



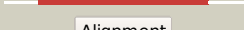

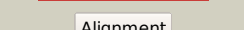

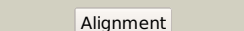





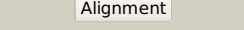

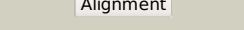

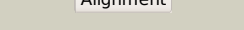

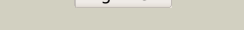



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0757_(phoP)_851611_852354
Date	Fri Jul 26 01:50:33 BST 2019
Unique Job ID	a3b2ca6bea77910e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ys7B_	 Alignment		100.0	46	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	c3r0jA_	 Alignment		100.0	96	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
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	29	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	c4kfcB_	 Alignment		100.0	34	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
6	c2gwrA_	 Alignment		100.0	39	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
7	c5u8mA_	 Alignment		100.0	28	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
8	c2hqrA_	 Alignment		100.0	18	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	29	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
10	c1kgsA_	 Alignment		100.0	35	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	32	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	35	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	26	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		100.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
15	c5f64C_	Alignment		99.9	20	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
16	c2ayxA_	Alignment		99.9	28	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
17	c4hyeB_	Alignment		99.9	24	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	c1w25B_	Alignment		99.9	32	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
19	c3eq2A_	Alignment		99.9	31	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas aeruginosa rssb
20	c3breA_	Alignment		99.9	32	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
21	c3c3wB_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
22	d1ys7a2	Alignment	not modelled	99.9	51	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
23	c4qpiC_	Alignment	not modelled	99.9	38	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
24	c1ny5A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
25	c3w9sB_	Alignment	not modelled	99.9	37	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
26	c5uicA_	Alignment	not modelled	99.9	43	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
27	c5ep0A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
28	d1ny5a1	Alianment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like

					Family:CheY-related
29	c6ifhA_	Alignment	not modelled	99.9	38 PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spoOf from paenisporosarcina sp. tg-14
30	d1kgsa2	Alignment	not modelled	99.9	38 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
31	d2pl1a1	Alignment	not modelled	99.9	43 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
32	d1krwa_	Alignment	not modelled	99.9	29 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
33	d2ayxa1	Alignment	not modelled	99.9	30 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	c3i5aA_	Alignment	not modelled	99.9	31 PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
35	c6od1A_	Alignment	not modelled	99.9	23 PDB header: signaling protein Chain: A: PDB Molecule: regulator of rpos; PDBTitle: irad-bound to rssb d58p variant
36	c1rn1A_	Alignment	not modelled	99.9	22 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
37	c3cfyA_	Alignment	not modelled	99.9	23 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
38	d1jbea_	Alignment	not modelled	99.9	33 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
39	c3dzdA_	Alignment	not modelled	99.9	25 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
40	d1mvoa_	Alignment	not modelled	99.9	49 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
41	c3rq1A_	Alignment	not modelled	99.9	20 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 and 3 citrate
42	d1s8na_	Alignment	not modelled	99.9	30 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c4if4A_	Alignment	not modelled	99.9	24 PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryllofluoride-activated vvar2 from staphylococcus aureus
44	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
45	d1qkka_	Alignment	not modelled	99.9	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	d2a9pa1	Alignment	not modelled	99.9	46 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	c5hevC_	Alignment	not modelled	99.9	24 PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryllofluoride-activated liar from 2 enterococcus faecium
48	c2zwmA_	Alignment	not modelled	99.9	45 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
49	d1peya_	Alignment	not modelled	99.9	32 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	d1dbwa_	Alignment	not modelled	99.9	24 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3nhzA_	Alignment	not modelled	99.9	46 PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
52	c2rjnA_	Alignment	not modelled	99.9	25 PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from 2 neptuniibacter caesariensis
53	c2jrlA_	Alignment	not modelled	99.9	28 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
					PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryllofluoride-activated liar from 2 enterococcus faecium

