

Table S4. PatSer motif search (Fig 6) and PWM for CenR binding motif in *Rhodobacter sphaeroides* 2.4.1

A. PatSer motif search

Identified gene ¹	Position (distance from start codon) ²	Score ³	ln(p-value)	Sequence
<i>Rhodobacter sphaeroides</i> 2.4.1				
<i>cenR</i>	183	7.4	-9.45	TTGCAGGAAATTGAA
<i>msrA</i>	199	9.98	-12.6	TGGCGGAGCGTGAT
<i>RSP1807</i>	231	8.59	-10.77	TCGCAAAACCTTGAT
<i>RSP1860</i>	177	7.11	-9.16	TGGCAAAAATGTCAC
<i>surA</i>	142	9.01	-11.28	TGACATGATCGTGTG
<i>tolQ</i>	213	9.98	-12.6	TGACGCAGATGTGTT
<i>Agrobacterium tumefaciens</i> BIM B-1315G				
<i>cenR</i> (IAI05_12475)	65	8.44	-10.6	TCACGAGATTTTGCT
<i>msrA</i> (IAI05_13425)	101	8.46	-10.62	TGGCGCTTCATTGAA
<i>RSP1807</i> (IAI05_12080)	197	10.11	-12.79	TGACTTTCTATTGAA
<i>RSP1860</i> (IAI05_01710)	171	9.5	-11.91	ACACATTAACGTGAA
<i>surA</i> (IAI05_17235)	239	3.26	-5.89	TGGAAGTTTTTTCAG
<i>tolQ</i> (IAI05_18005)	240	7.88	-9.96	TAACACGCGTTTGAA
<i>Brucella abortus</i> 2308				
<i>cenR</i> (BAB1_2006)	121	4.33	-6.68	TCAAGGTCTTTTCGAG
<i>msrA</i> (BAB2_1029)	116	7.5	-9.55	AGAAGCGACCGTGAC
<i>RSP1807</i> (BAB1_0088)	146	7.66	-9.73	TGAATTCCTATTGAT
<i>RSP1860</i> (BAB1_0408)	94	5.39	-7.55	TAGCAATGGTCTGAT
<i>surA</i> (BAB1_1944)	160	7.32	-9.37	TTGCTTCAAAGTGAT
<i>tolQ</i> (BAB1_1712)	238	5.9	-8	TAACGGATTTGCGAT
<i>Caulobacter crescentus</i> NA1000				
<i>cenR</i> (CCNA_03859)	195	4.02	-6.44	TCCCGCAAGCTCGAA
<i>msrA</i> (CCNA_01046)	65	3.7	-6.21	AGAGAGGGATTTCGAA
<i>RSP1807</i> (CCNA_03780)	259	8.04	-10.14	TCACGGCCTCGTGAA
<i>RSP1860</i> (CCNA_03062)	125	6.32	-8.39	TCAAGTGCTTGCGAG
<i>surA</i> (CCNA_03163)	145	3.6	-6.13	TGGTGTCAACGCGAA
<i>tolQ</i> (CCNA_03341)	66	2.49	-5.36	TGAGGTGCTGTTCGA
<i>Rhodopseudomonas palustris</i> RCB100				

<i>cenR</i> (RPA0283)	55	5.73	-7.85	ACAATCGCGCGTGAT
<i>msrA</i> (RPA4834)	100	7.19	-9.02	TGAAATTGAGTTGAG
<i>RSP1807</i> (RPA0201)	108	5.82	-7.93	TGAGTGGCAGGTGAA
<i>RSP1860</i> (RPA0201)	NA	NA	NA	NA
<i>surA</i> (RPA0511)	83	6.60	-8.65	TTTCATCATTTTGAC
<i>tolQ</i> (RPA1117)	143	7.19	-9.24	TGACAGGGGATTGAG

¹blastn search to identify homologs of each *Rb. sphaeroides* gene (locus tag listed).

²Identified in 300bp genomic region upstream of start codon using in search.

³Scores determined by comparison of the base position in the sequence to the same position in the PWM (below). Scores for each position are summed for the length of the sequence, larger score means more positions matched more frequent bases in the PWM.

NA - could not identify a homolog with high sequence homology.

B. PWM CenR binding motif in *Rhodobacter sphaeroides* 2.4.1 (Fig 4A) formatted for Patser

nucleotide	Logo Position														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
A	1	0	7	1	2	2	2	3	2	1	0	0	0	8	3
C	0	3	0	8	0	4	1	2	2	4	1	1	0	0	4
G	0	6	3	1	6	1	5	3	3	1	6	0	10	1	1
T	9	1	0	0	1	3	2	2	3	4	2	9	0	1	3