



















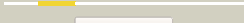

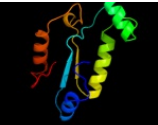


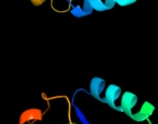







Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dqqB_	 Alignment		100.0	80	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative trna synthase; PDBTitle: the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
2	dlyzya1	 Alignment		100.0	54	Fold: YgbK-like Superfamily: YgbK-like Family: YgbK-like
3	dluana_	 Alignment		92.7	19	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
4	c3eqzB_	 Alignment		84.7	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea
5	c3c3mA_	 Alignment		83.5	11	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
6	c2jrlA_	 Alignment		83.3	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
7	c3a0rB_	 Alignment		81.9	15	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)
8	c3i42A_	 Alignment		81.8	15	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
9	dlqo0d_	 Alignment		80.2	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon AmiR
10	d2b4aa1	 Alignment		79.7	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
11	dlzgza1	 Alignment		78.1	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	c3dfmA	Alignment		77.7	12	PDB header: hydrolase Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
13	c3ghyA	Alignment		76.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
14	d2nv0a1	Alignment		75.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	d1xhfa1	Alignment		71.0	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	c3r0jA	Alignment		69.4	12	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
17	c2j48A	Alignment		68.4	11	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
18	c2qr3A	Alignment		67.0	9	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
19	c3plnA	Alignment		66.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
20	d1kgsa2	Alignment		66.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	c3hdvB	Alignment	not modelled	64.7	14	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
22	c1kgsA	Alignment	not modelled	64.3	14	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
23	d1zesa1	Alignment	not modelled	64.1	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
24	c3hdgE	Alignment	not modelled	63.6	14	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 wolinetella3 succinogenes
25	c3grcD	Alignment	not modelled	62.4	14	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
26	d1s8na	Alignment	not modelled	61.2	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
27	c3jteA	Alignment	not modelled	60.7	19	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
28	c3crnA	Alignment	not modelled	60.7	15	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
						PDB header: transcription

29	c1ny5A_	Alignment	not modelled	59.8	14	Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
30	c2ayxA_	Alignment	not modelled	59.0	17	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
31	d1ny5a1	Alignment	not modelled	57.4	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
32	c2rjnA_	Alignment	not modelled	57.2	5	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
33	c2qzjC_	Alignment	not modelled	56.7	15	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
34	c1ys7B_	Alignment	not modelled	56.4	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
35	c3dfiA_	Alignment	not modelled	56.1	14	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
36	c3hv2B_	Alignment	not modelled	56.1	5	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
37	c2zwmA_	Alignment	not modelled	55.9	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
38	c2cnwF_	Alignment	not modelled	55.7	16	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
39	c2ixdB_	Alignment	not modelled	55.1	11	PDB header: hydrolase Chain: B: PDB Molecule: lmbc-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
40	c3nhmA_	Alignment	not modelled	54.6	9	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
41	c3lwdA_	Alignment	not modelled	53.8	23	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
42	d1gsaa1	Alignment	not modelled	51.3	26	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
43	c3cg4A_	Alignment	not modelled	51.0	8	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
44	d1zh2a1	Alignment	not modelled	50.3	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	c2iy3A_	Alignment	not modelled	48.9	15	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein ffh; PDBTitle: structure of the e. coli signal recognition particle2 bound to a translating ribosome
46	c3lteH_	Alignment	not modelled	47.4	14	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
47	c3h1gA_	Alignment	not modelled	47.3	14	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
48	c3nhzA_	Alignment	not modelled	46.7	18	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
49	c3b2nA_	Alignment	not modelled	46.5	6	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
50	c3dzdA_	Alignment	not modelled	46.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
51	d1ys7a2	Alignment	not modelled	45.8	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
52	d1sula_	Alignment	not modelled	45.3	33	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
53	c1sulaA_	Alignment	not modelled	45.3	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
						PDB header: transcription Chain: B: PDB Molecule: response regulator receiver modulated

