

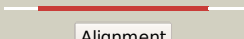

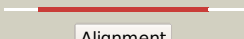










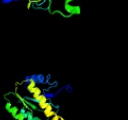


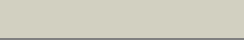







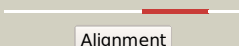

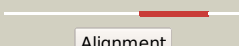

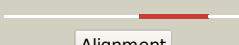

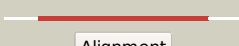


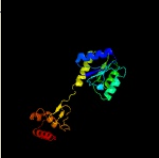

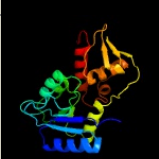

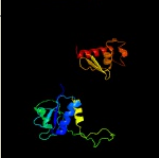




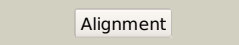





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0195 (-) _230897_231532
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	f6091da05c4e2aba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5hevC_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the berylofluoride-activated liar from 2 enterococcus faecium
2	<a href="#">c4yn8A_</a>	 Alignment		100.0	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chra; <b>PDBTitle:</b> crystal structure of response regulator chra in heme-sensing two2 component system
3	<a href="#">c4hyeB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription activator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
4	<a href="#">c4if4A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the magnesium and berylofluoride-activated vvar2 from staphylococcus aureus
5	<a href="#">c5f64C_</a>	 Alignment		100.0	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> putative positive transcription regulator (sensor evgs) from shigella2 flexneri
6	<a href="#">c3c3wB_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
7	<a href="#">c1rnlA_</a>	 Alignment		100.0	17	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
8	<a href="#">c5xt2C_</a>	 Alignment		100.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator fixj; <b>PDBTitle:</b> crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
9	<a href="#">c1zn2A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator sty
10	<a href="#">c5o8yG_</a>	 Alignment		100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
11	<a href="#">c3klnC_</a>	 Alignment		100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst

12	<a href="#">c1kgsA_</a>	 Alignment		99.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding response regulator d; <b>PDBTitle:</b> crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
13	<a href="#">c4lifuA_</a>	 Alignment		99.8	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
14	<a href="#">c3sztb_</a>	 Alignment		99.8	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
15	<a href="#">c1h0mD_</a>	 Alignment		99.8	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
16	<a href="#">c2q0oA_</a>	 Alignment		99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
17	<a href="#">c3q9sA_</a>	 Alignment		99.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of rra(1-215) from deinococcus radiodurans
18	<a href="#">c4s05B_</a>	 Alignment		99.8	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional regulator basr; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
19	<a href="#">c2gwrA_</a>	 Alignment		99.8	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator mtra; <b>PDBTitle:</b> crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
20	<a href="#">c4b09F_</a>	 Alignment		99.7	14	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein baer; <b>PDBTitle:</b> structure of unphosphorylated baer dimer
21	<a href="#">c3qp5C_</a>	 Alignment	not modelled	99.7	27	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
22	<a href="#">c4kfcB_</a>	 Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> B: <b>PDB Molecule:</b> kdp operon transcriptional regulatory protein kdpe; <b>PDBTitle:</b> crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
23	<a href="#">c3r0jA_</a>	 Alignment	not modelled	99.7	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible two component system response transcriptional <b>PDBTitle:</b> structure of phop from mycobacterium tuberculosis
24	<a href="#">c2oqrA_</a>	 Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory transduction protein regx3; <b>PDBTitle:</b> the structure of the response regulator regx3 from mycobacterium2 tuberculosis
25	<a href="#">c1ys7B_</a>	 Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed2 with mg2+
26	<a href="#">c3cloC_</a>	 Alignment	not modelled	99.7	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
27	<a href="#">c6jqsA_</a>	 Alignment	not modelled	99.7	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
28	<a href="#">c2krfB_</a>	 Alignment	not modelled	99.7	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of

