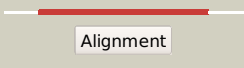

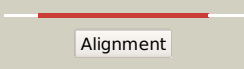

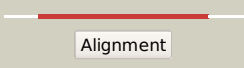
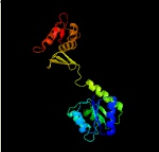
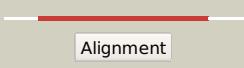

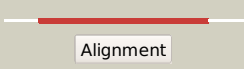

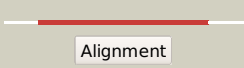

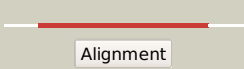
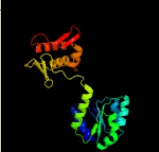
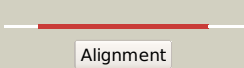

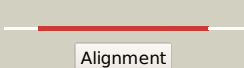
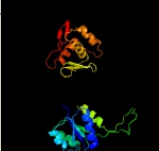
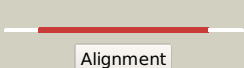

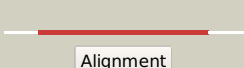



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1033c\_(trcR)\_1157967\_1158740  
 Date Wed Jul 31 22:05:10 BST 2019  
 Unique Job ID a97a04a5ef68997e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ys7B_</a>			100.0	42	<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+
2	<a href="#">c3r0jA_</a>			100.0	47	<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
3	<a href="#">c4s05B_</a>			100.0	37	<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
4	<a href="#">c2oqrA_</a>			100.0	41	<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
5	<a href="#">c4kfcB_</a>			100.0	33	<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
6	<a href="#">c2gwrA_</a>			100.0	40	<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
7	<a href="#">c5u8mA_</a>			100.0	28	<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
8	<a href="#">c2hqrA_</a>			100.0	24	<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
9	<a href="#">c4b09F_</a>			100.0	30	<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
10	<a href="#">c1kgsA_</a>			100.0	44	<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
11	<a href="#">c1p2fA_</a>			100.0	35	<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

12	<a href="#">c3q9sA_</a>	Alignment		100.0	37	<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
13	<a href="#">c5xt2C_</a>	Alignment		100.0	22	<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
14	<a href="#">c1zn2A_</a>	Alignment		99.9	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 styr
15	<a href="#">c2ayxA_</a>	Alignment		99.9	23	<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
16	<a href="#">c5f64C_</a>	Alignment		99.9	16	<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
17	<a href="#">c3eq2A_</a>	Alignment		99.9	30	<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
18	<a href="#">c4hyeB_</a>	Alignment		99.9	26	<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
19	<a href="#">c3breA_</a>	Alignment		99.9	33	<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
20	<a href="#">c4qpiC_</a>	Alignment		99.9	43	<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
21	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.9	31	<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
22	<a href="#">c6od1A_</a>	Alignment	not modelled	99.9	26	<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
23	<a href="#">d2ayxa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
24	<a href="#">c5uicA_</a>	Alignment	not modelled	99.9	44	<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
25	<a href="#">c3c3wB_</a>	Alignment	not modelled	99.9	27	<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
26	<a href="#">c1w25B_</a>	Alignment	not modelled	99.9	38	<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
27	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.9	50	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
28	<a href="#">d1s8na_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