54	c3n53B_	Alignment	not modelled	45.0	12	diguanylate cyclase; PDBTitle: crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
55	d1mvoa_	Alignment	not modelled	44.2	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	c2j289_	Alignment	not modelled	44.1	14	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
57	c1i8tB_	Alignment	not modelled	43.9	17	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
58	c1pbtA_	Alignment	not modelled	43.3	19	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 6-phosphoglucanactonase; PDBTitle: the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
59	c2j37W_	Alignment	not modelled	43.3	12	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
60	c3b9qA_	Alignment	not modelled	43.2	10	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
61	c2zayA_	Alignment	not modelled	43.1	8	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
62	d1vl1a_	Alignment	not modelled	42.9	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
63	d1w25a1	Alignment	not modelled	42.6	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	d2ayxa1	Alignment	not modelled	42.6	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	d1yioa2	Alignment	not modelled	42.4	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	c3f6cB_	Alignment	not modelled	42.0	11	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	d1heya_	Alignment	not modelled	41.8	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	d2a9pa1	Alignment	not modelled	41.6	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
69	c3t6kB_	Alignment	not modelled	41.0	14	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
70	c1zu4A_	Alignment	not modelled	40.7	18	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
71	c1gshA_	Alignment	not modelled	40.5	17	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
72	c3cg0A_	Alignment	not modelled	40.0	14	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
73	d1peya_	Alignment	not modelled	39.7	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
74	c2rdmB_	Alignment	not modelled	39.5	17	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
75	d1j8yf2	Alignment	not modelled	39.0	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c3smaD_	Alignment	not modelled	38.5	32	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
77	c2j7pA_	Alignment	not modelled	38.1	15	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyt
78	d1krwa_	Alignment	not modelled	37.5	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
79	d2nyga1	Alignment	not modelled	37.5	28	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like

80	d1mb3a_	Alignment	not modelled	37.1	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
81	c3dmdA_	Alignment	not modelled	36.9	15	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
82	c1j8yF_	Alignment	not modelled	36.6	7	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
83	c2ogrA_	Alignment	not modelled	36.2	16	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
84	c3cu5B_	Alignment	not modelled	35.3	14	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
85	c3khyA_	Alignment	not modelled	34.9	14	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
86	c2hqaA_	Alignment	not modelled	34.6	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
87	c2qy9A_	Alignment	not modelled	34.4	12	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
88	c3lhiA_	Alignment	not modelled	34.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
89	c2og2A_	Alignment	not modelled	33.0	12	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
90	d2a9va1	Alignment	not modelled	32.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
91	c3qfnA_	Alignment	not modelled	31.9	44	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
92	d1p2fa2	Alignment	not modelled	31.0	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	c3e4fB_	Alignment	not modelled	30.9	23	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
94	c3nwpA_	Alignment	not modelled	30.9	19	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
95	d2pl1a1	Alignment	not modelled	30.8	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c2yhsA_	Alignment	not modelled	30.6	12	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
97	c3dm5A_	Alignment	not modelled	30.6	13	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
98	c3gt7A_	Alignment	not modelled	30.2	14	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
99	c1tuuA_	Alignment	not modelled	30.1	18	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
100	c1w25B_	Alignment	not modelled	29.7	11	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
101	d1g99a2	Alignment	not modelled	29.1	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
102	c3cfyA_	Alignment	not modelled	29.1	6	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
103	d1u0sy_	Alignment	not modelled	29.1	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
104	c2jk1A_	Alignment	not modelled	28.6	11	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1;

						PDBTitle: crystal structure of the wild-type hupr receiver domain PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
105	c2iirJ_	Alignment	not modelled	28.4	18	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
106	c1x3nA_	Alignment	not modelled	27.6	17	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
107	c3t8yA_	Alignment	not modelled	27.4	14	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
108	c3lufB_	Alignment	not modelled	26.6	15	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
109	c3eq2A_	Alignment	not modelled	25.9	17	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
110	c3c3wB_	Alignment	not modelled	25.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
111	c3dojA_	Alignment	not modelled	25.0	20	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
112	c2gwrA_	Alignment	not modelled	24.8	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
113	d1dbwa_	Alignment	not modelled	24.3	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
114	d1p6qa_	Alignment	not modelled	23.6	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
115	d2bona1	Alignment	not modelled	23.2	23	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
116	d1v4aa2	Alignment	not modelled	23.0	16	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GlnE-like domain
117	c3i4fD_	Alignment	not modelled	22.9	14	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
118	d1jbea_	Alignment	not modelled	21.9	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
119	c2obnA_	Alignment	not modelled	21.8	13	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
120	d1xpja_	Alignment	not modelled	21.4	14	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232