Phyre^2

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Description	RVBD2859c_(-)_3170730_3171656
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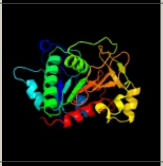
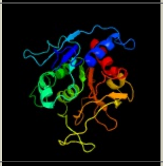
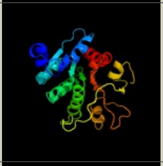
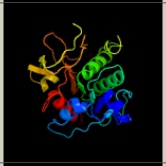
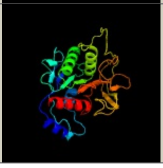
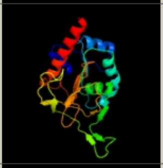
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fijD_	Alignment		100.0	36	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
2	c1l9xA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
3	d1l9xa_	Alignment		100.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
4	c4l8fA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
5	c2v4uA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
6	d1s1ma1	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
7	c2ad5B_	Alignment		100.0	20	**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.
8	c3nvaB_	Alignment		100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
9	c2w7tA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound acivicin
10	d1vcoa1	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
11	c4zdiE_	Alignment		100.0	21	**PDB header:**ligase **Chain:** E: **PDB Molecule:**ctp synthase; **PDBTitle:** crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)

12	c5u03C_	Alignment		100.0	20	**PDB header:**ligase, protein fibril **Chain:** C: **PDB Molecule:**ctp synthase 1; **PDBTitle:** cryo-em structure of the human ctp synthase filament
13	c1vcnA_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
14	d2a9va1	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
15	d1a9xb2	Alignment		100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
16	c2vxoB_	Alignment		100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
17	c1gpmD_	Alignment		100.0	21	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
18	c5tw7E_	Alignment		100.0	23	**PDB header:**ligase **Chain:** E: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
19	c2ywcC_	Alignment		100.0	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
20	c3d54D_	Alignment		100.0	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** structure of purlqs from thermotoga maritima
21	c1keeH_	Alignment	not modelled	100.0	24	**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
22	c2lxnA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit a; **PDBTitle:** solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
23	d1wl8a1	Alignment	not modelled	100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
24	d1qdlb_	Alignment	not modelled	100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
25	d1i7qb_	Alignment	not modelled	100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
26	d1gpma2	Alignment	not modelled	100.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
27	c3tqiB_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
28	c2vpiA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase;

						PDBTitle: human gmp synthetase - glutaminase domain
29	c6qurA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutaminase; **PDBTitle:** mapping the allosteric communication network of aminodeoxychorismate2 synthase
30	c3uowB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
31	c3l7nA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
32	d1q7ra_	Alignment	not modelled	100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
33	d1i1qb_	Alignment	not modelled	100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
34	d1jvna2	Alignment	not modelled	100.0	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
35	c2ywjA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
36	c4gudA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit hish; **PDBTitle:** crystal structure of amidotransferase hish from vibrio cholerae
37	c3r74B_	Alignment	not modelled	100.0	20	**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
38	c3l83A_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
39	d1k9vf_	Alignment	not modelled	100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	c2ywdA_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
41	d1o1ya_	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
42	d2nv0a1	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
43	c2issF_	Alignment	not modelled	99.9	20	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
44	d2abwa1	Alignment	not modelled	99.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
45	d1t3ta2	Alignment	not modelled	99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
46	d1ka9h_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
47	c1jvnB_	Alignment	not modelled	99.9	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
48	c5dotA_	Alignment	not modelled	99.9	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase [ammonia], mitochondrial; **PDBTitle:** crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
49	c5douC_	Alignment	not modelled	99.9	23	**PDB header:**ligase **Chain:** C: **PDB Molecule:**carbamoyl-phosphate synthase [ammonia], mitochondrial; **PDBTitle:** crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
50	c2h2wA_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
51	d2ghra1	Alignment	not modelled	99.8	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
52	c6mtgB_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
53	c6fqbE_	Alignment	not modelled	99.2	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**cobyric acid synthase;

		Alignment	not modelled	99.2	17	**PDBTitle:** murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
54	c5n9mA_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobyric acid synthase; **PDBTitle:** crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
55	c1t3tA_	Alignment	not modelled	97.8	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
56	c6a4tB_	Alignment	not modelled	97.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase e; **PDBTitle:** crystal structure of peptidase e from deinococcus radiodurans r1
57	c5j84A_	Alignment	not modelled	97.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxy-acid dehydratase; **PDBTitle:** crystal structure of l-arabinonate dehydratase in holo-form
58	c3l4eA_	Alignment	not modelled	97.2	14	**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
59	c5oynB_	Alignment	not modelled	96.9	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dehydratase, ilvd/edd family; **PDBTitle:** crystal structure of d-xylonate dehydratase in holo-form
60	c1sy7B_	Alignment	not modelled	96.9	15	**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.
61	c5ym0A_	Alignment	not modelled	96.8	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxy-acid dehydratase, chloroplastic; **PDBTitle:** the crystal structure of dhad
62	c3uk7B_	Alignment	not modelled	95.8	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
63	c3cneD_	Alignment	not modelled	95.7	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
64	c1p81A_	Alignment	not modelled	95.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
65	d1p80a1	Alignment	not modelled	95.4	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
66	c5ze4A_	Alignment	not modelled	95.2	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxy-acid dehydratase, chloroplastic; **PDBTitle:** the structure of holo- structure of dhad complex with [2fe-2s] cluster
67	c3l3bA_	Alignment	not modelled	94.3	19	**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
68	d1sy7a1	Alignment	not modelled	93.8	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
69	d1fyea_	Alignment	not modelled	93.6	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
70	c4hcjA_	Alignment	not modelled	92.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thij/pfpi domain protein; **PDBTitle:** crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
71	c3f5dA_	Alignment	not modelled	92.4	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from bacillus2 subtilis
72	d1vhqa_	Alignment	not modelled	92.1	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
73	c3n7tA_	Alignment	not modelled	91.8	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
74	c4lruA_	Alignment	not modelled	91.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase iii (glutathione-independent); **PDBTitle:** crystal structure of glyoxalase iii (orf 19.251) from candida albicans
75	d1g2ia_	Alignment	not modelled	91.4	30	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
76	c3kklA_	Alignment	not modelled	91.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
77	c3efeC_	Alignment	not modelled	91.2	26	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
78	c3fseB_	Alignment	not modelled	90.8	27	**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

79	d1p5fa_	Alignment	not modelled	90.3	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
80	c4i2nC_	Alignment	not modelled	90.1	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**intracellular protease/amidase; **PDBTitle:** crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
81	c3en0A_	Alignment	not modelled	89.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
82	d1qvwa_	Alignment	not modelled	89.1	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
83	d1oi4a1	Alignment	not modelled	89.1	36	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
84	d1n57a_	Alignment	not modelled	88.9	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
85	c5xr2D_	Alignment	not modelled	87.7	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**protein/nucleic acid deglycase hcha; **PDBTitle:** sav0551
86	c4y0nB_	Alignment	not modelled	86.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein sav1875; **PDBTitle:** sav1875
87	c4e08B_	Alignment	not modelled	85.6	29	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dj-1 beta; **PDBTitle:** crystal structure of drosophila melanogaster dj-1beta
88	c3nooB_	Alignment	not modelled	85.2	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
89	c4p5pA_	Alignment	not modelled	84.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
90	c3bhnA_	Alignment	not modelled	84.6	27	**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
91	d1j8ba_	Alignment	not modelled	81.0	19	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
92	c3graA_	Alignment	not modelled	80.8	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, arac family; **PDBTitle:** crystal structure of arac family transcriptional regulator from2 pseudomonas putida
93	c3mgkA_	Alignment	not modelled	79.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**intracellular protease/amidase related enzyme (thij **PDBTitle:** crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824
94	c3ot1B_	Alignment	not modelled	78.7	23	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
95	d1puga_	Alignment	not modelled	78.6	23	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
96	d1xi8a3	Alignment	not modelled	78.1	24	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
97	d1uz5a3	Alignment	not modelled	77.1	25	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
98	c4xllB_	Alignment	not modelled	76.9	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**dj-1 family protein; **PDBTitle:** toxoplasma gondii dj-1, oxidized
99	c4ge0C_	Alignment	not modelled	76.2	11	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein c22e12.03c; **PDBTitle:** schizosaccharomyces pombe dj-1 t114p mutant
100	c3ej6D_	Alignment	not modelled	76.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
101	c3ewnA_	Alignment	not modelled	75.8	27	**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
102	c2nqqA_	Alignment	not modelled	75.4	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
103	c3dzvB_	Alignment	not modelled	74.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
104	d2fexa1	Alignment	not modelled	73.2	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
						PDB header:structural genomics, unknown function

105	c1ybxA_	Alignment	not modelled	71.9	22	**Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
106	d1wd7a_	Alignment	not modelled	71.2	20	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
107	c3d8tB_	Alignment	not modelled	69.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
108	d1u9ca_	Alignment	not modelled	68.5	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
109	c3er6D_	Alignment	not modelled	68.0	27	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative transcriptional regulator protein; **PDBTitle:** crystal structure of a putative transcriptional regulator protein from2 vibrio parahaemolyticus
110	c2fu3A_	Alignment	not modelled	67.6	19	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
111	c5g2rA_	Alignment	not modelled	67.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein cnx1; **PDBTitle:** crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
112	d2ab0a1	Alignment	not modelled	64.6	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
113	d1sc6a2	Alignment	not modelled	62.3	15	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
114	c1uz5A_	Alignment	not modelled	62.1	25	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
115	d1wu2a3	Alignment	not modelled	56.7	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
116	c2vrnA_	Alignment	not modelled	55.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease i; **PDBTitle:** the structure of the stress response protein dr1199 from deinococcus2 radiodurans: a member of the dj-1 superfamily
117	c4k2hG_	Alignment	not modelled	53.6	20	**PDB header:**unknown function **Chain:** G: **PDB Molecule:**intracellular protease/amidase; **PDBTitle:** crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium
118	d1ekqa_	Alignment	not modelled	51.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
119	c1jr2A_	Alignment	not modelled	48.7	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
120	d1jr2a_	Alignment	not modelled	48.7	24	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like