
































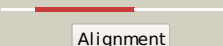
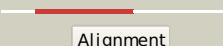


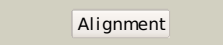
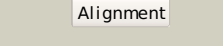
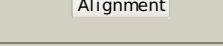
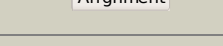
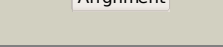
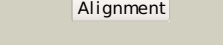
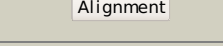
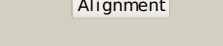
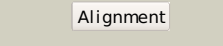
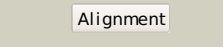
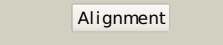

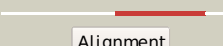
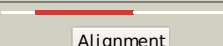

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv0A_	 Alignment		99.9	36	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of 2 protein mrke from klebsiella pneumoniae
2	c3breA_	 Alignment		99.9	25	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
3	c3eq2A_	 Alignment		99.9	27	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
4	c3b2nA_	 Alignment		99.9	24	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
5	c2ayxA_	 Alignment		99.9	21	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
6	c1a2oB_	 Alignment		99.9	28	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
7	c3t8yA_	 Alignment		99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
8	c3i5aA_	 Alignment		99.9	25	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
9	c1w25B_	 Alignment		99.9	23	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
10	d1s8na_	 Alignment		99.9	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
11	d1dz3a_	 Alignment		99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	d1ny5a1	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
13	c1ny5A_	Alignment		99.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
14	c3cu5B_	Alignment		99.9	27	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
15	d2a9pa1	Alignment		99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	d1jbea_	Alignment		99.9	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	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
18	d2ayxa1	Alignment		99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
19	d1kgsa2	Alignment		99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
20	d1a04a2	Alignment		99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	c3eulB_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
22	c2zwmA_	Alignment	not modelled	99.9	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
23	c3cnbC_	Alignment	not modelled	99.9	21	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 psycherythraea 34h
24	d1a2oa1	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
25	d1u0sy_	Alignment	not modelled	99.9	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
26	c3cg0A_	Alignment	not modelled	99.9	27	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
27	c3cz5B_	Alignment	not modelled	99.9	26	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
28	d1w25a1	Alignment	not modelled	99.9	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
29	d1ys7a2	Alignment	not modelled	99.9	29 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
30	c3dzdA	Alignment	not modelled	99.9	22 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
31	c2qr3A	Alignment	not modelled	99.9	24 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
32	c2rjnA	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
33	c2jrlA	Alignment	not modelled	99.9	25 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
34	d1k66a	Alignment	not modelled	99.9	18 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
35	c3jteA	Alignment	not modelled	99.9	26 PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
36	d1qkka	Alignment	not modelled	99.9	20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
37	c3cfyA	Alignment	not modelled	99.9	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
38	c3nhzA	Alignment	not modelled	99.9	27 PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
39	d1mvoa	Alignment	not modelled	99.9	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	d1dbwa	Alignment	not modelled	99.9	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
41	d1zh2a1	Alignment	not modelled	99.9	29 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
42	d1heya	Alignment	not modelled	99.9	24 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c3khtA	Alignment	not modelled	99.9	19 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
44	c3gt7A	Alignment	not modelled	99.9	24 PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
45	c3hdgE	Alignment	not modelled	99.9	32 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
46	c3hebB	Alignment	not modelled	99.9	15 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
47	c2qzjC	Alignment	not modelled	99.9	25 PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
48	d2pl1a1	Alignment	not modelled	99.9	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	d1zgza1	Alignment	not modelled	99.9	22 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	d1peya	Alignment	not modelled	99.9	23 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3crnA	Alignment	not modelled	99.9	20 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
52	d1p6qa	Alignment	not modelled	99.9	23 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
					PDB header: signaling protein

53	c3h1gA	Alignment	not modelled	99.9	27	Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
54	c2gwrA	Alignment	not modelled	99.9	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
55	c3hv2B	Alignment	not modelled	99.9	18	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
56	d1krwa	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	d1yioa2	Alignment	not modelled	99.9	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
58	d2r25b1	Alignment	not modelled	99.9	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c2zayA	Alignment	not modelled	99.9	20	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
60	c1ys7B	Alignment		99.9	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
61	d1zesa1	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	c2qvga	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
63	c3t6kB	Alignment	not modelled	99.9	28	PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
64	c3ilhA	Alignment	not modelled	99.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
65	c3i42A	Alignment	not modelled	99.9	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
66	d1xhfa1	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	d1i3ca	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	c3rqia	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 and3 citrate
69	c1kgsA	Alignment	not modelled	99.9	27	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
70	c3f6cB	Alignment	not modelled	99.9	23	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
71	c3c3mA	Alignment	not modelled	99.9	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 methanoculleus marisnigri jr1
72	d1p2fa2	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	c3q9sA	Alignment	not modelled	99.9	22	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
74	c1p2fA	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
75	c3lteH	Alignment	not modelled	99.9	23	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
76	d1mb3a	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
77	c2oqrA	Alignment	not modelled	99.9	17	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from

