



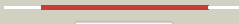









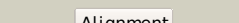

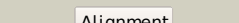







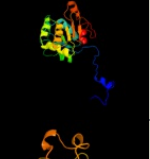
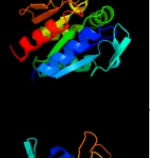
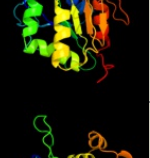
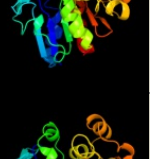
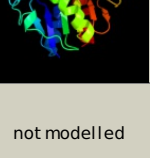


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1n57a_</a>	 Alignment		100.0	97	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
2	<a href="#">d1qvwa_</a>	 Alignment		100.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
3	<a href="#">c3n7ta_</a>	 Alignment		100.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage binding protein; <b>PDBTitle:</b> crystal structure of a macrophage binding protein from coccidioides2 immitis
4	<a href="#">c3kklA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chaperone protein hsp33; <b>PDBTitle:</b> crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
5	<a href="#">d1u9ca_</a>	 Alignment		100.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
6	<a href="#">d1vhqa_</a>	 Alignment		100.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
7	<a href="#">c3uk7B_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> class i glutamine amidotransferase-like domain-containing <b>PDBTitle:</b> crystal structure of arabidopsis thaliana dj-1d
8	<a href="#">c3fseB_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> two-domain protein containing dj-1/thij/pfpi-like and <b>PDBTitle:</b> 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
9	<a href="#">c3l3ba_</a>	 Alignment		100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> es1 family protein; <b>PDBTitle:</b> crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
10	<a href="#">d1oi4a1</a>	 Alignment		100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
11	<a href="#">c3cneD_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative protease i; <b>PDBTitle:</b> crystal structure of the putative protease i from bacteroides2 thetaiotaomicron

12	<a href="#">d1g2ia_</a>	Alignment		100.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
13	<a href="#">d1p5fa_</a>	Alignment		100.0	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
14	<a href="#">c2vrnA_</a>	Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease i; <b>PDBTitle:</b> the structure of the stress response protein dr1199 from2 deinococcus radiodurans: a member of the dj-1 superfamily
15	<a href="#">c3ot1B_</a>	Alignment		99.9	18	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate <b>PDBTitle:</b> crystal structure of vc2308 protein
16	<a href="#">c1sy7B_</a>	Alignment		99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase 1; <b>PDBTitle:</b> crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
17	<a href="#">d2ab0a1</a>	Alignment		99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
18	<a href="#">d1sy7a1</a>	Alignment		99.9	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
19	<a href="#">d2fexa1</a>	Alignment		99.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
20	<a href="#">c3efeC_</a>	Alignment		99.9	16	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
21	<a href="#">c3mgkA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular protease/amidase related enzyme <b>PDBTitle:</b> crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
22	<a href="#">c3f5dA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ydea; <b>PDBTitle:</b> crystal structure of a protein of unknown function from2 bacillus subtilis
23	<a href="#">c3ewnA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
24	<a href="#">c3nooB_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
25	<a href="#">c3bhnA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi domain protein; <b>PDBTitle:</b> crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
26	<a href="#">c3er6D_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator protein; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 protein from vibrio parahaemolyticus
27	<a href="#">c3graA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of arac family transcriptional regulator from2 pseudomonas putida
28	<a href="#">d1p80a1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like

					<b>Family:</b> Catalase, C-terminal domain
29	<a href="#">c1p81A</a>	Alignment	not modelled	99.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catalase hpii; <b>PDBTitle:</b> crystal structure of the d181e variant of catalase hpii2 from e. coli
30	<a href="#">d1t3ta2</a>	Alignment	not modelled	98.0	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
31	<a href="#">d1q7ra</a>	Alignment	not modelled	97.7	20 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
32	<a href="#">c3ej6D</a>	Alignment	not modelled	97.6	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catalase-3; <b>PDBTitle:</b> neurospora crassa catalase-3 crystal structure
33	<a href="#">c2issF</a>	Alignment	not modelled	97.2	21 <b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
34	<a href="#">d1o1ya</a>	Alignment	not modelled	97.2	13 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
35	<a href="#">c3l7nA</a>	Alignment	not modelled	97.1	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1228c
36	<a href="#">c3d54D</a>	Alignment	not modelled	96.9	20 <b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylformylglycinamidine synthase 1; <b>PDBTitle:</b> stucture of purlqs from thermotoga maritima
37	<a href="#">d1gpm2</a>	Alignment	not modelled	96.9	23 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
38	<a href="#">d1jvna2</a>	Alignment	not modelled	96.9	14 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
39	<a href="#">c3l4eA</a>	Alignment	not modelled	96.8	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
40	<a href="#">d1wl8a1</a>	Alignment	not modelled	96.7	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
41	<a href="#">c2ywjA</a>	Alignment	not modelled	96.6	24 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
42	<a href="#">d2nv0a1</a>	Alignment	not modelled	96.6	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
43	<a href="#">c2ywdA</a>	Alignment	not modelled	96.5	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of glutamine amidotransferase
44	<a href="#">c3l83A</a>	Alignment	not modelled	96.4	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amido transferase; <b>PDBTitle:</b> crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
45	<a href="#">d2a9va1</a>	Alignment	not modelled	96.4	8 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
46	<a href="#">d1a9xb2</a>	Alignment	not modelled	96.2	20 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
47	<a href="#">d1ka9h</a>	Alignment	not modelled	96.2	12 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
48	<a href="#">d1qdlb</a>	Alignment	not modelled	96.2	10 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
49	<a href="#">c1keeH</a>	Alignment	not modelled	96.0	20 <b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> carbamoyl-phosphate synthetase small chain; <b>PDBTitle:</b> inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
50	<a href="#">d2abwa1</a>	Alignment	not modelled	95.9	13 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
51	<a href="#">d1k9vf</a>	Alignment	not modelled	95.8	19 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
52	<a href="#">d1slma1</a>	Alignment	not modelled	95.6	25 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
53	<a href="#">d1vcoa1</a>	Alignment	not modelled	95.4	29 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
54	<a href="#">d1i1qb</a>	Alignment	not modelled	95.3	16 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
					<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase;

55	<a href="#">c2ad5B_</a>	Alignment	not modelled	95.1	27	<b>PDBTitle:</b> mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
56	<a href="#">c1jvnB_</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
57	<a href="#">c3r74B_</a>	Alignment	not modelled	95.0	19	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component I; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
58	<a href="#">d2ghra1</a>	Alignment	not modelled	94.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> HTS-like
59	<a href="#">c2w7tA_</a>	Alignment	not modelled	94.8	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytidine triphosphate synthase; <b>PDBTitle:</b> trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
60	<a href="#">c3nvaB_</a>	Alignment	not modelled	94.7	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> dimeric form of ctp synthase from sulfolobus solfataricus
61	<a href="#">c2iufA_</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
62	<a href="#">d1fyea_</a>	Alignment	not modelled	94.4	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Aspartyl dipeptidase PepE
63	<a href="#">d1e5da1</a>	Alignment	not modelled	94.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
64	<a href="#">d1ycga1</a>	Alignment	not modelled	94.0	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
65	<a href="#">c1vcnA_</a>	Alignment	not modelled	93.7	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp synthetase; <b>PDBTitle:</b> crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
66	<a href="#">c2h2wA_</a>	Alignment	not modelled	93.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> 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
67	<a href="#">d1i7qb_</a>	Alignment	not modelled	93.1	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
68	<a href="#">c3fijD_</a>	Alignment	not modelled	93.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> lin1909 protein; <b>PDBTitle:</b> crystal structure of a uncharacterized protein lin1909
69	<a href="#">d1t5ba_</a>	Alignment	not modelled	92.3	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
70	<a href="#">c3uowB_</a>	Alignment	not modelled	92.3	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
71	<a href="#">c2v4uA_</a>	Alignment	not modelled	91.5	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp synthase 2; <b>PDBTitle:</b> human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
72	<a href="#">c2ywcC_</a>	Alignment	not modelled	91.1	12	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
73	<a href="#">c3klbA_</a>	Alignment	not modelled	90.4	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavoprotein; <b>PDBTitle:</b> crystal structure of putative flavoprotein in complex with frn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
74	<a href="#">d2a5la1</a>	Alignment	not modelled	90.2	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
75	<a href="#">d1kwga3</a>	Alignment	not modelled	90.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> A4 beta-galactosidase middle domain
76	<a href="#">c2zkiH_</a>	Alignment	not modelled	89.3	15	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
77	<a href="#">c3fniA_</a>	Alignment	not modelled	88.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
78	<a href="#">c3en0A_</a>	Alignment	not modelled	88.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
79	<a href="#">c1gpmD_</a>	Alignment	not modelled	87.9	20	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate

80	<a href="#">c2q9uB_</a>	Alignment	not modelled	87.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> a-type flavoprotein; <b>PDBTitle:</b> crystal structure of the flavodiiron protein from giardia2 intestinalis
81	<a href="#">d1ydgA_</a>	Alignment	not modelled	86.5	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
82	<a href="#">d1f0ka_</a>	Alignment	not modelled	85.4	28	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
83	<a href="#">c1t3tA_</a>	Alignment	not modelled	85.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase; <b>PDBTitle:</b> structure of formylglycinamide synthetase
84	<a href="#">c2vpiA_</a>	Alignment	not modelled	84.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase; <b>PDBTitle:</b> human gmp synthetase - glutaminase domain
85	<a href="#">d1a9xa3</a>	Alignment	not modelled	83.6	10	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
86	<a href="#">c2vx0B_</a>	Alignment	not modelled	83.3	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
87	<a href="#">d1dxqa_</a>	Alignment	not modelled	82.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
88	<a href="#">d1l9xa_</a>	Alignment	not modelled	82.7	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
89	<a href="#">c1l9xA_</a>	Alignment	not modelled	82.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
90	<a href="#">c3ia7A_</a>	Alignment	not modelled	82.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
91	<a href="#">c1kwgA_</a>	Alignment	not modelled	81.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of thermus thermophilus a4 beta-galactosidase
92	<a href="#">c3tqiB_</a>	Alignment	not modelled	80.9	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
93	<a href="#">d2fz5a1</a>	Alignment	not modelled	79.9	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
94	<a href="#">c3edoA_</a>	Alignment	not modelled	78.2	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative trp repressor binding protein; <b>PDBTitle:</b> crystal structure of flavoprotein in complex with fnm2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
95	<a href="#">c2q62A_</a>	Alignment	not modelled	77.7	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
96	<a href="#">d1t0ia_</a>	Alignment	not modelled	77.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
97	<a href="#">d1mkza_</a>	Alignment	not modelled	73.2	14	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
98	<a href="#">c2p6pB_</a>	Alignment	not modelled	72.4	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
99	<a href="#">d1pn3a_</a>	Alignment	not modelled	68.8	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
100	<a href="#">c2iyaB_</a>	Alignment	not modelled	67.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
101	<a href="#">c3d0qB_</a>	Alignment	not modelled	67.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
102	<a href="#">d1qrda_</a>	Alignment	not modelled	66.7	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
103	<a href="#">d1rrva_</a>	Alignment	not modelled	65.5	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
104	<a href="#">d1vmea1</a>	Alignment	not modelled	65.4	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
105	<a href="#">d2gk3a1</a>	Alignment	not modelled	65.0	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> STM3548-like
106	<a href="#">c3rfqC_</a>	Alignment	not modelled	63.7	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2;

						<b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
107	<a href="#">dliira_</a>	Alignment	not modelled	63.5	9	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
108	<a href="#">c3hlyA_</a>	Alignment	not modelled	62.9	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin-like domain; <b>PDBTitle:</b> crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
109	<a href="#">c2iyfA_</a>	Alignment	not modelled	60.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
110	<a href="#">c3dahB_</a>	Alignment	not modelled	58.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
111	<a href="#">dly5ea1</a>	Alignment	not modelled	58.0	22	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
112	<a href="#">c3f6sl_</a>	Alignment	not modelled	57.7	25	<b>PDB header:</b> electron transport <b>Chain:</b> I: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
113	<a href="#">d1rzua_</a>	Alignment	not modelled	56.0	19	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
114	<a href="#">c3iaaB_</a>	Alignment	not modelled	55.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
115	<a href="#">d1d4aa_</a>	Alignment	not modelled	54.5	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
116	<a href="#">c2qzsA_</a>	Alignment	not modelled	53.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
117	<a href="#">d2qwxal</a>	Alignment	not modelled	53.0	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
118	<a href="#">c3othB_</a>	Alignment	not modelled	52.6	31	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
119	<a href="#">c1ps9A_</a>	Alignment	not modelled	48.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
120	<a href="#">c3lcmB_</a>	Alignment	not modelled	48.8	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159