



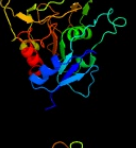


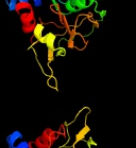



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2604c (- )_2931703_2932299
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	b52ef9566b3df2f2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1q7ra_</a>	Alignment		100.0	45	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
2	<a href="#">d2nv0a1</a>	Alignment		100.0	49	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
3	<a href="#">c2ywdA_</a>	Alignment		100.0	48	<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
4	<a href="#">c2issF_</a>	Alignment		100.0	44	<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
5	<a href="#">d2abwa1</a>	Alignment		100.0	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
6	<a href="#">c2ywjA_</a>	Alignment		100.0	41	<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
7	<a href="#">c1jvnB_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein highf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
8	<a href="#">d1k9vf_</a>	Alignment		100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
9	<a href="#">d1ka9h_</a>	Alignment		100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
10	<a href="#">d1wl8a1</a>	Alignment		100.0	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
11	<a href="#">c3fijD_</a>	Alignment		100.0	21	<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

12	<a href="#">c3d54D</a>	Alignment		100.0	20	<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
13	<a href="#">c4gudA</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit hish; <b>PDBTitle:</b> crystal structure of amidotransferase hish from vibrio cholerae
14	<a href="#">d1jvna2</a>	Alignment		100.0	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
15	<a href="#">d2a9va1</a>	Alignment		100.0	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
16	<a href="#">d1gpma2</a>	Alignment		100.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
17	<a href="#">d1i7qb</a>	Alignment		100.0	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
18	<a href="#">c2ywcC</a>	Alignment		100.0	26	<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
19	<a href="#">c1gpmD</a>	Alignment		100.0	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
20	<a href="#">c5tw7E</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
21	<a href="#">d1qdlb</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
22	<a href="#">c2vxob</a>	Alignment	not modelled	100.0	21	<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
23	<a href="#">c1l9xA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
24	<a href="#">d1l9xa</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
25	<a href="#">c4l8fA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx <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
26	<a href="#">c1keeH</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase; <b>PDBTitle:</b> human gmp synthetase - glutaminase domain
27	<a href="#">c2vpiA</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
28	<a href="#">d1t3ta2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Flavodoxin-like

29	<a href="#">d1i1qb_</a>	Alignment	not modelled	100.0	22	<b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
30	<a href="#">c6qurA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> mapping the allosteric communication network of aminodeoxychorismate2 synthase
31	<a href="#">d1s1ma1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
32	<a href="#">d1o1ya_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
33	<a href="#">d1a9xb2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
34	<a href="#">c3r74B_</a>	Alignment	not modelled	99.9	18	<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
35	<a href="#">c3l7nA_</a>	Alignment	not modelled	99.9	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="#">c3uowB_</a>	Alignment	not modelled	99.9	13	<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
37	<a href="#">c3tqiB_</a>	Alignment	not modelled	99.9	16	<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
38	<a href="#">c2lxnA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit a; <b>PDBTitle:</b> solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
39	<a href="#">c1vcnA_</a>	Alignment	not modelled	99.9	21	<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
40	<a href="#">c3nvaB_</a>	Alignment	not modelled	99.9	17	<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
41	<a href="#">c2ad5B_</a>	Alignment	not modelled	99.9	20	<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.
42	<a href="#">c3l83A_</a>	Alignment	not modelled	99.9	18	<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
43	<a href="#">d1vcoa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
44	<a href="#">c4zdiE_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
45	<a href="#">c5u03C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament
46	<a href="#">c2v4uA_</a>	Alignment	not modelled	99.9	16	<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
47	<a href="#">c6fqbe_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> cobyrinic acid synthase; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
48	<a href="#">c2w7tA_</a>	Alignment	not modelled	99.9	19	<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 bound acivicin
49	<a href="#">c5n9mA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyrinic acid synthase; <b>PDBTitle:</b> crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
50	<a href="#">c5dotA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
51	<a href="#">c5douC_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
52	<a href="#">d2ghra1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> HTS-like
53	<a href="#">c2h2wA_</a>	Alignment	not modelled	99.8	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

54	<a href="#">c6mtgB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
55	<a href="#">c1t3tA_</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase; <b>PDBTitle:</b> structure of formylglycinamide synthetase
56	<a href="#">c3l4eA_</a>	Alignment	not modelled	98.7	13	<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
57	<a href="#">c6a4tB_</a>	Alignment	not modelled	98.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase e; <b>PDBTitle:</b> crystal structure of peptidase e from deinococcus radiodurans r1
58	<a href="#">d1fyea_</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Aspartyl dipeptidase PepE
59	<a href="#">c1sy7B_</a>	Alignment	not modelled	98.6	22	<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.
60	<a href="#">c3cneD_</a>	Alignment	not modelled	98.4	25	<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
61	<a href="#">d1sy7a1</a>	Alignment	not modelled	98.4	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
62	<a href="#">c3uk7B_</a>	Alignment	not modelled	98.4	25	<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
63	<a href="#">d1p80a1</a>	Alignment	not modelled	98.4	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
64	<a href="#">c3fseB_</a>	Alignment	not modelled	98.4	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
65	<a href="#">c4e08B_</a>	Alignment	not modelled	98.2	21	<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
66	<a href="#">d1oi4a1</a>	Alignment	not modelled	98.2	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
67	<a href="#">d1g2ia_</a>	Alignment	not modelled	98.1	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
68	<a href="#">d1p5fa_</a>	Alignment	not modelled	98.1	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
69	<a href="#">c4y0nB_</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein sav1875; <b>PDBTitle:</b> sav1875
70	<a href="#">c3l3bA_</a>	Alignment	not modelled	97.9	20	<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
71	<a href="#">c4xllB_</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dj-1 family protein; <b>PDBTitle:</b> toxoplasma gondii dj-1, oxidized
72	<a href="#">c3ot1B_</a>	Alignment	not modelled	97.8	23	<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
73	<a href="#">c4hcjA_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi domain protein; <b>PDBTitle:</b> crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
74	<a href="#">c3kkIA_</a>	Alignment	not modelled	97.8	18	<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
75	<a href="#">d1u9ca_</a>	Alignment	not modelled	97.7	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
76	<a href="#">c4lruA_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase iii (glutathione-independent); <b>PDBTitle:</b> crystal structure of glyoxalase iii (orf 19.251) from candida albicans
77	<a href="#">c3nooB_</a>	Alignment	not modelled	97.7	18	<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
78	<a href="#">d1qvwa_</a>	Alignment	not modelled	97.6	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
79	<a href="#">c3ewnA_</a>	Alignment	not modelled	97.6	15	<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
80	<a href="#">c4k2hG</a>	Alignment	not modelled	97.6	20 <b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> intracellular protease/amidase; <b>PDBTitle:</b> crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium
81	<a href="#">d1vhqa</a>	Alignment	not modelled	97.5	22 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
82	<a href="#">c3mgkA</a>	Alignment	not modelled	97.5	17 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular protease/amidase related enzyme (thij <b>PDBTitle:</b> crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824
83	<a href="#">c3n7tA</a>	Alignment	not modelled	97.5	13 <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
84	<a href="#">d2fexa1</a>	Alignment	not modelled	97.5	27 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
85	<a href="#">d2ab0a1</a>	Alignment	not modelled	97.5	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
86	<a href="#">c3en0A</a>	Alignment	not modelled	97.5	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
87	<a href="#">c2vrnA</a>	Alignment	not modelled	97.4	22 <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 from deinococcus2 radiodurans: a member of the dj-1 superfamily
88	<a href="#">c4p5pA</a>	Alignment	not modelled	97.4	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
89	<a href="#">c3er6D</a>	Alignment	not modelled	97.4	21 <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 regulator protein from2 vibrio parahaemolyticus
90	<a href="#">c4ge0C</a>	Alignment	not modelled	97.4	17 <b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein c22e12.03c; <b>PDBTitle:</b> schizosaccharomyces pombe dj-1 t114p mutant
91	<a href="#">c3bhnA</a>	Alignment	not modelled	97.4	17 <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
92	<a href="#">c3f5dA</a>	Alignment	not modelled	97.4	20 <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 from bacillus2 subtilis
93	<a href="#">c1p81A</a>	Alignment	not modelled	97.3	21 <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
94	<a href="#">c3graA</a>	Alignment	not modelled	97.1	22 <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
95	<a href="#">c4i2nC</a>	Alignment	not modelled	96.7	19 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> intracellular protease/amidase; <b>PDBTitle:</b> crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
96	<a href="#">d1n57a</a>	Alignment	not modelled	96.3	20 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
97	<a href="#">c3efeC</a>	Alignment	not modelled	96.1	22 <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
98	<a href="#">c5xr2D</a>	Alignment	not modelled	95.9	21 <b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein/nucleic acid deglycase hcha; <b>PDBTitle:</b> sav0551
99	<a href="#">d1xi8a3</a>	Alignment	not modelled	95.0	29 <b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
100	<a href="#">c5vymB</a>	Alignment	not modelled	94.5	20 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase bgab; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bifidobacterium2 adollescens
101	<a href="#">d2gk3a1</a>	Alignment	not modelled	94.2	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> STM3548-like
102	<a href="#">c2an1D</a>	Alignment	not modelled	94.0	23 <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 typhimurium lt2
103	<a href="#">c3ej6D</a>	Alignment	not modelled	93.8	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catalase-3; <b>PDBTitle:</b> neurospora crassa catalase-3 crystal structure
104	<a href="#">c4uzsB</a>	Alignment	not modelled	92.6	18 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium bifidum beta-galactosidase
105	<a href="#">d1uz5a3</a>	Alignment	not modelled	92.3	29 <b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like



106	<a href="#">c4uozc</a>	Alignment	not modelled	91.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
107	<a href="#">c5e9aB</a>	Alignment	not modelled	91.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure analysis of the cold-adamped beta-galactosidase from2 rahnella sp. r3
108	<a href="#">c4ojyA</a>	Alignment	not modelled	90.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> 3d structure of the e323a catalytic mutant of gan42b, a gh42 beta-2 galactosidase from g. stearothermophilus
109	<a href="#">d2ftsa3</a>	Alignment	not modelled	90.8	25	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
110	<a href="#">d2jfga1</a>	Alignment	not modelled	90.2	26	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
111	<a href="#">c3ttsD</a>	Alignment	not modelled	90.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bacillus circulans sp.2 alkalophilus
112	<a href="#">c2zuaA</a>	Alignment	not modelled	89.9	20	<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
113	<a href="#">c2nqqA</a>	Alignment	not modelled	89.6	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
114	<a href="#">d1p3da1</a>	Alignment	not modelled	89.3	13	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
115	<a href="#">c2fu3A</a>	Alignment	not modelled	89.0	33	<b>PDB header:</b> biosynthetic protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin; <b>PDBTitle:</b> crystal structure of gephyrin e-domain
116	<a href="#">c3sozC</a>	Alignment	not modelled	88.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> cytoplasmic protein stm1381; <b>PDBTitle:</b> cytoplasmic protein stm1381 from salmonella typhimurium lt2
117	<a href="#">c5dteD</a>	Alignment	not modelled	88.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> monosaccharide-transporting atpase; <b>PDBTitle:</b> crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
118	<a href="#">c4e5vA</a>	Alignment	not modelled	88.0	9	<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
119	<a href="#">d1wu2a3</a>	Alignment	not modelled	87.6	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
120	<a href="#">c4jqsc</a>	Alignment	not modelled	87.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative thua-like protein (bacuni_01602) from2 bacteroides uniformis atcc 8492 at 2.30 a resolution