					competence protein2 a
29	<a href="#">d1l3la1</a>	Alignment	not modelled	99.7	24 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
30	<a href="#">d1fsea_</a>	Alignment	not modelled	99.6	29 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
31	<a href="#">c1p2fA_</a>	Alignment	not modelled	99.6	11 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
32	<a href="#">c1zljE_</a>	Alignment	not modelled	99.6	29 <b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
33	<a href="#">d1p4wa_</a>	Alignment	not modelled	99.6	22 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
34	<a href="#">c2rnjA_</a>	Alignment	not modelled	99.6	33 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vrar; <b>PDBTitle:</b> nmr structure of the s. aureus vrar dna binding domain
35	<a href="#">d1a04a1</a>	Alignment	not modelled	99.6	27 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
36	<a href="#">c2hqrA_</a>	Alignment	not modelled	99.6	10 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
37	<a href="#">c1x3uA_</a>	Alignment	not modelled	99.6	25 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
38	<a href="#">c5u8mA_</a>	Alignment	not modelled	99.6	11 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
39	<a href="#">d1s8na_</a>	Alignment	not modelled	99.6	9 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
40	<a href="#">c2jpcA_</a>	Alignment	not modelled	99.6	26 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
41	<a href="#">c6ideA_</a>	Alignment	not modelled	99.6	20 <b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator luxr family; <b>PDBTitle:</b> crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
42	<a href="#">d1yioa1</a>	Alignment	not modelled	99.5	31 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
43	<a href="#">c1a2oB_</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> bacterial chemotaxis <b>Chain:</b> B: <b>PDB Molecule:</b> cheb methyltransferase; <b>PDBTitle:</b> structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
44	<a href="#">c3b2nA_</a>	Alignment	not modelled	99.3	14 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4; <b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
45	<a href="#">d1a04a2</a>	Alignment	not modelled	99.3	13 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
46	<a href="#">c3eulB_</a>	Alignment	not modelled	99.3	17 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible nitrate/nitrite response transcriptional <b>PDBTitle:</b> structure of the signal receiver domain of the putative response2 regulator narl from mycobacterium tuberculosis
47	<a href="#">d1a2oa1</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
48	<a href="#">c5i4cA_</a>	Alignment	not modelled	99.3	13 <b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
49	<a href="#">c4e7pA_</a>	Alignment	not modelled	99.3	13 <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of receiver domain of putative narl family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryllifluoride
50	<a href="#">c6ekhY_</a>	Alignment	not modelled	99.2	13 <b>PDB header:</b> metal binding protein <b>Chain:</b> Y: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> crystal structure of activated chey from methanococcus maripaludis
51	<a href="#">c3cz5B_</a>	Alignment	not modelled	99.2	13 <b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two-component response regulator, luxr family; <b>PDBTitle:</b> crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
52	<a href="#">c5lwkB_</a>	Alignment	not modelled	99.2	9 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> maer response regulator bound to beryllium trifluoride
53	<a href="#">c3t8yA_</a>	Alignment	not modelled	99.2	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator protein-glutamate <b>PDBTitle:</b> crystal structure of the response regulator domain of

						thermotoga2 maritima cheb
54	<a href="#">d1dz3a_</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
55	<a href="#">c3eq2A_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> structure of hexagonal crystal form of pseudomonas aeruginosa rssb
56	<a href="#">c5wq0C_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> stage 0 sporulation protein; <b>PDBTitle:</b> receiver domain of spo0a from paenisporsarcina sp. tg-14
57	<a href="#">d1jbea_</a>	Alignment	not modelled	99.2	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
58	<a href="#">d2ayxa1</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
59	<a href="#">c2ayxA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase protein rcsc; <b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
60	<a href="#">c3f6cB_</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
61	<a href="#">c3cu5B_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
62	<a href="#">c3breA_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> crystal structure of p.aeruginosa pa3702
63	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/ggdef domain protein; <b>PDBTitle:</b> crystal structure of full-length wpsr from pseudomonas syringae
64	<a href="#">c6ifhA_</a>	Alignment	not modelled	99.1	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenisporsarcina sp. tg-14
65	<a href="#">d1u0sy_</a>	Alignment	not modelled	99.1	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
66	<a href="#">c6m8oA_</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of the receiver domain of lytr from staphylococcus2 aureus
67	<a href="#">d1dbwa_</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
68	<a href="#">c2qv0A_</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein mrke; <b>PDBTitle:</b> crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
69	<a href="#">c4dadA_</a>	Alignment	not modelled	99.0	9	<b>PDB header:</b> signaling protein, signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> putative pilus assembly-related protein; <b>PDBTitle:</b> crystal structure of a putative pilus assembly-related protein2 (bpss2195) from burkholderia pseudomallei k96243 at 2.50 a resolution3 (psi community target, shapiro l.)
70	<a href="#">d1p6qa_</a>	Alignment	not modelled	99.0	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
71	<a href="#">d1mvoa_</a>	Alignment	not modelled	99.0	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
72	<a href="#">c2rjnA_</a>	Alignment	not modelled	99.0	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver:metal-dependent <b>PDBTitle:</b> crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
73	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.0	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
74	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
75	<a href="#">c6od1A_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of rpos; <b>PDBTitle:</b> irad-bound to rssb d58p variant
76	<a href="#">d1krwa_</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">c1w25B_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein; <b>PDBTitle:</b> response regulator pled in complex with c-digmp
78	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>PDB header:</b> signaling protein

