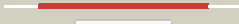



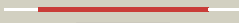



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0788_purQ_882763_883437
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	237a7f4ae90c5794

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t3ta2	 Alignment		100.0	29	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
2	c3d54D	 Alignment		100.0	44	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
3	c1t3ta	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
4	c1jvnB	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hisf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
5	c1i9xA	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
6	d1i9xa	 Alignment		100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
7	c4i8fA	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
8	d1ka9h	 Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
9	d1jvna2	 Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	d1q7ra	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
11	c3fijD	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909

12	d1k9vf_	Alignment		100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c3uowB_	Alignment		100.0	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
14	c5tw7E_	Alignment		100.0	22	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
15	c1gpmD_	Alignment		100.0	19	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
16	c2ywcC_	Alignment		100.0	23	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
17	c2ywjA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
18	d1vcoa1	Alignment		100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
19	d1wl8a1	Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
20	c6qurA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
21	d2a9va1	Alignment	not modelled	100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
22	d1qdlb_	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
23	c4gudA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
24	d1slma1	Alignment	not modelled	100.0	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	dli7qb_	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	c2vxob_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
27	d1gpmA2	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
28	c2issF_	Alignment	not modelled	100.0	17	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
						Fold: Flavodoxin-like

29	d2nv0a1	Alignment	not modelled	100.0	22	Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
30	c3tqiB	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
31	c2ad5B	Alignment	not modelled	100.0	25	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.
32	c1vcnA	Alignment	not modelled	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
33	c1keeH	Alignment	not modelled	100.0	18	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
34	d1i1qb	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c2vpiA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
36	c3nvaB	Alignment	not modelled	100.0	25	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
37	c2ywdA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
38	d1a9xb2	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	d2abwa1	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
40	c2lxnA	Alignment	not modelled	100.0	19	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
41	c4zdiE	Alignment	not modelled	100.0	24	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
42	c3r74B	Alignment	not modelled	100.0	16	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
43	c2w7tA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
44	c5u03C	Alignment	not modelled	100.0	18	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
45	c2v4uA	Alignment	not modelled	99.9	21	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
46	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
47	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
48	c3l7nA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
49	c3l83A	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
50	d1o1ya	Alignment	not modelled	99.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	d2ghra1	Alignment	not modelled	99.7	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
52	c6fqbe	Alignment	not modelled	99.7	17	PDB header: ligase Chain: E: PDB Molecule: cobryric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
53	c2h2wA	Alignment	not modelled	99.7	16	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

54	c5n9mA	Alignment	not modelled	99.7	16	PDB header: transferase Chain: A: PDB Molecule: cobyric acid synthase; PDBTitle: crystal structure of gatl - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
55	c6mtgB	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
56	c3cneD	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetalotaomicron
57	c1sy7B	Alignment	not modelled	98.9	18	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.
58	d1p80a1	Alignment	not modelled	98.9	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
59	d1sy7a1	Alignment	not modelled	98.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
60	c3uk7B	Alignment	not modelled	98.9	29	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
61	c4e08B	Alignment	not modelled	98.8	28	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
62	c3fseB	Alignment	not modelled	98.8	30	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 anaebaena variabilis3 atcc 29413 at 1.90 a resolution
63	d1oi4a1	Alignment	not modelled	98.7	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
64	c4y0nB	Alignment	not modelled	98.6	19	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sav1875; PDBTitle: sav1875
65	d1p5fa	Alignment	not modelled	98.6	29	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
66	d1q2ia	Alignment	not modelled	98.6	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
67	c6a4tB	Alignment	not modelled	98.5	21	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
68	c4xllB	Alignment	not modelled	98.5	26	PDB header: unknown function Chain: B: PDB Molecule: dj-1 family protein; PDBTitle: toxoplasma gondii dj-1, oxidized
69	c3l4eA	Alignment	not modelled	98.4	16	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
70	d1vhqa	Alignment	not modelled	98.4	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
71	c4hclA	Alignment	not modelled	98.4	21	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
72	c3ot1B	Alignment	not modelled	98.4	25	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
73	d2ab0a1	Alignment	not modelled	98.4	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
74	c3ewna	Alignment	not modelled	98.3	26	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
75	d2fexa1	Alignment	not modelled	98.3	32	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
76	c3l3bA	Alignment	not modelled	98.3	15	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
77	c4k2hg	Alignment	not modelled	98.3	28	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
78	c3f5dA	Alignment	not modelled	98.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
79	c3nooB	Alignment	not modelled	98.3	26	PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from

						pseudomonas2 fluorescens
80	d1qvwa	Alignment	not modelled	98.3	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
81	d1u9ca	Alignment	not modelled	98.2	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
82	c3n7tA	Alignment	not modelled	98.2	18	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from <i>coccidioides2 immitis</i>
83	c1p81A	Alignment	not modelled	98.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from <i>e. coli</i>
84	c3kkIA	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from <i>saccharomyces cerevisiae</i>
85	c3mgkA	Alignment	not modelled	98.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intracellular protease/amidase related enzyme (thij) PDBTitle: crystal structure of probable protease/amidase from <i>clostridium2 acetobutylicum atcc 824</i>
86	c2vrnA	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: protease i; PDBTitle: the structure of the stress response protein dr1199 from <i>deinococcus2 radiodurans</i> : a member of the dj-1 superfamily
87	c4lruA	Alignment	not modelled	98.1	19	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from <i>candida albicans</i>
88	c3efeC	Alignment	not modelled	98.0	18	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from <i>bacillus2 anthracis</i>
89	d1fyea	Alignment	not modelled	98.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
90	c4ge0C	Alignment	not modelled	98.0	21	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein c22e12.03c; PDBTitle: <i>schizosaccharomyces pombe dj-1 t114p mutant</i>
91	c3bhnA	Alignment	not modelled	98.0	25	PDB header: unknown function Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of a dj-1/pfpi-like protein (shew_2856) from <i>shewanella loihica pv-4</i> at 1.76 a resolution
92	c4p5pA	Alignment	not modelled	97.9	15	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi family protein; PDBTitle: x-ray structure of <i>francisella tularensis</i> rapid encystment protein 242 kda (rep24), gene product of <i>ftn_0841</i>
93	c3graA	Alignment	not modelled	97.7	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from <i>2 pseudomonas putida</i>
94	c3er6D	Alignment	not modelled	97.7	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein; PDBTitle: crystal structure of a putative transcriptional regulator protein from <i>2 vibrio parahaemolyticus</i>
95	c5xr2D	Alignment	not modelled	97.5	24	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
96	d1n57a	Alignment	not modelled	97.3	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
97	c4i2nC	Alignment	not modelled	97.2	19	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from <i>vibrio2 cholerae</i>
98	c3ej6D	Alignment	not modelled	97.1	23	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: <i>neurospora crassa catalase-3 crystal structure</i>
99	c3en0A	Alignment	not modelled	96.6	25	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
100	c4jqsC	Alignment	not modelled	96.2	12	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative thua-like protein (bacuni_01602) from <i>2 bacteroides uniformis atcc 8492</i> at 2.30 a resolution
101	d1z0sa1	Alignment	not modelled	95.0	23	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
102	c1z0zC	Alignment	not modelled	95.0	23	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from <i>archaeoglobus2 fulgidus</i> in complex with nad
103	d1xi8a3	Alignment	not modelled	94.8	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
104	c2iufA	Alignment	not modelled	94.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the structures of <i>penicillium vitale</i> catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
105	c2an1D	Alignment	not modelled	94.5	28	PDB header: transferase Chain: D: PDB Molecule: putative kinase;

105	c2am1D_	Alignment	not modelled	94.5	28	PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
106	d2a5la1	Alignment	not modelled	92.4	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
107	d2fts3	Alignment	not modelled	91.9	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
108	d1uz5a3	Alignment	not modelled	91.7	29	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
109	c2nqqA_	Alignment	not modelled	91.6	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
110	d2jfga1	Alignment	not modelled	90.9	22	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
111	c2fu3A_	Alignment	not modelled	90.7	18	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
112	c5mp4C_	Alignment	not modelled	90.4	13	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
113	c2zkih_	Alignment	not modelled	89.2	24	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
114	d1u0ta_	Alignment	not modelled	89.1	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
115	d1wu2a3	Alignment	not modelled	88.8	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
116	c5vymB_	Alignment	not modelled	88.6	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase bgab; PDBTitle: crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
117	c4e5vA_	Alignment	not modelled	87.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thua-like protein; PDBTitle: crystal structure of a putative thua-like protein (parmer_02418) from2 parabacteroides merdae atcc 43184 at 1.75 a resolution
118	c4uozC_	Alignment	not modelled	84.6	20	PDB header: hydrolase Chain: C: PDB Molecule: beta-galactosidase; PDBTitle: beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
119	c1uz5A_	Alignment	not modelled	84.1	28	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
120	c2vlbC_	Alignment	not modelled	84.0	22	PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase