





















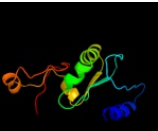










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fyea_	 Alignment		100.0	88	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
2	c3en0A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
3	c3l4eA_	 Alignment		100.0	26	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
4	c1jvnB_	 Alignment		99.1	19	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
5	d1q7ra_	 Alignment		98.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
6	d1ka9h_	 Alignment		98.8	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
7	c2issF_	 Alignment		98.7	17	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
8	d1t3ta2	 Alignment		98.6	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
9	d2nv0a1	 Alignment		98.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	d1jvna2	 Alignment		98.5	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
11	c2ywdA_	 Alignment		98.5	22	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase

12	d1k9vf_	Alignment		98.4	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c2ywjA_	Alignment		98.2	23	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdx; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
14	d2abwa1	Alignment		98.0	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	c3d54D_	Alignment		97.8	16	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: stucture of purlqs from thermotoga maritima
16	d1i1qb_	Alignment		97.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
17	d1qdlb_	Alignment		97.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	d1i7qb_	Alignment		97.7	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
19	d1wl8a1	Alignment		97.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
20	c1vcnA_	Alignment		97.4	18	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
21	d1vcoa1	Alignment	not modelled	97.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
22	c3fijD_	Alignment	not modelled	97.4	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
23	d1s1ma1	Alignment	not modelled	97.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
24	c3r74B_	Alignment	not modelled	97.3	18	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
25	d1gpma2	Alignment	not modelled	97.1	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	c3l3ba_	Alignment	not modelled	97.1	14	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
27	c2vpiA_	Alignment	not modelled	97.1	14	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
28	c3nvaB_	Alignment	not modelled	97.0	18	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus

29	c2ad5B_	Alignment	not modelled	97.0	16	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.
30	d1o1ya_	Alignment	not modelled	97.0	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
31	c1keeH_	Alignment	not modelled	96.9	15	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
32	d1p80a1	Alignment	not modelled	96.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
33	d1oi4a1	Alignment	not modelled	96.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
34	c3uk7B_	Alignment	not modelled	96.8	10	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
35	d1qvwa_	Alignment	not modelled	96.8	8	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
36	c3l7nA_	Alignment	not modelled	96.8	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
37	c2w7tA_	Alignment	not modelled	96.7	16	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
38	d1a9xb2	Alignment	not modelled	96.6	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c3kk1A_	Alignment	not modelled	96.6	13	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
40	d2a9va1	Alignment	not modelled	96.6	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	d1p5fa_	Alignment	not modelled	96.6	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
42	c3l83A_	Alignment	not modelled	96.4	20	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
43	c1sy7B_	Alignment	not modelled	96.4	11	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.
44	d1sy7a1	Alignment	not modelled	96.3	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
45	d1q2ia_	Alignment	not modelled	96.2	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
46	c3ot1B_	Alignment	not modelled	96.1	17	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
47	c2v4uA_	Alignment	not modelled	96.1	15	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
48	c3fseB_	Alignment	not modelled	96.1	16	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
49	c3n7tA_	Alignment	not modelled	96.0	18	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
50	c3cneD_	Alignment	not modelled	95.8	19	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
51	c1gpmD_	Alignment	not modelled	95.8	20	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
52	d1u9ca_	Alignment	not modelled	95.7	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
53	c2ywcC_	Alignment	not modelled	95.6	17	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
54	c1l9xA_	Alignment	not modelled	95.5	14	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase;

					PDBTitle: structure of gamma-glutamyl hydrolase
55	d1l9xa_	Alignment	not modelled	95.5	14 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
56	d1vhqa_	Alignment	not modelled	95.0	19 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
57	c3uowB_	Alignment	not modelled	94.9	13 PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
58	c2vrnA_	Alignment	not modelled	94.7	14 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
59	d2fexa1	Alignment	not modelled	94.2	18 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
60	c3efeC_	Alignment	not modelled	93.9	18 PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
61	c3ewnA_	Alignment	not modelled	93.8	20 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
62	d1n57a_	Alignment	not modelled	93.1	13 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
63	c3mgkA_	Alignment	not modelled	92.2	21 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
64	d2ab0a1	Alignment	not modelled	92.0	19 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
65	c3tqiB_	Alignment	not modelled	91.8	18 PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
66	c2vxob_	Alignment	not modelled	91.2	15 PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
67	c3nooB_	Alignment	not modelled	90.7	16 PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
68	c3f5dA_	Alignment	not modelled	90.3	11 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from2 bacillus subtilis
69	c3bhnA_	Alignment	not modelled	89.9	13 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
70	d1u0ta_	Alignment	not modelled	89.8	23 Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
71	c3s40C_	Alignment	not modelled	88.4	22 PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
72	c2qv7A_	Alignment	not modelled	88.3	21 PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
73	c2an1D_	Alignment	not modelled	87.4	17 PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
74	c3gjzB_	Alignment	not modelled	86.4	22 PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
75	c3rhtB_	Alignment	not modelled	85.5	14 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
76	c3graA_	Alignment	not modelled	84.8	19 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
77	d2nqra3	Alignment	not modelled	82.6	29 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
78	d2gk3a1	Alignment	not modelled	82.5	20 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
79	c3kbqA_	Alignment	not modelled	81.9	28 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
80	c3er6D_	Alignment	not modelled	81.0	11 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein;

						PDBTitle: crystal structure of a putative transcriptional regulator2 protein from vibrio parahaemolyticus
81	d2qv7a1	Alignment	not modelled	78.5	21	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
82	c3a0rB_	Alignment	not modelled	78.5	11	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)
83	c3u80A_	Alignment	not modelled	77.8	11	PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquinate dehydratase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
84	d1uz5a3	Alignment	not modelled	77.4	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
85	d1xi8a3	Alignment	not modelled	76.3	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
86	d1a9xa4	Alignment	not modelled	75.8	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
87	d1ycga1	Alignment	not modelled	74.3	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
88	d1ydga_	Alignment	not modelled	74.3	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
89	d2fts a3	Alignment	not modelled	74.1	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
90	c3nhzA_	Alignment	not modelled	73.6	16	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
91	c2amjD_	Alignment	not modelled	70.1	23	PDB header: oxidoreductase Chain: D: PDB Molecule: modulator of drug activity b; PDBTitle: crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
92	c3hlyA_	Alignment	not modelled	70.0	20	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
93	d2p1ra1	Alignment	not modelled	69.2	21	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
94	d2jgra1	Alignment	not modelled	67.6	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
95	d1peya_	Alignment	not modelled	67.5	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3ag5A_	Alignment	not modelled	67.1	17	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
97	d2a84a1	Alignment	not modelled	67.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
98	d2auna2	Alignment	not modelled	65.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
99	c2jrlA_	Alignment	not modelled	65.5	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
100	c2hqoA_	Alignment	not modelled	65.1	14	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
101	c2g4rB_	Alignment	not modelled	65.0	26	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
102	c2fu3A_	Alignment	not modelled	64.9	21	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
103	c3ke8A_	Alignment	not modelled	64.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate PDBTitle: crystal structure of isph:hmbpp-complex
104	d2qwx a1	Alignment	not modelled	63.9	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
105	c3dzdA_	Alignment	not modelled	62.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
106	c2bonB_	Alignment	not modelled	62.5	21	PDB header: transferase Chain: B: PDB Molecule: lipid kinase;

						PDBTitle: structure of an escherichia coli lipid kinase (yegs)
107	c2pjkA_	Alignment	not modelled	59.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
108	c2ejcA_	Alignment	not modelled	59.5	18	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
109	c3rpeA_	Alignment	not modelled	59.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: modulator of drug activity b; PDBTitle: 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
110	c3innB_	Alignment	not modelled	59.0	13	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
111	c3gt7A_	Alignment	not modelled	58.4	11	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
112	dlihoa_	Alignment	not modelled	58.4	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
113	c2zwmA_	Alignment	not modelled	57.9	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
114	c2is8A_	Alignment	not modelled	57.7	21	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
115	dlccwa_	Alignment	not modelled	57.2	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
116	c1t3tA_	Alignment	not modelled	57.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
117	dlw25a1	Alignment	not modelled	56.8	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	d2a5la1	Alignment	not modelled	56.8	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
119	dlmvoa_	Alignment	not modelled	56.7	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
120	d2g2ca1	Alignment	not modelled	56.3	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like