

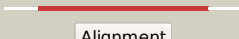

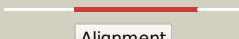












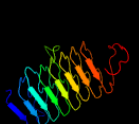















Phyre2

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 Description RVBD3859c_gltB_4331676_4336259
 Date Sat Aug 10 22:05:04 BST 2019
 Unique Job ID c2b0950e1fb575e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vdcF_	 Alignment		100.0	45	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
2	c1lm1A_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
3	d1ofda2	 Alignment		100.0	50	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
4	d1ea0a2	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
5	d1ea0a3	 Alignment		100.0	39	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
6	d1ofda3	 Alignment		100.0	41	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
7	d1ea0a1	 Alignment		100.0	45	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
8	d1ofda1	 Alignment		100.0	44	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
9	c5t5iK_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: K: PDB Molecule: tungsten-containing formylmethanofuran dehydrogenase 2 PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
10	d1p0ka_	 Alignment		99.9	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
11	c4af0B_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase

12	d1tb3a1	Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
13	c4n02A	Alignment		99.9	20	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
14	c1ecjB	Alignment		99.9	22	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
15	c1gph1	Alignment		99.9	30	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
16	c2e77B	Alignment		99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
17	c2rduA	Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
18	d1ecfa2	Alignment		99.9	21	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
19	d1kbia1	Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
20	d1vrda1	Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
21	d1p4ca	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
22	d2cu0a1	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
23	c6a0gA	Alignment	not modelled	99.9	18	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
24	d1goxa	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
25	c4q33F	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110
26	c5upxA	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate
27	c4mz1A	Alignment	not modelled	99.8	16	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from

						campylobacter jejuni complexed3 with inhibitor compound p12 PDB header: oxidoreductase
28	c2rtdA_	Alignment	not modelled	99.8	15	Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
29	c4xtiA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
30	c1vrdA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
31	c2cu0B_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
32	d1xffa_	Alignment	not modelled	99.8	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
33	d1eepa_	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
34	d1gph12	Alignment	not modelled	99.8	21	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
35	c3sr7C_	Alignment	not modelled	99.8	20	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
36	c4avfD_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
37	d1pvna1	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
38	c4ff0B_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
39	c1ypfB_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
40	c6dvhF_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
41	c4mjmD_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a short internal deletion of cbs domain from bacillus anthracis str.3 ames
42	c3r2gA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
43	c2zrvC_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfobolus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
44	c2a7nA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
45	c1kbiB_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
46	c1fcbA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
47	c3ffsC_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
48	c3khjE_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
49	d1jr1a1	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
50	d1vcfa1	Alignment	not modelled	99.7	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
						PDB header: oxidoreductase

51	c4zqrD_	Alignment	not modelled	99.7	18	Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
52	c1me9A_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
53	c6gk9C_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
54	c2a7rD_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
55	c1jxaA_	Alignment	not modelled	99.6	22	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
56	d1zfja1	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
57	c2cdh1_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
58	c4z38B_	Alignment	not modelled	99.5	17	PDB header: transferase Chain: B: PDB Molecule: mlna; PDBTitle: crystal structure of enoyl reductase domain of mlna from the2 macrolactin biosynthesis cluster from bacillus amyloliquefaciens
59	c2qr6A_	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
60	d1juba_	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
61	c1jcnA_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
62	d1jcna1	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
63	c3tsdA_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
64	c3oixA_	Alignment	not modelled	99.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
65	c4xq6A_	Alignment	not modelled	99.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
66	c2fptA_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
67	c4z87B_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
68	d1d3ga_	Alignment	not modelled	99.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
69	c6bkaA_	Alignment	not modelled	99.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monoxygenase; PDBTitle: crystal structure of nitronate monoxygenase from cyberlindnera2 saturnus
70	c3bw2A_	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
71	d1te5a_	Alignment	not modelled	99.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
72	d1uuma_	Alignment	not modelled	99.0	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	c5x8oA_	Alignment	not modelled	99.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
74	c4dqwb_	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770

75	c6b8sB_	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
76	c3mdnD_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
77	c4z9rA_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: omega-3 polyunsaturated fatty acid synthase subunit pfad; PDBTitle: crystal structure of pfad from shewanella oneidensis in complex with2 nad+ determined by in-situ diffraction.
78	c4zfb_	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase egtc; PDBTitle: ergothioneine-biosynthetic ntn hydrolase egtc, apo form
79	d2b4ga1	Alignment	not modelled	98.8	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
80	d1ct9a2	Alignment	not modelled	98.7	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
81	c5lsmF_	Alignment	not modelled	98.7	20	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
82	d1tv5a1	Alignment	not modelled	98.7	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c1tv5A_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
84	c1zfa_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
85	d1ep3a_	Alignment	not modelled	98.7	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
86	c2z6jB_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
87	c4fxsA_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
88	c1ct9D_	Alignment	not modelled	98.6	20	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
89	c3gyeA_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major
90	c2qjIA_	Alignment	not modelled	98.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
91	c3bo9B_	Alignment	not modelled	98.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
92	d1jgta2	Alignment	not modelled	98.2	23	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
93	c4iqjB_	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn
94	c1m1zB_	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
95	c4cw5B_	Alignment	not modelled	97.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens
96	d1f76a_	Alignment	not modelled	97.6	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
97	c2htmB_	Alignment	not modelled	97.5	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
98	d1gtea2	Alignment	not modelled	97.4	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
99	c5zknA_	Alignment	not modelled	97.0	20	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum PDB header: lyase/biosynthetic protein

100	c4n6eA_	Alignment	not modelled	96.9	24	Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
101	c1gthD_	Alignment	not modelled	96.8	14	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
102	c5z9yB_	Alignment	not modelled	96.7	20	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
103	d1wv2a_	Alignment	not modelled	96.6	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
104	d1vhna_	Alignment	not modelled	96.6	26	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c2c3zA_	Alignment	not modelled	96.6	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
106	d1n7ka_	Alignment	not modelled	96.5	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
107	c1q15A_	Alignment	not modelled	96.5	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: scara; PDBTitle: carbapenam synthetase
108	d1l6wa_	Alignment	not modelled	96.5	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
109	d1yxya1	Alignment	not modelled	96.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
110	d1o0ya_	Alignment	not modelled	96.3	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
111	d1y0ea_	Alignment	not modelled	96.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
112	d1xm3a_	Alignment	not modelled	96.2	19	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
113	c3tsmB_	Alignment	not modelled	96.1	10	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
114	c6bmaA_	Alignment	not modelled	96.0	13	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
115	c3w9zA_	Alignment	not modelled	96.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
116	c3qjaA_	Alignment	not modelled	95.9	16	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
117	c4xbsA_	Alignment	not modelled	95.8	25	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
118	d1p1xa_	Alignment	not modelled	95.8	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
119	d1mzha_	Alignment	not modelled	95.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
120	d1ub3a_	Alignment	not modelled	95.7	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase