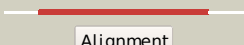

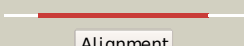

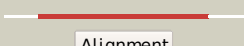

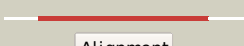











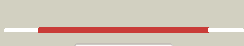





# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A0K3
Date	Tue Jul 17 17:05:07 BST 2012
Unique Job ID	092efac2c43050e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3fseB_</a>	 Alignment		100.0	39	<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
2	<a href="#">c3cneD_</a>	 Alignment		100.0	19	<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
3	<a href="#">c4e08B_</a>	 Alignment		100.0	26	<b>PDB header:</b> motor protein <b>Chain:</b> B; <b>PDB Molecule:</b> dj-1 beta; <b>PDBTitle:</b> crystal structure of drosophila melanogaster dj-1beta
4	<a href="#">c3uk7B_</a>	 Alignment		100.0	30	<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
5	<a href="#">d1g2ia_</a>	 Alignment		100.0	40	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
6	<a href="#">c3ot1B_</a>	 Alignment		100.0	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
7	<a href="#">d1oi4a1</a>	 Alignment		100.0	47	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
8	<a href="#">d1p5fa_</a>	 Alignment		100.0	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
9	<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
10	<a href="#">c3kk1A_</a>	 Alignment		100.0	20	<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
11	<a href="#">c2vrnA_</a>	 Alignment		100.0	38	<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

12	<a href="#">d1qvwa_</a>	Alignment		100.0	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
13	<a href="#">c3ewnA_</a>	Alignment		100.0	20	<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
14	<a href="#">c3efeC_</a>	Alignment		100.0	21	<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
15	<a href="#">c3n7tA_</a>	Alignment		100.0	27	<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
16	<a href="#">d2ab0a1</a>	Alignment		100.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
17	<a href="#">c3f5dA_</a>	Alignment		100.0	21	<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
18	<a href="#">d1n57a_</a>	Alignment		100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
19	<a href="#">c3bhnA_</a>	Alignment		100.0	23	<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
20	<a href="#">c3nooB_</a>	Alignment		100.0	22	<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
21	<a href="#">d2fexa1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
22	<a href="#">c3mgkA_</a>	Alignment	not modelled	100.0	21	<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
23	<a href="#">d1vhqa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
24	<a href="#">d1sy7a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
25	<a href="#">c3graA_</a>	Alignment	not modelled	100.0	17	<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
26	<a href="#">c1sy7B_</a>	Alignment	not modelled	100.0	18	<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.
27	<a href="#">c3er6D_</a>	Alignment	not modelled	100.0	16	<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
28	<a href="#">c3l3bA_</a>	Alignment	not modelled	100.0	23	<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
29	<a href="#">d1p80a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
30	<a href="#">c1p81A_</a>	Alignment	not modelled	99.7	18	<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
31	<a href="#">c3ej6D_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catalase-3; <b>PDBTitle:</b> neurospora crassa catalase-3 crystal structure
32	<a href="#">d1t3ta2</a>	Alignment	not modelled	98.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
33	<a href="#">d1q7ra_</a>	Alignment	not modelled	98.7	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
34	<a href="#">c2iufA_</a>	Alignment	not modelled	98.7	21	<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
35	<a href="#">c3d54D_</a>	Alignment	not modelled	98.6	28	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 1; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
36	<a href="#">c2issF_</a>	Alignment	not modelled	98.6	24	<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
37	<a href="#">d2nv0a1</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
38	<a href="#">d1ka9h_</a>	Alignment	not modelled	98.3	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
39	<a href="#">d1o1ya_</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
40	<a href="#">c3l7nA_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1228c
41	<a href="#">c2ywdA_</a>	Alignment	not modelled	98.1	23	<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
42	<a href="#">c2ywjA_</a>	Alignment	not modelled	98.1	23	<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
43	<a href="#">d1jvna2</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
44	<a href="#">d1gpma2</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
45	<a href="#">c3l83A_</a>	Alignment	not modelled	97.9	15	<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
46	<a href="#">d2abwa1</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
47	<a href="#">d1wl8a1</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)
48	<a href="#">c1t3tA_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase; <b>PDBTitle:</b> structure of formylglycinamide synthetase
49	<a href="#">c1keeH_</a>	Alignment	not modelled	97.6	18	<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="#">c3r74B_</a>	Alignment	not modelled	97.6	28	<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
51	<a href="#">d1a9xb2</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
52	<a href="#">d1k9vf_</a>	Alignment	not modelled	97.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
53	<a href="#">d1qdlb_</a>	Alignment	not modelled	97.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
54	<a href="#">d2a9va1</a>	Alignment	not modelled	97.4	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)

55	<a href="#">c3fijD_</a>	Alignment	not modelled	97.3	19	<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
56	<a href="#">dli1qb_</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
57	<a href="#">c1jvnB_</a>	Alignment	not modelled	97.2	17	<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
58	<a href="#">c3l4eA_</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase Imo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
59	<a href="#">dli7qb_</a>	Alignment	not modelled	96.9	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
60	<a href="#">d1fyea_</a>	Alignment	not modelled	96.6	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Aspartyl dipeptidase PepE
61	<a href="#">c2vpiA_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase; <b>PDBTitle:</b> human gmp synthetase - glutaminase domain
62	<a href="#">d2ghra1</a>	Alignment	not modelled	96.4	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> HTS-like
63	<a href="#">c2h2wA_</a>	Alignment	not modelled	96.3	12	<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
64	<a href="#">c1gpmD_</a>	Alignment	not modelled	96.0	17	<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
65	<a href="#">c3nvaB_</a>	Alignment	not modelled	95.8	21	<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
66	<a href="#">c2ad5B_</a>	Alignment	not modelled	95.8	35	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <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.
67	<a href="#">d1s1ma1</a>	Alignment	not modelled	95.6	34	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
68	<a href="#">c3tqiB_</a>	Alignment	not modelled	95.5	14	<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
69	<a href="#">c2ywcC_</a>	Alignment	not modelled	95.4	22	<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
70	<a href="#">c3uowB_</a>	Alignment	not modelled	95.3	23	<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="#">c2w7tA_</a>	Alignment	not modelled	95.2	27	<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
72	<a href="#">c3en0A_</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
73	<a href="#">d1e5da1</a>	Alignment	not modelled	95.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
74	<a href="#">d1vcoa1</a>	Alignment	not modelled	95.1	33	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
75	<a href="#">c2ax3A_</a>	Alignment	not modelled	95.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0922; <b>PDBTitle:</b> crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
76	<a href="#">c3d3jA_</a>	Alignment	not modelled	95.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
77	<a href="#">d1ycga1</a>	Alignment	not modelled	94.9	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
78	<a href="#">c3d3kD_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
79	<a href="#">d2ax3a2</a>	Alignment	not modelled	94.4	10	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
80	<a href="#">c2v4uA_</a>	Alignment	not modelled	93.3	22	<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

81	<a href="#">c1vcnA</a>	Alignment	not modelled	93.3	30	<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
82	<a href="#">c3klbA</a>	Alignment	not modelled	92.5	9	<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 fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
83	<a href="#">c2vxob</a>	Alignment	not modelled	90.9	19	<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
84	<a href="#">d1iowa1</a>	Alignment	not modelled	89.3	24	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> D-Alanine ligase N-terminal domain
85	<a href="#">c2dg2D</a>	Alignment	not modelled	89.1	10	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> apolipoprotein a-i binding protein; <b>PDBTitle:</b> crystal structure of mouse apolipoprotein a-i binding2 protein
86	<a href="#">c3fniA</a>	Alignment	not modelled	85.3	9	<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 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
87	<a href="#">c3okfA</a>	Alignment	not modelled	85.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
88	<a href="#">d1u0ta</a>	Alignment	not modelled	84.4	20	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> NAD kinase-like
89	<a href="#">d1vmea1</a>	Alignment	not modelled	83.4	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
90	<a href="#">d1d4aa</a>	Alignment	not modelled	81.8	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
91	<a href="#">c2iyaB</a>	Alignment	not modelled	81.4	8	<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
92	<a href="#">d1g5qa</a>	Alignment	not modelled	79.7	15	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
93	<a href="#">d1l9xa</a>	Alignment	not modelled	76.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
94	<a href="#">c1l9xA</a>	Alignment	not modelled	76.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
95	<a href="#">c2dlnA</a>	Alignment	not modelled	74.9	21	<b>PDB header:</b> ligase(peptidoglycan synthesis) <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
96	<a href="#">c3edoA</a>	Alignment	not modelled	73.3	14	<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 fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
97	<a href="#">c3ragA</a>	Alignment	not modelled	71.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
98	<a href="#">c2an1D</a>	Alignment	not modelled	70.7	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
99	<a href="#">d1kwga3</a>	Alignment	not modelled	69.4	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> A4 beta-galactosidase middle domain
100	<a href="#">d1jzta</a>	Alignment	not modelled	67.6	15	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
101	<a href="#">d2a5la1</a>	Alignment	not modelled	66.9	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
102	<a href="#">c4e5vA</a>	Alignment	not modelled	63.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thua-like protein; <b>PDBTitle:</b> crystal structure of a putative thua-like protein (parmer_02418) from2 parabacteroides merdae atcc 43184 at 1.75 a resolution
103	<a href="#">c2qv7A</a>	Alignment	not modelled	58.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol kinase dgkb; <b>PDBTitle:</b> crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
104	<a href="#">c3pfnB</a>	Alignment	not modelled	58.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nad kinase; <b>PDBTitle:</b> crystal structure of human nad kinase
105	<a href="#">d1ccwa</a>	Alignment	not modelled	57.8	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain

106	<a href="#">d2qv7a1</a>	Alignment	not modelled	57.4	23	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
107	<a href="#">d1l5xa_</a>	Alignment	not modelled	56.6	10	<b>Fold:</b> SurE-like <b>Superfamily:</b> SurE-like <b>Family:</b> SurE-like
108	<a href="#">d2jgra1</a>	Alignment	not modelled	56.6	11	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
109	<a href="#">c3qbeA</a>	Alignment	not modelled	56.1	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate synthase; <b>PDBTitle:</b> crystal structure of the 3-dehydroquinate synthase (arob) from2 mycobacterium tuberculosis
110	<a href="#">c1e5dA</a>	Alignment	not modelled	52.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin);oxygen oxidoreductase; <b>PDBTitle:</b> rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
111	<a href="#">d1fmfa_</a>	Alignment	not modelled	51.1	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
112	<a href="#">c2r47C_</a>	Alignment	not modelled	51.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein mth_862; <b>PDBTitle:</b> crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
113	<a href="#">d1mkza_</a>	Alignment	not modelled	50.7	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
114	<a href="#">c3mcfuF_</a>	Alignment	not modelled	50.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
115	<a href="#">c1mbbA</a>	Alignment	not modelled	49.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine diphospho-n-acetylenolpyruvylglucosamine <b>PDBTitle:</b> oxidoreductase
116	<a href="#">c2zuuA</a>	Alignment	not modelled	47.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lacto-n-biose phosphorylase; <b>PDBTitle:</b> crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
117	<a href="#">d1p3y1_</a>	Alignment	not modelled	46.9	17	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
118	<a href="#">c3ff4A</a>	Alignment	not modelled	44.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
119	<a href="#">d2p1ra1</a>	Alignment	not modelled	43.8	12	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
120	<a href="#">d2bona1</a>	Alignment	not modelled	43.7	10	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like