

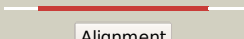

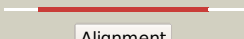













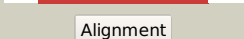



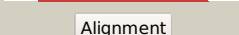





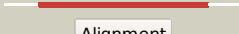












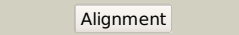
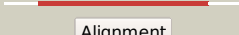


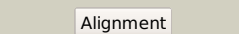

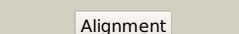


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3133c_(devR)_3499259_3499912
 Date Thu Aug 8 16:20:31 BST 2019
 Unique Job ID 5a6646a02223e5e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c3wB_	 Alignment		100.0	100	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
2	c5hevC_	 Alignment		100.0	36	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
3	c4hyeB_	 Alignment		100.0	29	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
4	c5f64C_	 Alignment		100.0	25	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
5	c4if4A_	 Alignment		100.0	32	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryllofluoride-activated vvar2 from staphylococcus aureus
6	c1rn1A_	 Alignment		100.0	30	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
7	c1zn2A_	 Alignment		100.0	26	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator sty
8	c5xt2C_	 Alignment		100.0	20	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
9	c5o8yG_	 Alignment		100.0	17	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
10	c4yn8A_	 Alignment		100.0	36	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
11	c3klnC_	 Alignment		99.9	17	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst

12	c1kgsA	 Alignment		99.9	17	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
13	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
14	c4s05B	 Alignment		99.9	20	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
15	c3r0jA	 Alignment		99.9	25	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
16	c1ys7B	 Alignment		99.9	25	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
17	c4b09F	 Alignment		99.8	21	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
18	c4kfcB	 Alignment		99.8	25	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
19	c2oqrA	 Alignment		99.8	25	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
20	c2gwrA	 Alignment		99.8	24	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
21	c2hqrA	 Alignment	not modelled	99.8	11	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
22	c1p2fA	 Alignment	not modelled	99.8	22	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
23	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
24	d1s8na	 Alignment	not modelled	99.8	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
25	c3sztB	 Alignment	not modelled	99.8	20	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
26	c4lfuA	 Alignment	not modelled	99.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
27	c1h0mD	 Alignment	not modelled	99.7	17	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
28	c2q0oA	 Alignment	not modelled	99.7	24	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial

					quorum2 sensing
29	c3qp5C_	Alignment	not modelled	99.7	32 PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
30	c1zljE_	Alignment	not modelled	99.7	97 PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
31	c3b2nA_	Alignment	not modelled	99.7	18 PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
32	c6ekhY_	Alignment	not modelled	99.7	28 PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
33	c4e7pA_	Alignment	not modelled	99.7	24 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
34	c6jqsA_	Alignment	not modelled	99.7	34 PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
35	c5lwkB_	Alignment	not modelled	99.7	20 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
36	c3cz5B_	Alignment	not modelled	99.7	37 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
37	d1a04a2	Alignment	not modelled	99.7	28 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
38	c3eulB_	Alignment	not modelled	99.7	34 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
39	c5i4cA_	Alignment	not modelled	99.6	23 PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
40	c3cloC_	Alignment	not modelled	99.6	26 PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: 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
41	d1p4wa_	Alignment	not modelled	99.6	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
42	d1dz3a_	Alignment	not modelled	99.6	22 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c2krfB_	Alignment	not modelled	99.6	26 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
44	c1a2oB_	Alignment	not modelled	99.6	21 PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
45	c3t8yA_	Alignment	not modelled	99.6	25 PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
46	d1fsea_	Alignment	not modelled	99.6	36 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
47	d1l3la1	Alignment	not modelled	99.6	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
48	c6ifhA_	Alignment	not modelled	99.6	27 PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporosarcina sp. tg-14
49	c6m8oA_	Alignment	not modelled	99.6	26 PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
50	c2ayxA_	Alignment	not modelled	99.6	19 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
51	c2rnjA_	Alignment	not modelled	99.6	35 PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
52	c3eq2A_	Alignment	not modelled	99.6	23 PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas aeruginosa rssb
53	c2f6cB_	Alignment	not modelled	99.6	22 PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga;

53	c3t0cB	Alignment	not modelled	99.6	22	PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli PDB header: transcription
54	c1x3uA	Alignment	not modelled	99.6	22	Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
55	c3cu5B	Alignment	not modelled	99.6	28	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
56	c3breA	Alignment	not modelled	99.6	23	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
57	d1a04a1	Alignment	not modelled	99.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
58	c2qv0A	Alignment	not modelled	99.6	17	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
59	c5wq0C	Alignment	not modelled	99.6	22	PDB header: signaling protein Chain: C: PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from paenisporsarcina sp. tg-14
60	c1ny5A	Alignment	not modelled	99.6	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
61	d1ny5a1	Alignment	not modelled	99.6	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	d1jbea	Alignment	not modelled	99.6	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
63	d1kgsa2	Alignment	not modelled	99.6	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	d1ys7a2	Alignment	not modelled	99.6	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	d1a2oa1	Alignment	not modelled	99.6	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	c5uicA	Alignment	not modelled	99.6	23	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
67	d1u0sy	Alignment	not modelled	99.5	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	c6od1A	Alignment	not modelled	99.5	17	PDB header: signaling protein Chain: A: PDB Molecule: regulator of rpos; PDBTitle: irad-bound to rssb d58p variant
69	c2qr3A	Alignment	not modelled	99.5	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
70	c4qpiC	Alignment	not modelled	99.5	22	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
71	c2jr1A	Alignment	not modelled	99.5	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
72	c2jpcA	Alignment	not modelled	99.5	27	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
73	c3i5aA	Alignment	not modelled	99.5	24	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
74	c3rqiA	Alignment	not modelled	99.5	21	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
75	c5ep0A	Alignment	not modelled	99.5	20	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
76	c1w25B	Alignment	not modelled	99.5	25	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
77	c6ideA	Alignment	not modelled	99.5	29	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
78	c3jteA	Alignment	not modelled	99.5	24	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain

						protein from2 clostridium thermocellum 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
79	c3w9sB_	Alignment	not modelled	99.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
80	d1yioa1	Alignment	not modelled	99.5	33	PDB header: signaling protein Chain: A: PDB Molecule: candidate response regulator, chey; PDBTitle: bacteriophytochrome response regulator rtbrr
81	c5bria_	Alignment	not modelled	99.5	22	PDB header: transcription Chain: B: PDB Molecule: response regulator rsta; PDBTitle: the response regulator rsta is a potential drug target for2 acinetobacter baumannii
82	c5e3jB_	Alignment	not modelled	99.5	28	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
83	c4h60A_	Alignment	not modelled	99.5	29	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
84	c3dzdA_	Alignment	not modelled	99.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
85	d1peya_	Alignment	not modelled	99.5	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
86	c3crnA_	Alignment	not modelled	99.5	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	d2ayxa1	Alignment	not modelled	99.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	d1mvoa_	Alignment	not modelled	99.5	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	d1dbwa_	Alignment	not modelled	99.5	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
90	d2pl1a1	Alignment	not modelled	99.5	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	c3c3mA_	Alignment	not modelled	99.5	22	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 methanococcus marisnigri jr1
92	c3to5A_	Alignment	not modelled	99.5	25	PDB header: signaling protein Chain: A: PDB Molecule: chey homolog; PDBTitle: high resolution structure of chey3 from vibrio cholerae
93	c3cnbC_	Alignment	not modelled	99.5	17	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
94	c3hdgE_	Alignment	not modelled	99.5	20	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
95	d2a9pa1	Alignment	not modelled	99.5	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c2rjnA_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
97	c5brjA_	Alignment	not modelled	99.5	24	PDB header: signaling protein Chain: A: PDB Molecule: two component response regulator; PDBTitle: structure of the bacteriophytochrome response regulator atbrr
98	c3cg0A_	Alignment	not modelled	99.5	23	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
99	c5t3yA_	Alignment	not modelled	99.5	25	PDB header: signaling protein Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: solution structure of response regulator protein from burkholderia2 multivorans
100	d1qkka_	Alignment	not modelled	99.5	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
101	c5te9A_	Alignment	not modelled	99.5	22	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a response regulator receiver protein from2 burkholderia phymatum
102	c4lzlA_	Alignment	not modelled	99.5	18	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) PDB header: transcription

103	c2zwmA_	Alignment	not modelled	99.5	29	Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
104	c4q7eA_	Alignment	not modelled	99.5	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
105	c3cfyA_	Alignment	not modelled	99.5	19	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
106	c5m7nA_	Alignment	not modelled	99.5	20	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
107	c4dadA_	Alignment	not modelled	99.5	21	PDB header: signaling protein, signal transduction Chain: A: PDB Molecule: putative pilus assembly-related protein; PDBTitle: crystal structure of a putative pilus assembly-related protein2 (bpps2195) from burkholderia pseudomallei k96243 at 2.50 a resolution3 (psi community target, shapiro l.)
108	d1k66a_	Alignment	not modelled	99.4	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c3nhzA_	Alignment	not modelled	99.4	28	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
110	d1yioa2	Alignment	not modelled	99.4	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
111	d1p6qa_	Alignment	not modelled	99.4	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
112	c3i42A_	Alignment	not modelled	99.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (cheY-like); PDBTitle: structure of response regulator receiver domain (cheY-like) from2 methylobacillus flagellatus
113	c3khtA_	Alignment	not modelled	99.4	23	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
114	c2qsjB_	Alignment	not modelled	99.4	28	PDB header: transcription Chain: B: PDB Molecule: dna-binding response regulator, luxr family; PDBTitle: crystal structure of a luxr family dna-binding response regulator from2 silicibacter pomeroyi
115	d1zh2a1	Alignment	not modelled	99.4	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	d1krwa_	Alignment	not modelled	99.4	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	c3h1gA_	Alignment	not modelled	99.4	26	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
118	c3hv2B_	Alignment	not modelled	99.4	23	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
119	d1heya_	Alignment	not modelled	99.4	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
120	d1w25a1	Alignment	not modelled	99.4	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related