54	c2qzjC_	Alignment	not modelled	99.9	26	Chain: C; PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
55	d1p6qa_	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	d1w25a1	Alignment	not modelled	99.9	44	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	c4lzIA_	Alignment	not modelled	99.9	25	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)
58	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
59	d1yioa2	Alignment	not modelled	99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	c5e3jB_	Alignment	not modelled	99.9	41	PDB header: transcription Chain: B; PDB Molecule: response regulator rsta; PDBTitle: the response regulator rsta is a potential drug target for2 acinetobacter baumannii
61	c4eukA_	Alignment	not modelled	99.9	27	PDB header: signaling protein Chain: A; PDB Molecule: histidine kinase 5; PDBTitle: crystal structure
62	d1zh2a1	Alignment	not modelled	99.9	42	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
63	c3to5A_	Alignment	not modelled	99.9	29	PDB header: signaling protein Chain: A; PDB Molecule: chey homolog; PDBTitle: high resolution structure of chey3 from vibrio cholerae
64	c3hv2B_	Alignment	not modelled	99.9	25	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
65	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
66	d1u0sy_	Alignment	not modelled	99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	c3cu5B_	Alignment	not modelled	99.9	23	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
68	c2qr3A_	Alignment	not modelled	99.9	22	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
69	c4h60A_	Alignment	not modelled	99.9	37	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
70	d1zga1	Alignment	not modelled	99.9	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
71	c5t3yA_	Alignment	not modelled	99.9	30	PDB header: signaling protein Chain: A; PDB Molecule: two-component system response regulator; PDBTitle: solution structure of response regulator protein from burkholderia2 multivorans
72	c3hdgE_	Alignment	not modelled	99.9	22	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
73	d1zesa1	Alignment	not modelled	99.9	41	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
74	c3t6kB_	Alignment	not modelled	99.9	39	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
75	c3eulB_	Alignment	not modelled	99.9	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
76	d1a04a2	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
77	c6ekhY_	Alignment	not modelled	99.9	26	PDB header: metal binding protein Chain: Y; PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
78	c5kbxB_	Alignment	not modelled	99.9	23	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
79	c3jteA_	Alignment	not modelled	99.9	28	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
80	c4e7pA_	Alignment	not modelled	99.9	25	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of receiver domain of putative narI family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog berylliofluoride
81	c5lwkB_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
82	c3crnA_	Alignment	not modelled	99.9	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
83	d1xhfa1	Alignment	not modelled	99.9	37	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	c3b2nA_	Alignment	not modelled	99.9	26	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
85	d1heya_	Alignment	not modelled	99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
86	d1dz3a_	Alignment	not modelled	99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c3lteH_	Alignment	not modelled	99.9	28	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
88	c3cg4A_	Alignment	not modelled	99.9	27	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
89	c3cz5B_	Alignment	not modelled	99.9	27	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
90	c5x5jA_	Alignment	not modelled	99.9	37	PDB header: dna binding protein Chain: A: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader receiver domain
91	c6m8oA_	Alignment	not modelled	99.9	25	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
92	c5wq0C_	Alignment	not modelled	99.9	26	PDB header: signaling protein Chain: C: PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from paenisporosarcina sp. tg-14
93	c4uhsA_	Alignment	not modelled	99.9	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)
94	c2zayA_	Alignment	not modelled	99.9	23	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
95	d1k66a_	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c1a2oB_	Alignment	not modelled	99.9	30	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
97	c3h1gA_	Alignment	not modelled	99.9	27	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
98	c5briA_	Alignment	not modelled	99.9	33	PDB header: signaling protein Chain: A: PDB Molecule: candidate response regulator, chey; PDBTitle: bacteriophytochrome response regulator rtbrr
99	c5tqjA_	Alignment	not modelled	99.9	37	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 burkholderia phymatum
100	c3cnbC_	Alignment	not modelled	99.9	22	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
101	c2qv0A_	Alignment	not modelled	99.9	22	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
102	c3grcD_	Alignment	not modelled	99.9	24	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666

103	d1i3ca_	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
104	c2rv8A_	Alignment	not modelled	99.9	85	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
105	c5dc1B_	Alignment	not modelled	99.9	30	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
106	c2jk1A_	Alignment	not modelled	99.9	24	PDB header: dna-binding Chain: A; PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
107	c2hqoA_	Alignment	not modelled	99.9	20	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
108	c3hdvB_	Alignment	not modelled	99.9	23	PDB header: transcription regulator Chain: B; PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
109	c3c3mA_	Alignment	not modelled	99.9	29	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
110	c3khtA_	Alignment	not modelled	99.9	26	PDB header: signaling protein Chain: A; PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
111	c4d6yA_	Alignment	not modelled	99.9	25	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
112	d2r25b1	Alignment	not modelled	99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
113	c2qxyB_	Alignment	not modelled	99.9	29	PDB header: transcription Chain: B; PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
114	c3hebB_	Alignment	not modelled	99.9	21	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
115	c3hzhA_	Alignment	not modelled	99.9	24	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
116	c5brjA_	Alignment	not modelled	99.9	28	PDB header: signaling protein Chain: A; PDB Molecule: two component response regulator; PDBTitle: structure of the bacteriophytochrome response regulator atbr
117	d1p2fa2	Alignment	not modelled	99.9	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c3a0rB_	Alignment	not modelled	99.9	37	PDB header: transferase Chain: B; PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
119	c2qvqA_	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A; PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
120	c3kcnA_	Alignment	not modelled	99.9	24	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica