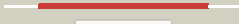



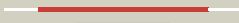



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0903c_prrA_1005855_1006565
 Date Fri Jul 26 01:50:49 BST 2019
 Unique Job ID 08c1f13491d07ff0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ys7B_	 Alignment		100.0	100	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
2	c4kfcB_	 Alignment		100.0	36	PDB header: transcription regulator/dna Chain: B: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
3	c2oqrA_	 Alignment		100.0	40	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
4	c4s05B_	 Alignment		100.0	35	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
5	c5u8mA_	 Alignment		100.0	30	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
6	c3r0jA_	 Alignment		100.0	45	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
7	c2gwrA_	 Alignment		100.0	43	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
8	c2hqrA_	 Alignment		100.0	24	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
9	c4b09F_	 Alignment		100.0	30	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
10	c1kgsA_	 Alignment		100.0	39	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
11	c1p2fA_	 Alignment		100.0	33	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog

12	c3q9sA_	Alignment		100.0	40	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
13	c5xt2C_	Alignment		100.0	25	PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
14	c1zn2A_	Alignment		99.9	26	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styf
15	c2ayxA_	Alignment		99.9	27	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
16	c5f64C_	Alignment		99.9	19	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
17	c4hyeB_	Alignment		99.9	23	PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
18	c3eq2A_	Alignment		99.9	35	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas aeruginosa rssb
19	c1w25B_	Alignment		99.9	41	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
20	c6od1A_	Alignment		99.9	26	PDB header: signaling protein Chain: A: PDB Molecule: regulator of rpos; PDBTitle: irad-bound to rssb d58p variant
21	d1ys7a2	Alignment	not modelled	99.9	100	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
22	c3c3wB_	Alignment	not modelled	99.9	25	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
23	c5hevC_	Alignment	not modelled	99.9	22	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
24	c6ifhA_	Alignment	not modelled	99.9	31	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporsarcina sp. tg-14
25	c4if4A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
26	c2qr3A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
27	c3rqjA_	Alignment	not modelled	99.9	25	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate PDB header: signal transduction protein

28	c1rnA_	Alignment	not modelled	99.9	23	Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
29	c3i5aA_	Alignment	not modelled	99.9	36	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
30	d2ayxa1	Alignment	not modelled	99.9	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
31	c3w9sB_	Alignment	not modelled	99.9	41	PDB header: signaling protein/antimicrobial protein Chain: B: PDB Molecule: ompr family response regulator in two-component regulatory PDBTitle: crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
32	c5e3jB_	Alignment	not modelled	99.9	39	PDB header: transcription Chain: B: PDB Molecule: response regulator rsta; PDBTitle: the response regulator rsta is a potential drug target for2 acinetobacter baumannii
33	c4qpiC_	Alignment	not modelled	99.9	39	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
34	c3cfyA_	Alignment	not modelled	99.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
35	c3breA_	Alignment	not modelled	99.9	34	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
36	c3dzdA_	Alignment	not modelled	99.8	32	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
37	d1krwa_	Alignment	not modelled	99.8	34	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
38	d1mvoa_	Alignment	not modelled	99.8	46	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
39	d1qkka_	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	c5ep0A_	Alignment	not modelled	99.8	31	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
41	c1ny5A_	Alignment	not modelled	99.8	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
42	c4q7eA_	Alignment	not modelled	99.8	28	PDB header: signaling protein Chain: A: PDB Molecule: response regulator of a two component regulatory system; PDBTitle: non-phosphorylated hemr receiver domain from leptospira biflexa
43	d2pl1a1	Alignment	not modelled	99.8	40	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	d1dbwa_	Alignment	not modelled	99.8	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	d1w25a1	Alignment	not modelled	99.8	36	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	d2a9pa1	Alignment	not modelled	99.8	46	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	c4h60A_	Alignment	not modelled	99.8	36	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey; PDBTitle: high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
48	c2rjnA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
49	d1ny5a1	Alignment	not modelled	99.8	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	c5uicA_	Alignment	not modelled	99.8	42	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
51	c4eukA_	Alignment	not modelled	99.8	26	PDB header: signaling protein Chain: A: PDB Molecule: histidine kinase 5; PDBTitle: crystal structure
52	c4lzlA_	Alignment	not modelled	99.8	21	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
53	c5m7nA_	Alignment	not modelled	99.8	27	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex

						with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
54	c2jrlA_	Alignment	not modelled	99.8	32	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
55	d1yioa2	Alignment	not modelled	99.8	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	c2zwmA_	Alignment	not modelled	99.8	50	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
57	c2qzjC_	Alignment	not modelled	99.8	31	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
58	d1xhfa1	Alignment	not modelled	99.8	35	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c5t3yA_	Alignment	not modelled	99.8	30	PDB header: signaling protein Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: solution structure of response regulator protein from burkholderia2 multivorans
60	d1peva_	Alignment	not modelled	99.8	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	d1kgsa2	Alignment	not modelled	99.8	44	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	c3nhzA_	Alignment	not modelled	99.8	47	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
63	d1zh2a1	Alignment	not modelled	99.8	42	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c3jteA_	Alignment	not modelled	99.8	29	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
65	d1s8na_	Alignment	not modelled	99.8	34	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	c3hv2B_	Alignment	not modelled	99.8	20	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
67	c3gt7A_	Alignment	not modelled	99.8	32	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
68	c2rv8A_	Alignment	not modelled	99.8	37	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
69	c3crnA_	Alignment	not modelled	99.8	25	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
70	d1jbea_	Alignment	not modelled	99.8	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
71	d1u0sy_	Alignment	not modelled	99.8	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	c2qxyB_	Alignment	not modelled	99.8	30	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
73	c6ekhY_	Alignment	not modelled	99.8	27	PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
74	c3cz5B_	Alignment	not modelled	99.8	29	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
75	d1zgza1	Alignment	not modelled	99.8	37	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c3t6kB_	Alignment	not modelled	99.8	42	PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a putative response regulator (caur_3799) from2 chloroflexus aurantiacus j-10-fl at 1.86 a resolution
77	c3c3mA_	Alignment	not modelled	99.8	26	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
78	d1zesa1	Alignment	not modelled	99.8	42	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

79	c3to5A_	Alignment	not modelled	99.8	27	PDB header: signaling protein Chain: A: PDB Molecule: chey homolog; PDBTitle: high resolution structure of chey3 from vibrio cholerae
80	c5lwkB_	Alignment	not modelled	99.8	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
81	c3b2nA_	Alignment	not modelled	99.8	21	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
82	c3hdgE_	Alignment	not modelled	99.8	27	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinnella3 succinogenes
83	c5kxbB_	Alignment	not modelled	99.8	28	PDB header: signaling protein Chain: B: PDB Molecule: osmolarity two-component system protein ssk1; PDBTitle: co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
84	c2zayA_	Alignment	not modelled	99.8	28	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
85	c2jzyA_	Alignment	not modelled	99.8	37	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of 2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
86	d1p6qa_	Alignment	not modelled	99.8	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	d1a04a2	Alignment	not modelled	99.8	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c5x5jA_	Alignment	not modelled	99.8	38	PDB header: dna binding protein Chain: A: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader receiver domain
89	c4uhsA_	Alignment	not modelled	99.8	44	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cpxr; PDBTitle: crystal structure of the receiver domain of cpxr from e. coli2 (tetragonal form)
90	c3eulB_	Alignment	not modelled	99.8	33	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative response2 regulator narl from mycobacterium tuberculosis
91	d1dz3a_	Alignment	not modelled	99.8	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
92	d1k66a_	Alignment	not modelled	99.8	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	c3cu5B_	Alignment	not modelled	99.8	25	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
94	c2jk1A_	Alignment	not modelled	99.8	24	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
95	d1gxqa_	Alignment	not modelled	99.8	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
96	c1a2oB_	Alignment	not modelled	99.8	30	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
97	c3cg4A_	Alignment	not modelled	99.8	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
98	c2hqna_	Alignment	not modelled	99.8	27	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
99	c3lteH_	Alignment	not modelled	99.8	34	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
100	c5tqjA_	Alignment	not modelled	99.8	36	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 burkholderia phymatum
101	c3q9vB_	Alignment	not modelled	99.8	39	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
102	c5bria_	Alignment	not modelled	99.8	29	PDB header: signaling protein Chain: A: PDB Molecule: candidate response regulator, chey; PDBTitle: bacteriophytochrome response regulator rtbr
						PDB header: transcription regulator Chain: A: PDB Molecule: response regulator;

103	c4e7pA_	Alignment	not modelled	99.8	26	PDBTitle: crystal structure of receiver domain of putative narI family response2 regulator spr1814 from streptococcus pneumoniae in the presence of 3 the phosphoryl analog beryll fluoride
104	c4d6yA_	Alignment	not modelled	99.8	28	PDB header: signaling protein Chain: A: PDB Molecule: bacterial regulatory, fis family protein; PDBTitle: crystal structure of the receiver domain of ntrX from <i>Brucella abortus</i> in complex with beryll fluoride and 3 magnesium
105	c3rjpA_	Alignment	not modelled	99.8	41	PDB header: dna binding protein Chain: A: PDB Molecule: covr; PDBTitle: crystal structure of the dna binding domain of covr from <i>Streptococcus pyogenes</i>
106	c3cg0A_	Alignment	not modelled	99.8	27	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate 2 cyclase from <i>Desulfovibrio desulfuricans</i> g20, an example of alternate 3 folding
107	c3a0rB_	Alignment	not modelled	99.8	35	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with 2 response regulator protein trra (tm1360)
108	d1heya_	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c2mswA_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
110	c3khtA_	Alignment	not modelled	99.8	29	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from <i>Haemella chejuensis</i>
111	c3hdvB_	Alignment	not modelled	99.8	26	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from <i>Pseudomonas putida</i>
112	c4ixaA_	Alignment	not modelled	99.8	33	PDB header: transcription Chain: A: PDB Molecule: response regulator saer; PDBTitle: structure of dna-binding domain of the response regulator saer from <i>Staphylococcus epidermidis</i>
113	c2zxB_	Alignment	not modelled	99.8	38	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein walr; PDBTitle: crystal structure of yycF dna-binding domain from <i>Staphylococcus aureus</i>
114	c3cnbC_	Alignment	not modelled	99.8	20	PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding response regulator, merr family; PDBTitle: crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from <i>Colwellia psychrerythraea</i> 34h
115	c3zq7A_	Alignment	not modelled	99.8	32	PDB header: transcription Chain: A: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: the structure of dna-binding domain of response regulator from <i>Escherichia coli</i> k-12
116	d1mb3a_	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	c5wq0C_	Alignment	not modelled	99.8	29	PDB header: signaling protein Chain: C: PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from <i>Paenisporsarcina</i> sp. tg-14
118	c3kcnA_	Alignment	not modelled	99.8	26	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from <i>Rhodospirella baltica</i>
119	c3hzhA_	Alignment	not modelled	99.8	29	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (cheY-3); PDBTitle: crystal structure of the cheX-cheY-bef3-mg+2 complex from <i>Borrelia burgdorferi</i>
120	d2r25b1	Alignment	not modelled	99.8	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related