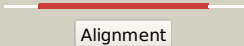

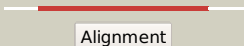

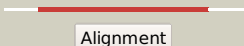







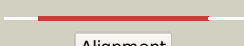











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0844c_(narL)_940459_941109
 Date Fri Jul 26 01:50:43 BST 2019
 Unique Job ID c66873285704cde2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hyeB_	 Alignment		100.0	27	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
2	c4if4A_	 Alignment		100.0	31	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus
3	c5hevC_	 Alignment		100.0	34	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the berylliofluoride-activated liar from2 enterococcus faecium
4	c5f64C_	 Alignment		100.0	24	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
5	c1rn1A_	 Alignment		100.0	35	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
6	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
7	c3c3wB_	 Alignment		100.0	31	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
8	c1zn2A_	 Alignment		100.0	27	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styx
9	c5o8yG_	 Alignment		100.0	20	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	31	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	14	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst

12	c1kgsA_	Alignment		99.9	18	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	24	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	19	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	23	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
16	c4b09F_	Alignment		99.8	21	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
17	c2gwrA_	Alignment		99.8	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
18	c1ys7B_	Alignment		99.8	29	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
19	c2oqrA_	Alignment		99.8	20	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	d1s8na_	Alignment		99.8	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	c2hqrA_	Alignment	not modelled	99.8	14	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	c4kfcB_	Alignment	not modelled	99.8	20	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
23	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
24	c5u8mA_	Alignment	not modelled	99.8	14	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
25	c3sztB_	Alignment	not modelled	99.7	32	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	99.7	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	c3eulB_	Alignment	not modelled	99.7	100	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
						PDB header: transcription/dna

28	c1h0mD_	Alignment	not modelled	99.7	26	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
29	c2q0oA_	Alignment	not modelled	99.7	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
30	d1a04a2	Alignment	not modelled	99.7	36	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
31	c1a2oB_	Alignment	not modelled	99.7	25	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
32	c4e7pA_	Alignment	not modelled	99.7	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 beryllifluoride
33	c3qp5C_	Alignment	not modelled	99.6	30	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
34	c3cz5B_	Alignment	not modelled	99.6	31	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
35	c3b2nA_	Alignment	not modelled	99.6	25	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
36	c5i4cA_	Alignment	not modelled	99.6	27	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
37	c2ayxA_	Alignment	not modelled	99.6	25	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
38	c5wq0C_	Alignment	not modelled	99.6	30	PDB header: signaling protein Chain: C: PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from paenisporsarcina sp. tg-14
39	d1dz3a_	Alignment	not modelled	99.6	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	c3eq2A_	Alignment	not modelled	99.6	24	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas aeruginosa rssb
41	c3cloC_	Alignment	not modelled	99.6	43	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
42	c6jqsA_	Alignment	not modelled	99.6	33	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
43	d1jbea_	Alignment	not modelled	99.6	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	c5lwkB_	Alignment	not modelled	99.6	22	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
45	c6ekhY_	Alignment	not modelled	99.6	25	PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
46	d1fsea_	Alignment	not modelled	99.6	38	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	d1a2oa1	Alignment	not modelled	99.6	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
48	c6m8oA_	Alignment	not modelled	99.6	24	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
49	c1w25B_	Alignment	not modelled	99.6	29	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
50	c2krfB_	Alignment	not modelled	99.6	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
51	c3breA_	Alignment	not modelled	99.6	26	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
52	d1p4wa_	Alignment	not modelled	99.6	24	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) PDB header: transcription regulator

53	c3cu5B_	Alignment	not modelled	99.6	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
54	d1l3la1	Alignment	not modelled	99.6	26	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)
55	c3f6cB_	Alignment	not modelled	99.5	24	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
56	c2qv0A_	Alignment	not modelled	99.5	20	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
57	c3t8yA_	Alignment	not modelled	99.5	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
58	c6od1A_	Alignment	not modelled	99.5	28	PDB header: signaling protein Chain: A: PDB Molecule: regulator of rpos; PDBTitle: irad-bound to rssb d58p variant
59	d1u0sy_	Alignment	not modelled	99.5	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	d2ayxa1	Alignment	not modelled	99.5	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	c1ny5A_	Alignment	not modelled	99.5	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
62	c1zljE_	Alignment	not modelled	99.5	31	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
63	d1ny5a1	Alignment	not modelled	99.5	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c2rnjA_	Alignment	not modelled	99.5	40	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
65	c3i5aA_	Alignment	not modelled	99.5	27	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
66	c3to5A_	Alignment	not modelled	99.5	26	PDB header: signaling protein Chain: A: PDB Molecule: chey homolog; PDBTitle: high resolution structure of chey3 from vibrio cholerae
67	c5uicA_	Alignment	not modelled	99.5	27	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
68	c4qpjC_	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
69	d1ys7a2	Alignment	not modelled	99.5	34	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
70	c1x3uA_	Alignment	not modelled	99.5	30	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
71	c2jpcA_	Alignment	not modelled	99.5	34	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
72	d1a04a1	Alignment	not modelled	99.5	32	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)
73	d1dbwa_	Alignment	not modelled	99.5	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
74	d1kgsa2	Alignment	not modelled	99.5	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d1p6qa_	Alignment	not modelled	99.5	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c6ifhA_	Alignment	not modelled	99.5	25	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporsarcina sp. tg-14
77	c2rjnA_	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
78	d1mvoa_	Alignment	not modelled	99.5	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						PDB header: transcription

79	c3rqjA	Alignment	not modelled	99.5	21	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
80	d1krwa	Alignment	not modelled	99.5	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
81	d1peya	Alignment	not modelled	99.5	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	c5ep0A	Alignment	not modelled	99.5	26	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
83	c3hv2B	Alignment	not modelled	99.5	18	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
84	c3w9sB	Alignment	not modelled	99.5	22	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
85	c3hdqE	Alignment	not modelled	99.5	24	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
86	d2a9pa1	Alignment	not modelled	99.5	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c3dzdA	Alignment	not modelled	99.5	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
88	c5m7nA	Alignment	not modelled	99.4	24	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 crystalldirect automated mounting and cryo-cooling3 technology
89	c6ideA	Alignment	not modelled	99.4	24	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
90	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
91	d1yioa2	Alignment	not modelled	99.4	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
92	c3t6kB	Alignment	not modelled	99.4	25	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
93	d2pl1a1	Alignment	not modelled	99.4	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
94	c4q7eA	Alignment	not modelled	99.4	21	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
95	d1heya	Alignment	not modelled	99.4	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3cfyA	Alignment	not modelled	99.4	21	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
97	d1k66a	Alignment	not modelled	99.4	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	c2jrIA	Alignment	not modelled	99.4	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
99	c2lpmA	Alignment	not modelled	99.4	18	PDB header: transcription regulator Chain: A: PDB Molecule: two-component response regulator; PDBTitle: chemical shift and structure assignments for sma0114
100	c3cnbC	Alignment	not modelled	99.4	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 colwellia psychrerythraea 34h
101	d1qkka	Alignment	not modelled	99.4	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
102	c5kxbB	Alignment	not modelled	99.4	17	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
103	c2zwuA	Alignment	not modelled	99.4	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf;

103	c2zw11A_	Alignment	not modelled	99.4	20	PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis PDB header: transcription Chain: A; PDB Molecule: two-component system response regulator;
104	c2qr3A_	Alignment	not modelled	99.4	18	PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
105	c5briA_	Alignment	not modelled	99.4	27	PDB header: signaling protein Chain: A; PDB Molecule: candidate response regulator, chey; PDBTitle: bacteriophytochrome response regulator rtbr
106	d1yioa1	Alignment	not modelled	99.4	34	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)
107	c3khtA_	Alignment	not modelled	99.4	24	PDB header: signaling protein Chain: A; PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
108	c3cg4A_	Alignment	not modelled	99.4	23	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
109	c2qvqA_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: A; PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
110	c4h60A_	Alignment	not modelled	99.4	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
111	c3hebB_	Alignment	not modelled	99.4	18	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
112	c5e3jB_	Alignment	not modelled	99.4	23	PDB header: transcription Chain: B; PDB Molecule: response regulator rsta; PDBTitle: the response regulator rsta is a potential drug target for2 acinetobacter baumannii
113	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
114	d1zh2a1	Alignment	not modelled	99.4	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
115	c3kyiB_	Alignment	not modelled	99.4	24	PDB header: transferase Chain: B; PDB Molecule: chey6 protein; PDBTitle: crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
116	d1i3ca_	Alignment	not modelled	99.4	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	c4eukA_	Alignment	not modelled	99.4	18	PDB header: signaling protein Chain: A; PDB Molecule: histidine kinase 5; PDBTitle: crystal structure
118	c3ilhA_	Alignment	not modelled	99.4	19	PDB header: transcription regulator Chain: A; PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
119	c3gt7A_	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: A; PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
120	d1w25a1	Alignment	not modelled	99.4	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related