					mycobacterium2 tuberculosis
78	c3hzhA_	Alignment	not modelled	99.9	17 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
79	c3mmnA_	Alignment	not modelled	99.9	25 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+
80	c3m6mF_	Alignment	not modelled	99.9	29 PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc
81	c3n0rA_	Alignment	not modelled	99.9	21 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
82	c2jk1A_	Alignment	not modelled	99.9	17 PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
83	c3kcnA_	Alignment	not modelled	99.9	20 PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
84	c3a0rB_	Alignment	not modelled	99.9	31 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)
85	d1k68a_	Alignment	not modelled	99.9	15 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
86	c3grcD_	Alignment	not modelled	99.9	23 PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
87	c2qxyB_	Alignment	not modelled	99.9	20 PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
88	c3eqzB_	Alignment	not modelled	99.9	21 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea
89	c3cg4A_	Alignment	not modelled	99.9	24 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (cheY-like); PDBTitle: crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1
90	c3hdvB_	Alignment	not modelled	99.9	25 PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
91	c2rdmB_	Alignment	not modelled	99.9	18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
92	c3gl9B_	Alignment	not modelled	99.9	26 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
93	c3nhmA_	Alignment	not modelled	99.8	25 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
94	d1w25a2	Alignment	not modelled	99.8	20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c3snkA_	Alignment	not modelled	99.8	17 PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
96	c3h5iA_	Alignment	not modelled	99.8	20 PDB header: transcription Chain: A: PDB Molecule: response regulator/sensory box protein/ggdef PDBTitle: crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydothermus hydrogenoformans
97	c2qsjB_	Alignment	not modelled	99.8	19 PDB header: transcription Chain: B: PDB Molecule: dna-binding response regulator, luxr family; PDBTitle: crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
98	c3luaA_	Alignment	not modelled	99.8	23 PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
99	d2b4aa1	Alignment	not modelled	99.8	20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
100	c3c97A_	Alignment	not modelled	99.8	25 PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
101	c1zn2A_	Alignment	not modelled	99.8	28 PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr

102	c2hgoA	 Alignment	not modelled	99.8	16	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
103	c2j48A	 Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
104	d1dcfa	 Alignment	not modelled	99.8	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
105	c2hqrA	 Alignment	not modelled	99.8	12	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
106	c3eodA	 Alignment	not modelled	99.8	24	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
107	c2nt3A	 Alignment	not modelled	99.8	22	PDB header: signaling protein Chain: A: PDB Molecule: response regulator homolog; PDBTitle: receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
108	c3kviB	 Alignment	not modelled	99.8	25	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
109	c3ktoA	 Alignment	not modelled	99.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
110	c3lufB	 Alignment	not modelled	99.8	21	PDB header: signaling protein Chain: B: PDB Molecule: two-component system response regulator/ggdef PDBTitle: structure of probable two-component system response2 regulator/ggdef domain protein
111	c3c3wB	 Alignment	not modelled	99.8	30	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
112	d1qo0d	 Alignment	not modelled	99.8	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon AmiR
113	c3n53B	 Alignment	not modelled	99.8	30	PDB header: transcription Chain: B: PDB Molecule: response regulator receiver modulated diguanylate cyclase; PDBTitle: crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
114	c1rnlA	 Alignment	not modelled	99.7	32	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
115	c2yxbA	 Alignment	not modelled	99.6	15	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
116	c3d6wA	 Alignment	not modelled	99.6	24	PDB header: dna binding protein Chain: A: PDB Molecule: methyl-accepting/dna response regulator; PDBTitle: lyttr dna-binding domain of putative methyl-accepting/dna response2 regulator from bacillus cereus.
117	c3cwoX	 Alignment	not modelled	99.6	20	PDB header: de novo protein Chain: X: PDB Molecule: beta/alpha-barrel protein based on 1thf and 1trny; PDBTitle: a beta/alpha-barrel built by the combination of fragments2 from different folds
118	c3bs1A	 Alignment	not modelled	99.4	18	PDB header: transcription regulator Chain: A: PDB Molecule: accessory gene regulator protein a; PDBTitle: structure of the staphylococcus aureus agra lyttr domain2 bound to dna reveals a beta fold with a novel mode of3 binding
119	d1fmfa	 Alignment	not modelled	99.2	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
120	c3klnC	 Alignment	not modelled	99.0	11	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst