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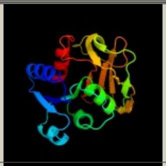
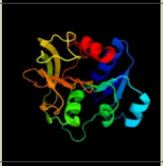
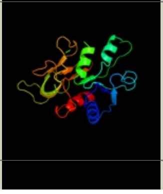
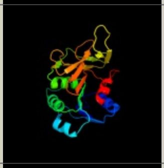
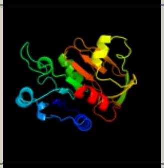
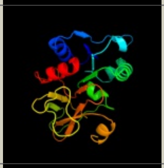
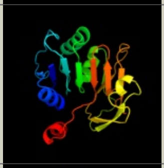
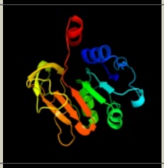
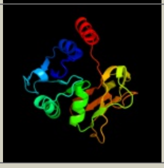
Description	P00903
Date	Thu Jan 5 10:57:07 GMT 2012
Unique Job ID	cec0dd2f8179cb46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qdlb_	Alignment		100.0	49	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
2	c2ywcC_	Alignment		100.0	32	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
3	d1i7qb_	Alignment		100.0	45	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
4	c1gpmD_	Alignment		100.0	26	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
5	d1wl8a1	Alignment		100.0	33	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
6	c2vxoB_	Alignment		100.0	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
7	d1gpma2	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
8	d1i1qb_	Alignment		100.0	46	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
9	c3r74B_	Alignment		100.0	24	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
10	d2a9va1	Alignment		100.0	30	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
11	c3tqiB_	Alignment		100.0	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii

12	c1keeH_	Alignment		100.0	23	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
13	d1a9xb2	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
14	c2vpiA_	Alignment		100.0	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
15	c3uowB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
16	c1jvnB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hisHF; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
17	c3l83A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
18	c3l7nA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
19	d1jvna2	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
20	d1o1ya_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
21	d1ka9h_	Alignment	not modelled	100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
22	d1vcoa1	Alignment	not modelled	100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
23	d1s1ma1	Alignment	not modelled	100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
24	d1k9vf_	Alignment	not modelled	100.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
25	c3nvaB_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
26	c2v4uA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
27	c2w7tA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
28	c2ad5B_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
29	c3fijD_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein;

						PDBTitle: crystal structure of a uncharacterized protein lin1909
30	c3d54D_	Alignment	not modelled	100.0	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
31	c1vcnA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
32	c2issF_	Alignment	not modelled	100.0	13	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
33	d2nv0a1	Alignment	not modelled	100.0	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
34	c1l9xA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
35	d1l9xa_	Alignment	not modelled	100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
36	d1q7ra_	Alignment	not modelled	100.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
37	c2ywjA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
38	c2ywdA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
39	d1t3ta2	Alignment	not modelled	99.9	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	d2abwa1	Alignment	not modelled	99.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
41	d2ghra1	Alignment	not modelled	99.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
42	c2h2wA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
43	c1t3tA_	Alignment	not modelled	99.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
44	c3l3bA_	Alignment	not modelled	98.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
45	c3uk7B_	Alignment	not modelled	98.2	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
46	c1sy7B_	Alignment	not modelled	98.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
47	d1vhqa_	Alignment	not modelled	98.1	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
48	d1sy7a1	Alignment	not modelled	97.8	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
49	c3n7tA_	Alignment	not modelled	97.8	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
50	c3kklA_	Alignment	not modelled	97.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
51	c3cneD_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
52	d1qvwa_	Alignment	not modelled	97.7	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
53	c3l4eA_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
54	d1p80a1	Alignment	not modelled	97.6	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
55	d1oi4a1	Alignment	not modelled	97.5	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI

56	d1g2ia_	Alignment	not modelled	97.4	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
57	c3fseB_	Alignment	not modelled	97.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
58	d1fyea_	Alignment	not modelled	97.3	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
59	d1p5fa_	Alignment	not modelled	97.2	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
60	d1u9ca_	Alignment	not modelled	97.1	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
61	d1n57a_	Alignment	not modelled	97.1	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
62	c3ot1B_	Alignment	not modelled	97.0	13	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
63	c3f5dA_	Alignment	not modelled	96.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
64	d2fexa1	Alignment	not modelled	96.7	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
65	c2vrnA_	Alignment	not modelled	96.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease i; **PDBTitle:** the structure of the stress response protein dr1199 from2 deinococcus radiodurans: a member of the dj-1 superfamily
66	c3nooB_	Alignment	not modelled	96.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
67	d2ab0a1	Alignment	not modelled	96.0	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
68	d1t0ba_	Alignment	not modelled	95.8	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
69	c1p81A_	Alignment	not modelled	95.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
70	c3efeC_	Alignment	not modelled	95.5	11	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
71	c3ewnA_	Alignment	not modelled	95.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
72	c3rhtB_	Alignment	not modelled	94.6	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
73	c3mgkA_	Alignment	not modelled	94.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**intracellular protease/amidase related enzyme **PDBTitle:** crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
74	c3bhnA_	Alignment	not modelled	94.4	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thij/pfpi domain protein; **PDBTitle:** crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
75	d1xhfa1	Alignment	not modelled	94.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c2zwmA_	Alignment	not modelled	93.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
77	c3nhzA_	Alignment	not modelled	93.6	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
78	c1ys7B_	Alignment	not modelled	93.2	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
79	d1w25a1	Alignment	not modelled	93.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c3t6kB_	Alignment	not modelled	92.9	21	**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
81	c2i48A	Alignment	not modelled	92.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase;

81	c2j48A_	Alignment	not modelled	92.8	19	**PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
82	d1ny5a1	Alignment	not modelled	92.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
83	d1mvoa_	Alignment	not modelled	92.4	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	d1peya_	Alignment	not modelled	92.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	c2ayxA_	Alignment	not modelled	92.0	16	**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
86	c3graA_	Alignment	not modelled	92.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, arac family; **PDBTitle:** crystal structure of arac family transcriptional regulator from2 pseudomonas putida
87	c3en0A_	Alignment	not modelled	91.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
88	c3gt7A_	Alignment	not modelled	91.9	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
89	c3c3mA_	Alignment	not modelled	91.8	13	**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
90	d1krwa_	Alignment	not modelled	91.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	d1kgsa2	Alignment	not modelled	91.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	d2gk3a1	Alignment	not modelled	91.5	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
93	d1ys7a2	Alignment	not modelled	91.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	c2an1D_	Alignment	not modelled	91.4	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
95	d2a9pa1	Alignment	not modelled	91.4	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	c3lteH_	Alignment	not modelled	91.3	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
97	c3cg4A_	Alignment	not modelled	91.0	5	**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
98	c2gwrA_	Alignment	not modelled	90.9	17	**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
99	d1zgza1	Alignment	not modelled	90.9	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
100	c3cfyA_	Alignment	not modelled	90.7	14	**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
101	c2qzjC_	Alignment	not modelled	90.7	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
102	d1dbwa_	Alignment	not modelled	90.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
103	c3i42A_	Alignment	not modelled	90.5	8	**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
104	d2pl1a1	Alignment	not modelled	90.3	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c3ej6D_	Alignment	not modelled	90.2	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
106	d1zesa1	Alignment	not modelled	90.1	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
107	c2oqrA	Alignment	not modelled	90.1	11	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3;

107	c2oqrA_	Alignment	not modelled	90.1	11	**PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
108	d1qkka_	Alignment	not modelled	89.7	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c3hv2B_	Alignment	not modelled	89.6	13	**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
110	c2zayA_	Alignment	not modelled	89.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
111	c2hqoA_	Alignment	not modelled	89.6	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
112	c3h5iA_	Alignment	not modelled	89.5	9	**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
113	d1xi8a3	Alignment	not modelled	89.5	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
114	c3sozC_	Alignment	not modelled	89.5	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**cytoplasmic protein stm1381; **PDBTitle:** cytoplasmic protein stm1381 from salmonella typhimurium lt2
115	c1z0zC_	Alignment	not modelled	89.3	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
116	c3hdvB_	Alignment	not modelled	89.3	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
117	d1z0sa1	Alignment	not modelled	89.1	19	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
118	d1mb3a_	Alignment	not modelled	89.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
119	d1yioa2	Alignment	not modelled	89.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
120	c3a0rB_	Alignment	not modelled	88.9	12	**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)