79	<a href="#">c3to5A_</a>	Alignment	not modelled	99.0	9	<b>Chain:</b> A: <b>PDB Molecule:</b> chey homolog; <b>PDBTitle:</b> high resolution structure of chey3 from vibrio cholerae
80	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
81	<a href="#">c3rqjA_</a>	Alignment	not modelled	99.0	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein; <b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and 3 citrate
82	<a href="#">c5ep0A_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
83	<a href="#">c2qr3A_</a>	Alignment	not modelled	99.0	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
84	<a href="#">c5briA_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> candidate response regulator, chey; <b>PDBTitle:</b> bacteriophytochrome response regulator rtbrr
85	<a href="#">c3cg0A_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver modulated diguanylate cyclase <b>PDBTitle:</b> crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
86	<a href="#">c5e3jB_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator rsta; <b>PDBTitle:</b> the response regulator rsta is a potential drug target for2 acinetobacter baumannii
87	<a href="#">c4qpiC_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle response regulator ctra; <b>PDBTitle:</b> 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
88	<a href="#">c3dzdA_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
89	<a href="#">c5brjA_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> structure of the bacteriophytochrome response regulator atbrr
90	<a href="#">c5uicA_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> structure of the francisella response regulator receiver domain, qseb
91	<a href="#">c3ilhA_</a>	Alignment	not modelled	98.9	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> crystal structure of two component response regulator from cytophaga2 hutchinsonii
92	<a href="#">c3nhzA_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> two component system transcriptional regulator mtra; <b>PDBTitle:</b> structure of n-terminal domain of mtra
93	<a href="#">d1k66a_</a>	Alignment	not modelled	98.9	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
94	<a href="#">c3snkA_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chey-like protein; <b>PDBTitle:</b> crystal structure of a response regulator chey-like protein (mll6475)2 from mesorhizobium loti at 2.02 a resolution
95	<a href="#">c3kylB_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> chey6 protein; <b>PDBTitle:</b> crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
96	<a href="#">c3jteA_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
97	<a href="#">c5te9A_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of a response regulator receiver protein from2 burkholderia phymatum
98	<a href="#">c3h1gA_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chey homolog; <b>PDBTitle:</b> crystal structure of chey mutant t84a of helicobacter pylori
99	<a href="#">d1peva_</a>	Alignment	not modelled	98.9	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
100	<a href="#">c2jrlA_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
101	<a href="#">c3mmnA_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase homolog; <b>PDBTitle:</b> crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
102	<a href="#">c3w9sB_</a>	Alignment	not modelled	98.9	8	<b>PDB header:</b> signaling protein/antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> ompf family response regulator in two-component regulatory <b>PDBTitle:</b> crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
103	<a href="#">d1yioa2</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

104	<a href="#">c5m7nA</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
105	<a href="#">c4q7eA</a>	Alignment	not modelled	98.9	6	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator of a two component regulatory system; <b>PDBTitle:</b> non-phosphorylated hemr receiver domain from leptospira biflexa
106	<a href="#">c4h60A</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
107	<a href="#">c3t6kB</a>	Alignment	not modelled	98.9	8	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of a putative response regulator (caur_3799) from2 chloroflexus aurantiacus j-10-fl at 1.86 a resolution
108	<a href="#">c3crnA</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
109	<a href="#">d1qkka</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
110	<a href="#">d2a9pa1</a>	Alignment	not modelled	98.9	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
111	<a href="#">c3cfyA</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative luxo repressor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
112	<a href="#">c2zwmA</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein yycf; <b>PDBTitle:</b> crystal structure of yycf receiver domain from bacillus2 subtilis
113	<a href="#">d2p1a1</a>	Alignment	not modelled	98.8	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
114	<a href="#">c3hdgE</a>	Alignment	not modelled	98.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
115	<a href="#">c3hzhA</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator (chey-3); <b>PDBTitle:</b> crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
116	<a href="#">d2r25b1</a>	Alignment	not modelled	98.8	6	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
117	<a href="#">d1heya</a>	Alignment	not modelled	98.8	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
118	<a href="#">d1i3ca</a>	Alignment	not modelled	98.8	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
119	<a href="#">c3hv2B</a>	Alignment	not modelled	98.8	6	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator/hd domain protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
120	<a href="#">c4g97A</a>	Alignment	not modelled	98.8	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of the response regulator phyr from brucella abortus