regulatory proteins, merR family
47	28	42	32	30	Bacterial regulatory proteins, tetR family
7	9	9	8	0	Bacterial transcriptional regulator
1	1	0	1	1	CarD-like transcriptional regulator
10	8	6	6	4	Cold-shock DNA-binding domain
2	3	2	3	2	Ferric uptake regulator family
32	17	33	29	11	GGDEF domain
6	8	3	5	1	Helix-turn-helix domain, rpiR family
43	33	55	40	44	His Kinase A (phosphoacceptor) domain
57	43	67	50	56	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase
0	0	0	0	0	LuxS protein
32	22	17	27	9	MarR family
2	2	1	2	3	Nitrogen regulatory protein P-II
69	63	91	64	71	Response regulator receiver domain
7	10	0	10	3	ROK family
2	1	1	1	1	Sigma-54 factors family
13	12	22	9	5	Sigma-54 interaction domain
7	4	9	2	3	Sigma-70 factor
19	11	17	11	13	Sigma-70 factor (ECF subfamily)
13	13	6	6	5	SIS domain
28	18	24	22	12	Transcriptional regulatory protein, C terminal
7281	6206	5565	5420	3737	Total genes in organism
7.59	6.68	6.3	5.68	4.01	Genome size (Mb)
736	642	716	599	361	Total regulatory motifs
603	539	549	486	257	Distinct regulatory genes
8.28	8.69	9.87	8.97	6.88	% regulatory genes