29	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
30	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.9	46	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
31	<a href="#">c3w9sB</a>	Alignment	not modelled	99.9	43	<b>PDB header:</b> signaling protein/antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> ompr family response regulator in two-component regulatory <b>PDBTitle:</b> crystal structure analysis of the n-terminal receiver domain of 2 response regulator pmra
32	<a href="#">c5ep0A</a>	Alignment	not modelled	99.9	30	<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
33	<a href="#">c3dzdA</a>	Alignment	not modelled	99.9	30	<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
34	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.9	45	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
35	<a href="#">d1jbea</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">c4if4A</a>	Alignment	not modelled	99.9	24	<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 beryll fluoride-activated vvar2 from staphylococcus aureus
37	<a href="#">c6ifhA</a>	Alignment	not modelled	99.9	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenibacillus sp. tg-14
38	<a href="#">c1rnlA</a>	Alignment	not modelled	99.9	25	<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
39	<a href="#">c5hevC</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the beryll fluoride-activated liar from 2 enterococcus faecium
40	<a href="#">c3rqiA</a>	Alignment	not modelled	99.9	21	<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
41	<a href="#">d2a9pa1</a>	Alignment	not modelled	99.9	47	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
42	<a href="#">d1mvoa</a>	Alignment	not modelled	99.9	47	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
43	<a href="#">c3i5aA</a>	Alignment	not modelled	99.9	32	<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
44	<a href="#">c3cfyA</a>	Alignment	not modelled	99.9	29	<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
45	<a href="#">d1zgza1</a>	Alignment	not modelled	99.9	37	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
46	<a href="#">c2zwmA</a>	Alignment	not modelled	99.9	48	<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
47	<a href="#">c2rjnA</a>	Alignment	not modelled	99.9	17	<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 from 2 heptuniibacter caesariensis
48	<a href="#">d1dbwa</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
49	<a href="#">c4lzlA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
50	<a href="#">c2jrlA</a>	Alignment	not modelled	99.9	30	<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
51	<a href="#">c2rv8A</a>	Alignment	not modelled	99.9	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
52	<a href="#">c5m7nA</a>	Alignment	not modelled	99.9	29	<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
53	<a href="#">c5e3jB</a>	Alignment	not modelled	99.9	45	<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 for 2 acinetobacter baumannii
						<b>Fold:</b> Flavodoxin-like

54	<a href="#">d1w25a1</a>	Alignment	not modelled	99.9	38	<b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
55	<a href="#">d1peva</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
56	<a href="#">c3cu5B</a>	Alignment	not modelled	99.9	21	<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
57	<a href="#">c4q7eA</a>	Alignment	not modelled	99.9	32	<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
58	<a href="#">d1krwa</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
59	<a href="#">c5t3yA</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> solution structure of response regulator protein from burkholderia2 multivorans
60	<a href="#">c3nhzA</a>	Alignment	not modelled	99.9	42	<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
61	<a href="#">c4eukA</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase 5; <b>PDBTitle:</b> crystal structure
62	<a href="#">c3hdgE</a>	Alignment	not modelled	99.9	22	<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 wolinnella3 succinogenes
63	<a href="#">c3t6kB</a>	Alignment	not modelled	99.9	36	<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
64	<a href="#">c2qr3A</a>	Alignment	not modelled	99.9	21	<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
65	<a href="#">c4h60A</a>	Alignment	not modelled	99.9	37	<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
66	<a href="#">d1qkka</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
67	<a href="#">d1zh2a1</a>	Alignment	not modelled	99.9	41	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
68	<a href="#">c3gt7A</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
69	<a href="#">c3eulB</a>	Alignment	not modelled	99.9	28	<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
70	<a href="#">d1dz3a</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
71	<a href="#">c2qzjC</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> crystal structure of a two-component response regulator from2 clostridium difficile
72	<a href="#">c3to5A</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chey homolog; <b>PDBTitle:</b> high resolution structure of chey3 from vibrio cholerae
73	<a href="#">d1yioa2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
74	<a href="#">c6ekhY</a>	Alignment	not modelled	99.9	24	<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
75	<a href="#">d1a04a2</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
76	<a href="#">d1zesa1</a>	Alignment	not modelled	99.9	39	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">d1p6qa</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
78	<a href="#">c3hv2B</a>	Alignment	not modelled	99.9	22	<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
						<b>PDB header:</b> transcription

79	<a href="#">c5lwkB_</a>	Alignment	not modelled	99.9	23	<b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> maer response regulator bound to beryllium trifluoride
80	<a href="#">c3cz5B_</a>	Alignment	not modelled	99.9	28	<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
81	<a href="#">d1u0sy_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
82	<a href="#">d1heya_</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
83	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.9	40	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
84	<a href="#">c6m8oA_</a>	Alignment	not modelled	99.9	25	<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
85	<a href="#">c1a2oB_</a>	Alignment	not modelled	99.9	30	<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
86	<a href="#">c5kxbB_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> osmolarity two-component system protein ssk1; <b>PDBTitle:</b> co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
87	<a href="#">c5briA_</a>	Alignment	not modelled	99.9	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> candidate response regulator, chey; <b>PDBTitle:</b> bacteriophytochrome response regulator rtbr
88	<a href="#">c3b2nA_</a>	Alignment	not modelled	99.9	22	<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
89	<a href="#">c2zayA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator from desulfuromonas2 acetoxidans
90	<a href="#">c4e7pA_</a>	Alignment	not modelled	99.9	26	<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 berylliofluoride
91	<a href="#">c3jteA_</a>	Alignment	not modelled	99.9	24	<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
92	<a href="#">c3crnA_</a>	Alignment	not modelled	99.9	29	<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
93	<a href="#">d1k66a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
94	<a href="#">c2qv0A_</a>	Alignment	not modelled	99.9	21	<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
95	<a href="#">c5wq0C_</a>	Alignment	not modelled	99.9	26	<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
96	<a href="#">c4uhsA_</a>	Alignment	not modelled	99.9	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cpxr; <b>PDBTitle:</b> crystal structure of the receiver domain of cpxr from e. coli2 (tetragonal form)
97	<a href="#">c3cg4A_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> structural genomics, unknown function <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
98	<a href="#">c5x5jA_</a>	Alignment	not modelled	99.9	37	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of response regulator ader receiver domain
99	<a href="#">c3h1gA_</a>	Alignment	not modelled	99.9	30	<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
100	<a href="#">c3cnbC_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna-binding response regulator, merr family; <b>PDBTitle:</b> crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
101	<a href="#">d2r25b1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
102	<a href="#">c3lteH_</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
103	<a href="#">c3c3mA_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein;

103	<a href="#">c3c9m7A</a>	Alignment	not modelled	99.8	40	<b>PDBTitle:</b> crystal structure of the n-terminal domain of response regulator2 receiver protein from methanococcus marisnigri jr1 <b>PDB header:</b> hydrolase
104	<a href="#">c3t8yA</a>	Alignment	not modelled	99.8	29	<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
105	<a href="#">d2b4aa1</a>	Alignment	not modelled	99.8	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
106	<a href="#">c3a0rB</a>	Alignment	not modelled	99.8	35	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
107	<a href="#">c4d6yA</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacterial regulatory, fis family protein; <b>PDBTitle:</b> crystal structure of the receiver domain of ntrx from2 brucella abortus in complex with beryll fluoride and3 magnesium
108	<a href="#">c2hqoA</a>	Alignment	not modelled	99.8	25	<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
109	<a href="#">c3hzhA</a>	Alignment	not modelled	99.8	25	<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
110	<a href="#">c5tqjA</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 burkholderia phymatum
111	<a href="#">c3hebB</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> response regulator receiver domain protein (cheY); <b>PDBTitle:</b> crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
112	<a href="#">c5dclB</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> phob family transcriptional regulator; <b>PDBTitle:</b> structure of a lantibiotic response regulator: n terminal domain of2 the nisin resistance regulator nsrr
113	<a href="#">c3khtA</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator from hahella chejuensis
114	<a href="#">c2qxyB</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator from thermotoga2 maritima
115	<a href="#">c2jk1A</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> dna-binding <b>Chain:</b> A; <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1; <b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain
116	<a href="#">d1w25a2</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
117	<a href="#">c3c97A</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> signal transduction histidine kinase; <b>PDBTitle:</b> crystal structure of the response regulator receiver domain of a2 signal transduction histidine kinase from aspergillus oryzae
118	<a href="#">c3hdvB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 pseudomonas putida
119	<a href="#">c3f6cB</a>	Alignment	not modelled	99.8	15	<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
120	<a href="#">c2qvgA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> the crystal structure of a two-component response regulator2 from legionella pneumophila