

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zn2A_	 Alignment		100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
2	c1kgsA_	 Alignment		100.0	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
3	c3r0jA_	 Alignment		100.0	20	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
4	c3c3wB_	 Alignment		100.0	18	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
5	c1ys7B_	 Alignment		100.0	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
6	c1rnlA_	 Alignment		100.0	23	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	c2ayxA_	 Alignment		100.0	22	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
8	dls8na_	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
9	c3q9sA_	 Alignment		100.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
10	c3breA_	 Alignment		100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
11	d1a04a2	 Alignment		100.0	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	c3eulB	Alignment		100.0	16	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narI from mycobacterium tuberculosis
13	c1a2oB	Alignment		99.9	20	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheB regulation by a2 phosphorylation-activated domain
14	c3cz5B	Alignment		99.9	17	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
15	c3eq2A	Alignment		99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
16	c3b2nA	Alignment		99.9	25	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
17	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
18	d1jbea	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
19	c1w25B	Alignment		99.9	21	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
20	c3i5aA	Alignment		99.9	19	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
21	d1ny5a1	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
22	d1dz3a	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
23	c2gwrA	Alignment	not modelled	99.9	21	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
24	c1p2fA	Alignment	not modelled	99.9	17	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompR/phob homolog
25	c2oqrA	Alignment	not modelled	99.9	19	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
26	c3rqIA	Alignment	not modelled	99.9	22	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
27	d1qkka	Alignment	not modelled	99.9	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c3cu5B	Alignment	not modelled	99.9	24	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

29	d1p6qa_	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
30	c2qv0A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
31	d2ayxa1	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
32	d1u0sy_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
33	d1dbwa_	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	c2rjnA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
35	d1ys7a2	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
36	d2a9pa1	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
37	d1kgsa2	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
38	c3cfyA_	Alignment	not modelled	99.9	30	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
39	d1mvoa_	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	d2pl1a1	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
41	c2hqrA_	Alignment	not modelled	99.9	13	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
42	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
43	d1w25a1	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	d1heya_	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	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
46	d1peya_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	d1krwa_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
48	c3jteA_	Alignment	not modelled	99.9	21	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
49	c3hdgE_	Alignment	not modelled	99.9	29	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 wolinetlla3 succinogenes
50	c3hv2B_	Alignment	not modelled	99.9	20	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
51	d1k66a_	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
52	c2jrlA_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the berylliofluoride-activated ntrc4 receiver2 domain dimer
53	d1zh2a1	Alignment	not modelled	99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
54	c3cnbC_	Alignment	not modelled	99.9	23	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

55	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
56	dlzga1	Alignment	not modelled	99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	c3gt7A_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
58	dli3ca_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	dlyioa2	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	c3t6kB_	Alignment	not modelled	99.9	27	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
61	c3h1gA_	Alignment	not modelled	99.9	19	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
62	c3nhzA_	Alignment	not modelled	99.9	30	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
63	c2qzjC_	Alignment	not modelled	99.9	26	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
64	dlzesal	Alignment	not modelled	99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	c3khtA_	Alignment	not modelled	99.9	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
66	c3f6cB_	Alignment	not modelled	99.9	15	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
67	d1xhfa1	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	dla2oa1	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
69	d2r25b1	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
70	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
71	c2zayA_	Alignment	not modelled	99.9	19	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
72	c3lteH_	Alignment	not modelled	99.9	22	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
73	c3hebB_	Alignment	not modelled	99.9	23	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
74	c2qvga_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
75	c3hzha_	Alignment	not modelled	99.9	19	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
76	c2jk1A_	Alignment	not modelled	99.9	18	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
77	c3kcnA_	Alignment	not modelled	99.9	19	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
78	c3t8yA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
79	c3hdvB_	Alignment	not modelled	99.9	20	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein

					from2 pseudomonas putida
80	c3cg0A_	Alignment	not modelled	99.9	26 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
81	d1p2fa2	Alignment	not modelled	99.9	22 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	c2qxyB_	Alignment	not modelled	99.9	19 PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
83	c3c3mA_	Alignment	not modelled	99.9	19 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
84	c3m6mF_	Alignment	not modelled	99.9	19 PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc
85	c3snkA_	Alignment	not modelled	99.9	15 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
86	c3mmnA_	Alignment	not modelled	99.9	14 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+
87	c3gl9B_	Alignment	not modelled	99.9	22 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
88	c3cg4A_	Alignment	not modelled	99.9	20 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	d1w25a2	Alignment	not modelled	99.9	17 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
90	c2hqaA_	Alignment	not modelled	99.9	15 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
91	c3c97A_	Alignment	not modelled	99.9	19 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
92	c3grcD_	Alignment	not modelled	99.9	22 PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
93	d1mb3a_	Alignment	not modelled	99.9	24 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
94	c3ilhA_	Alignment	not modelled	99.9	16 PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
95	d1k68a_	Alignment	not modelled	99.9	15 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3luaA_	Alignment	not modelled	99.9	20 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
97	d1dcfa_	Alignment	not modelled	99.9	14 Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
98	d2b4aa1	Alignment	not modelled	99.9	20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
99	c2rdmB_	Alignment	not modelled	99.9	15 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
100	c3a0rB_	Alignment	not modelled	99.9	21 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)
101	d1qo0d_	Alignment	not modelled	99.9	11 Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon AmiR
102	c3eodA_	Alignment	not modelled	99.9	27 PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
103	c3nhmA_	Alignment	not modelled	99.9	18 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
					PDB header: structural genomics, unknown function

104	c3i42A_	Alignment	not modelled	99.9	23	Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
105	c3n0rA_	Alignment	not modelled	99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
106	c3eqzB_	Alignment	not modelled	99.9	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea
107	c3ktoA_	Alignment	not modelled	99.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
108	c3h5iA_	Alignment	not modelled	99.8	23	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
109	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.
110	c3kyiB_	Alignment	not modelled	99.8	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
111	c2qsjB_	Alignment	not modelled	99.8	17	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
112	c3klnC_	Alignment	not modelled	99.8	12	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
113	c3lufB_	Alignment	not modelled	99.8	19	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
114	c2nt3A_	Alignment	not modelled	99.8	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator homolog; PDBTitle: receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
115	c2yxbA_	Alignment	not modelled	99.8	11	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	c3n53B_	Alignment	not modelled	99.7	20	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
117	c3cwoX_	Alignment	not modelled	99.7	18	PDB header: de novo protein Chain: X: PDB Molecule: beta/alpha-barrel protein based on 1thf and 1tmy; PDBTitle: a beta/alpha-barrel built by the combination of fragments2 from different folds
118	d1fmfa_	Alignment	not modelled	99.5	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
119	c3fkqA_	Alignment	not modelled	98.0	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
120	c3sztB_	Alignment	not modelled	97.9	12	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