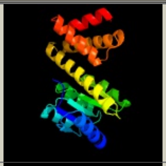
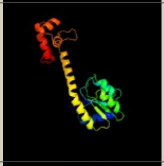
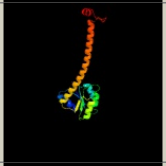
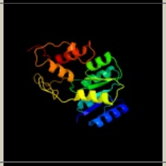
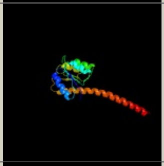
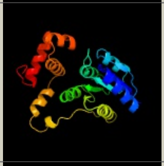
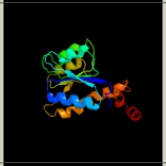
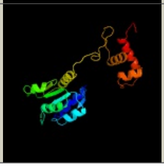
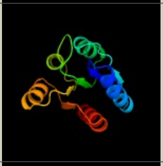
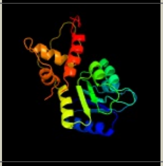
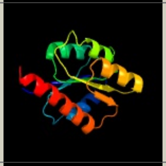
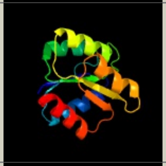
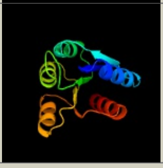
Email	mdejesus@rockefeller.edu
Description	RVBD1626_(-)_1828187_1828804
Date	Fri Aug 2 13:30:22 BST 2019
Unique Job ID	c3ef8401bc4111cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s8na_	Alignment		100.0	100	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
2	c1zn2A_	Alignment		99.9	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
3	c2ayxA_	Alignment		99.9	23	**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
4	d1qo0d_	Alignment		99.9	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
5	c5xt2C_	Alignment		99.9	22	**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
6	c3breA_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
7	c3q9sA_	Alignment		99.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
8	c3eq2A_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas aeruginosa rssb
9	c5f64C_	Alignment		99.9	21	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** putative positive transcription regulator (sensor evgs) from shigella2 flexneri
10	c6od1A_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of rpos; **PDBTitle:** irad-bound to rssb d58p variant
11	c3r0jA_	Alignment		99.9	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis

12	c1w25B_	Alignment		99.9	26	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
13	d2a9pa1	Alignment		99.9	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
14	c1kgsA_	Alignment		99.9	22	**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
15	c3i5aA_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
16	c2gwrA_	Alignment		99.9	22	**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
17	c3nhzA_	Alignment		99.9	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
18	c3cfyA_	Alignment		99.9	28	**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
19	c2zwmA_	Alignment		99.9	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
20	c5e3jB_	Alignment		99.9	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator rsta; **PDBTitle:** the response regulator rsta is a potential drug target for2 acinetobacter baumannii
21	c4kfcB_	Alignment	not modelled	99.9	28	**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
22	d1w25a1	Alignment	not modelled	99.9	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	c3dzdA_	Alignment	not modelled	99.9	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
24	c5ep0A_	Alignment	not modelled	99.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor protein luxo; **PDBTitle:** quorum-sensing signal integrator luxo - receiver+catalytic domains
25	d1u0sy_	Alignment	not modelled	99.9	43	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	c1ny5A_	Alignment	not modelled	99.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
27	c4s05B_	Alignment	not modelled	99.9	24	**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
28	d1zh2a1	Alignment	not modelled	99.9	38	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

29	d1qkka_	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
30	c3c3wB_	Alignment	not modelled	99.9	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
31	d1zgza1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	d1mvoa_	Alignment	not modelled	99.9	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c2qzjC_	Alignment	not modelled	99.9	23	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
34	c3to5A_	Alignment	not modelled	99.9	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chey homolog; **PDBTitle:** high resolution structure of chey3 from vibrio cholerae
35	c4qpjC_	Alignment	not modelled	99.9	27	**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
36	d1jbea_	Alignment	not modelled	99.9	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	c4q7eA_	Alignment	not modelled	99.9	29	**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
38	c6ifhA_	Alignment	not modelled	99.9	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sporulation initiation phosphotransferase f; **PDBTitle:** unphosphorylated spo0f from paenisporosarcina sp. tg-14
39	c4uhsA_	Alignment	not modelled	99.9	29	**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)
40	c3b2nA_	Alignment	not modelled	99.9	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
41	c5uicA_	Alignment	not modelled	99.9	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** structure of the francisella response regulator receiver domain, qseb
42	c4b09F_	Alignment	not modelled	99.9	17	**PDB header:**transcription **Chain:** F: **PDB Molecule:**transcriptional regulatory protein baer; **PDBTitle:** structure of unphosphorylated baer dimer
43	d1p6qa_	Alignment	not modelled	99.9	31	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	c5m7nA_	Alignment	not modelled	99.9	23	**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
45	c3w9sB_	Alignment	not modelled	99.9	28	**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
46	d1ny5a1	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c3gt7A_	Alignment	not modelled	99.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
48	d2ayxa1	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c3cz5B_	Alignment	not modelled	99.9	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
50	d2pl1a1	Alignment	not modelled	99.9	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	d1peya_	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	c3cg0A_	Alignment	not modelled	99.9	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
53	d1a04a2	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

54	c1a2oB_	Alignment	not modelled	99.9	32	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
55	c3hzhA_	Alignment	not modelled	99.9	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis response regulator (chey-3); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
56	c4hyeB_	Alignment	not modelled	99.9	28	**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
57	c4h60A_	Alignment	not modelled	99.9	30	**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
58	c5t3yA_	Alignment	not modelled	99.9	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component system response regulator; **PDBTitle:** solution structure of response regulator protein from burkholderia2 multivorans
59	c3eulB_	Alignment	not modelled	99.8	28	**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
60	c3rqiA_	Alignment	not modelled	99.8	23	**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
61	c2rjnA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
62	c1ys7B_	Alignment	not modelled	99.8	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra complexed2 with mg2+
63	d1xhfa1	Alignment	not modelled	99.8	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
64	d1zesa1	Alignment	not modelled	99.8	35	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	c2qr3A_	Alignment	not modelled	99.8	21	**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
66	d1dz3a_	Alignment	not modelled	99.8	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3f6cB_	Alignment	not modelled	99.8	26	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
68	d1heya_	Alignment	not modelled	99.8	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	d1dbwa_	Alignment	not modelled	99.8	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c4eukA_	Alignment	not modelled	99.8	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**histidine kinase 5; **PDBTitle:** crystal structure
71	c3t6kB_	Alignment	not modelled	99.8	31	**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
72	d1krwa_	Alignment	not modelled	99.8	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	d1ys7a2	Alignment	not modelled	99.8	33	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	c4lzlA_	Alignment	not modelled	99.8	22	**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)
75	c2oqrA_	Alignment	not modelled	99.8	23	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
76	c2jrlA_	Alignment	not modelled	99.8	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
77	c5x5jA_	Alignment	not modelled	99.8	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ader; **PDBTitle:** crystal structure of response regulator ader receiver domain
						PDB header:transcription regulator

78	c3cu5B_	Alignment	not modelled	99.8	26	**Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
79	c3lteH_	Alignment	not modelled	99.8	21	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
80	c4if4A_	Alignment	not modelled	99.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** crystal structure of the magnesium and beryllofluoride-activated vrar2 from staphylococcus aureus
81	c5briA_	Alignment	not modelled	99.8	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**candidate response regulator, chey; **PDBTitle:** bacteriophytochrome response regulator rtbrr
82	c3h1gA_	Alignment	not modelled	99.8	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
83	d1kgsa2	Alignment	not modelled	99.8	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	c5wq0C_	Alignment	not modelled	99.8	28	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**stage 0 sporulation protein; **PDBTitle:** receiver domain of spo0a from paenisporosarcina sp. tg-14
85	c1rnlA_	Alignment	not modelled	99.8	25	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
86	c3khtA_	Alignment	not modelled	99.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
87	c4e7pA_	Alignment	not modelled	99.8	34	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of receiver domain of putative narl family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryllofluoride
88	c2zayA_	Alignment	not modelled	99.8	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
89	d1k66a_	Alignment	not modelled	99.8	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
90	d2r25b1	Alignment	not modelled	99.8	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	d1yioa2	Alignment	not modelled	99.8	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	c5lwkB_	Alignment	not modelled	99.8	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** maer response regulator bound to beryllium trifluoride
93	c3jteA_	Alignment	not modelled	99.8	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
94	c3hv2B_	Alignment	not modelled	99.8	24	**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
95	c6ekhY_	Alignment	not modelled	99.8	34	**PDB header:**metal binding protein **Chain:** Y: **PDB Molecule:**chemotaxis protein chey; **PDBTitle:** crystal structure of activated chey from methanoccocus maripaludis
96	c3hdgE_	Alignment	not modelled	99.8	28	**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 wolinella3 succinogenes
97	c4g97A_	Alignment	not modelled	99.8	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of the response regulator phyr from brucella abortus
98	c3crnA_	Alignment	not modelled	99.8	23	**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
99	c5kbxB_	Alignment	not modelled	99.8	30	**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
100	d1w25a2	Alignment	not modelled	99.8	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
101	c5u8mA_	Alignment	not modelled	99.8	19	**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
102	c5dclB_	Alignment	not modelled	99.8	21	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**phob family transcriptional regulator; **PDBTitle:** structure of a lantibiotic response regulator: n terminal domain of2 the nisin resistance regulator nsrr

103	c5hevC_	Alignment	not modelled	99.8	23	**PDB header:**transcription **Chain:** C: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
104	c1p2fA_	Alignment	not modelled	99.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
105	c4qicC_	Alignment	not modelled	99.8	33	**PDB header:**signaling protein/dna binding protein **Chain:** C: **PDB Molecule:**sensory transduction regulatory protein, anti-anti-sigma **PDBTitle:** co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
106	c3cnbC_	Alignment	not modelled	99.8	26	**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 colwellia psychrerythraea 34h
107	c3hdvB_	Alignment	not modelled	99.8	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
108	c3t8yA_	Alignment	not modelled	99.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
109	c2qv0A_	Alignment	not modelled	99.8	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
110	c6m8oA_	Alignment	not modelled	99.8	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of the receiver domain of lytr from staphylococcus2 aureus
111	c3gl9B_	Alignment	not modelled	99.8	32	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
112	c5tqjA_	Alignment	not modelled	99.8	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 burkholderia phymatum
113	c3mmnA_	Alignment	not modelled	99.8	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
114	c6oecD_	Alignment	not modelled	99.8	26	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**response regulator/sensory box protein/ggdef domain **PDBTitle:** yeast spc42 trimeric coiled-coil amino acids 181-211 fused to pdb:2 3h5i
115	c3hebB_	Alignment	not modelled	99.8	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey); **PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
116	c4d6yA_	Alignment	not modelled	99.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bacterial regulatory, fis family protein; **PDBTitle:** crystal structure of the receiver domain of ntrx from2 brucella abortus in complex with beryllofluoride and3 magnesium
117	c3snkA_	Alignment	not modelled	99.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator chey-like protein; **PDBTitle:** crystal structure of a response regulator chey-like protein (mll6475)2 from mesorhizobium loti at 2.02 a resolution
118	d1mb3a_	Alignment	not modelled	99.8	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
119	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
120	c2jk1A_	Alignment	not modelled	99.8	21	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain