Table S4. Data collection and refinement statistics for GapR structures, related to Figure 6.

	Apo *Bosea sp.* Root 381 GapR	***Caulobacter crescentus* GapR-DNA**	***Bosea sp.* Root 381 GapR-DNA**
Data collection			
Pdb code	6CFY	6CG8	6CFX
Space group	$P4_122$	C2	$P2_1$
Crystallization Conditions	15% MPD, 10 mM $MgCl_2$, HEPES (7.5) 0.001 M spermine	28% PEG 400, 0.002 M spermine, HEPES (7.5), 0.2 M $CaCl_2$	1.7 M Ammonium sulphate, MES (6.5)
Cell dimensions			
a, b, c (Å)	39.6, 39.6, 205.1,	95.9, 35.6, 115.6	51.3, 44.5, 107.1
α, β, γ (°)	90.0, 90.0, 120.0	90.0, 90.2, 90.0	90.0, 101.8, 90.0
Resolution (Å)	2.40 (38.8)*	2.30 (57.8)	2.0 (50.2)
R_{sym}	0.099 (1.89)	0.079 (0.358)	0.059 (0.174)
R_{pim}	0.041 (1.19)	0.071 (0.267)	0.042 (0.105)
I/σI	9.8 (1.5)	7.6 (2.4)	10.5 (2.9)
Redundancy	11.2 (8.0)	3.5 (3.5)	2.5 (2.0)
CC(1/2)	0.997 (0.319)	0.977 (0.956)	0.994 (0.075)
Refinement			
Resolution (Å)	2.40 (38.8)	2.30 (57.8)	2.0 (50.2)
No. reflections	12187	32492	29679
R_{work}/R_{free}	22.2/25.9	24.1/26.8	19.6/22.1
R.m.s. deviations			
Bond lengths (Å)	0.018	0.002	0.003
Bond angles (°)	1.657	0.690	0.504
Ramachandran analyses			
Favored (%)	100.0	98.7	99.3
Disallowed (%)	0.0	0.0	0.0

*Data for highest resolution shell