

Table S3. Deposited ALR Structures.

ALR	PDB code	Bacterial Species	Function	Domains ^a	Y/T Coupling Residues	Y/T Rotomer	Acidic Triad Residues ^b	Oligo-meric State ^c	Ref. ^d
RitR	4LZL	<i>Streptococcus pneumoniae</i>	iron/redox regulation, pathogenesis	REC-wHTH	Y/D	out/in	E,K,N	M	This work
AmiR	1QO0	<i>Pseudomonas aeruginosa</i>	transcriptional termination	REC-ANTAR	V/V	in	P,P,S	D	[17]
ChxR	3Q7R	<i>Chlamydia trachomatis</i>	development, pathogenesis	REC-wHTH	Y/L	out	S,E,E	D	[27]
HP1043	2PLN	<i>Helicobacter pylori</i>	growth <i>in vitro</i>	REC-wHTH	Y/S	in	E,K,S	D	[25]
FrzS	2I6F	<i>Myxococcus xanthus</i>	polar localization, motility	REC-Coiled-Coil-GluZincin	Y/T	in	E,S,A	T*,H*	[28]
KaiA	1M2E	<i>Synechococcus elongatus</i>	circadian clock regulation	REC-PP2C phosphatase	H/G	in	V,E,V	M	[29]
n/a	2B4A	<i>Bacillus halodurans</i>	unknown	REC-wHTH	Y/T	in	E,D,S	M	Unch.
n/a	2QZJ	<i>Clostridium difficile</i>	unknown	REC	Y/T	in	D,G,E	D	Sugadev <i>et al.</i> Unch.
n/a	2ZAY	<i>Desulfuromonas acetoxidans</i>	unknown	Type II Secretion system protein-REC	F/S	in	D,T,E	D	Fedorov <i>et al.</i> Unch.

n/a	3HV2	<i>Pseudomonas fluorescens</i>	unknown	REC-HD	Y/T	in	D,S,A	D	Patskovsky <i>et al.</i> Unch.
n/a	3KTO	<i>Pseudo-alteromonas atlantica</i>	unknown	REC	F/A	in	D,H,E	T*	Damodharan <i>et al.</i> Unch.

^awHTH, winged helix-turn-helix; ANTAR, RNA binding domain; GluZincin, aminopeptidase domain; HD, phosphohydrolase domain.

^bAcidic triad residue in their order of appearance (N-C terminus: Acidic triad-1, acidic triad-2, changed phospho-accepting aspartate coordinate).

^cM, monomer; D, dimer; T, trimer; H, hexamer.

^dUnch. Uncharacterized protein or soon to be published. See entry in the RCSB PDB protein databank.

*Dimer is not facilitated through the canonical REC alpha4-beta4-alpha5 interface.