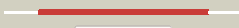


























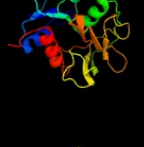


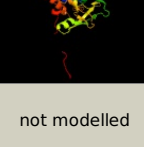


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0013_(trpG)_14914_15612
Date	Tue Jul 23 14:50:04 BST 2019
Unique Job ID	fbe28929d6b1006f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ywcC_	Alignment 		100.0	26	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermophilus in2 complex with xmp
2	c5tw7E_	Alignment 		100.0	23	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthetase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
3	c3r74B_	Alignment 		100.0	28	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
4	c1gpmD_	Alignment 		100.0	23	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
5	c2vx0B_	Alignment 		100.0	22	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
6	d1i7qb_	Alignment 		100.0	41	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
7	d2a9va1	Alignment 		100.0	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
8	d1wl8a1	Alignment 		100.0	32	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
9	d1qdlb_	Alignment 		100.0	44	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	c6qurA_	Alignment 		100.0	53	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
11	d1i1qb_	Alignment 		100.0	37	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	d1a9xb2	Alignment		100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c3tqiB	Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
14	c1keeH	Alignment		100.0	22	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
15	c2lxnA	Alignment		100.0	29	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
16	d1gpm2	Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
17	c2vpiA	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
18	c3uowB	Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
19	c5dotA	Alignment		100.0	20	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
20	c5douC	Alignment		100.0	20	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
21	d1vcoa1	Alignment	not modelled	100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
22	d1s1ma1	Alignment	not modelled	100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
23	c1jvnB	Alignment	not modelled	100.0	24	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
24	c3l7nA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
25	c2v4uA	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
26	d1o1ya	Alignment	not modelled	100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
27	c2w7tA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
28	d1ka9h	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

29	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
30	c3fijD	Alignment	not modelled	100.0	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
31	c3l83A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
32	d1k9vf	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
33	d1jvna2	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
34	c1l9xA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
35	d1l9xa	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
36	c2ad5B	Alignment	not modelled	100.0	21	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.
37	c3nvaB	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
38	c4l8fA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
39	c5u03C	Alignment	not modelled	100.0	25	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
40	d2nv0a1	Alignment	not modelled	100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	c4zdiE	Alignment	not modelled	100.0	23	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
42	c3d54D	Alignment	not modelled	100.0	16	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
43	c2issF	Alignment	not modelled	100.0	21	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
44	c2ywjA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
45	c1vcnA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
46	d1q7ra	Alignment	not modelled	100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
47	c2ywdA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
48	d2ghra1	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
49	d2abwa1	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	c2h2wA	Alignment	not modelled	99.9	17	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	d1t3ta2	Alignment	not modelled	99.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
52	c6mtgB	Alignment	not modelled	99.9	17	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	99.5	14	PDB header: ligase Chain: E: PDB Molecule: cohyric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
54	c5n9mA	Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: cohyric acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation

55	c1t3tA	Alignment	not modelled	98.6	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
56	c3uk7B	Alignment	not modelled	98.5	21	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
57	c3l3bA	Alignment	not modelled	98.2	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
58	c1sy7B	Alignment	not modelled	98.0	12	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.
59	c4lruA	Alignment	not modelled	98.0	21	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
60	c3kkIA	Alignment	not modelled	97.9	18	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
61	c3l4eA	Alignment	not modelled	97.9	15	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
62	d1vhqa	Alignment	not modelled	97.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
63	c4xllB	Alignment	not modelled	97.9	15	PDB header: unknown function Chain: B: PDB Molecule: dj-1 family protein; PDBTitle: toxoplasma gondii dj-1, oxidized
64	c6a4tB	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
65	d1sy7a1	Alignment	not modelled	97.8	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
66	c3cneD	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
67	c4hcia	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
68	d1oi4a1	Alignment	not modelled	97.7	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
69	c4p5pA	Alignment	not modelled	97.7	22	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
70	c3fseB	Alignment	not modelled	97.6	20	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 anaerobaculum variabilis3 atcc 29413 at 1.90 a resolution
71	d1p80a1	Alignment	not modelled	97.5	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
72	d1p5fa	Alignment	not modelled	97.5	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
73	d1n57a	Alignment	not modelled	97.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
74	d1q2ia	Alignment	not modelled	97.4	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
75	d1fyea	Alignment	not modelled	97.3	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
76	c3n7tA	Alignment	not modelled	97.3	17	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
77	c3f5dA	Alignment	not modelled	97.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
78	c4y0nB	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sav1875; PDBTitle: sav1875
79	c4e08B	Alignment	not modelled	97.2	16	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
80	d1qvwa	Alignment	not modelled	97.2	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl

81	d1u9ca	Alignment	not modelled	97.2	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
82	d1t0ba	Alignment	not modelled	97.1	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
83	c3ot1B	Alignment	not modelled	97.0	21	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
84	c4i2nC	Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
85	d2ab0a1	Alignment	not modelled	96.7	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
86	c5xr2D	Alignment	not modelled	96.6	14	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
87	c1p81A	Alignment	not modelled	96.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
88	c4k2hG	Alignment	not modelled	96.6	21	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
89	c4ge0C	Alignment	not modelled	96.5	11	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein c22e12.03c; PDBTitle: schizosaccharomyces pombe dj-1 t114p mutant
90	d2fexa1	Alignment	not modelled	96.5	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
91	c1z0zC	Alignment	not modelled	96.4	27	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
92	d1z0sa1	Alignment	not modelled	96.4	27	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
93	c2vrnA	Alignment	not modelled	96.2	13	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
94	c3nooB	Alignment	not modelled	96.2	16	PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
95	d1p3da1	Alignment	not modelled	95.6	10	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
96	c4jqsc	Alignment	not modelled	95.5	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative thua-like protein (bacuni_01602) from2 bacteroides uniformis atcc 8492 at 2.30 a resolution
97	d1j6ua1	Alignment	not modelled	95.4	11	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
98	c3efeC	Alignment	not modelled	95.2	14	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
99	c3vvpC	Alignment	not modelled	95.1	16	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfobolus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
100	d2jfga1	Alignment	not modelled	95.1	21	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
101	c2an1D	Alignment	not modelled	94.7	22	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
102	c3graA	Alignment	not modelled	94.6	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
103	c2zklA	Alignment	not modelled	93.8	9	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
104	c3en0A	Alignment	not modelled	93.7	14	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
105	c3bhnA	Alignment	not modelled	93.6	12	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
106	d1xi8a3	Alignment	not modelled	93.4	11	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like

107	c2f00A_	Alignment	not modelled	93.3	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
108	d1e5da1	Alignment	not modelled	93.3	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
109	d1u0ta_	Alignment	not modelled	93.1	30	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
110	c1j6uA_	Alignment	not modelled	93.1	11	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
111	c5uicA_	Alignment	not modelled	93.0	22	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
112	c2i2aA_	Alignment	not modelled	93.0	20	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of Imnadk1 from listeria monocytogenes
113	c4s05B_	Alignment	not modelled	93.0	15	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
114	d1ycga1	Alignment	not modelled	92.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
115	c3pfnB_	Alignment	not modelled	92.3	19	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
116	c3mgkA_	Alignment	not modelled	92.3	14	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
117	d1ydga_	Alignment	not modelled	92.2	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
118	c5f4bB_	Alignment	not modelled	92.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
119	c3ewnA_	Alignment	not modelled	92.1	19	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
120	c4qpiC_	Alignment	not modelled	92.0	18	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain