







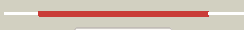















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0823c_(-)_916480_917649
Date	Fri Jul 26 01:50:41 BST 2019
Unique Job ID	ba428b9f27c8bc63

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ei9A_	 Alignment		100.0	36	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
2	d1vhna_	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
3	c3b0vD_	 Alignment		100.0	27	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
4	c3w9zA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
5	c4xp7A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)-like]; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
6	c3gr7A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
7	c4ot7A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
8	c3hf3A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
9	c3kruC_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
10	d1z41a1	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
11	c5ocsB_	 Alignment		100.0	21	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depntdent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans

12	c1djnB_	Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
13	c1ps9A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
14	c2h90A_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
15	d1ps9a1	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
16	c6qkgB_	Alignment		100.0	13	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
17	d1djqa1	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
18	c3k30B_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioles simplex
19	d1vyra_	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
20	c4a3uB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
21	c4jicB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
22	c6mywA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
23	d1gwja_	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
24	c3gkaB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
25	c2gq8A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
26	d1vjia_	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
27	c4qnwA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
28	c4b5nA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
29	d1oyaa_	Alianment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases

					Family:FMN-linked oxidoreductases
30	d1lcpa_	Alignment	not modelled	100.0	20 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
31	c3atyA_	Alignment	not modelled	100.0	19 PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tocoye
32	c5dxxA_	Alignment	not modelled	100.0	20 PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
33	d1q45a_	Alignment	not modelled	100.0	18 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
34	c3l5aA_	Alignment	not modelled	100.0	16 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
35	c4tmcB_	Alignment	not modelled	100.0	19 PDB header: flavoprotein Chain: B: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
36	c6de6B_	Alignment	not modelled	100.0	20 PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9
37	c4df2A_	Alignment	not modelled	100.0	16 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: p. stiptitis oye2.6 complexed with p-chlorophenol
38	c5epdA_	Alignment	not modelled	100.0	20 PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol trinitrate reductase; PDBTitle: crystal structure of glycerol trinitrate reductase xdpb from2 agrobacterium sp. r89-1 (apo form)
39	c6agzA_	Alignment	not modelled	100.0	18 PDB header: oxidoreductase Chain: A: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from pichia sp. aku4542
40	d1gtea2	Alignment	not modelled	100.0	16 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
41	d1ep3a_	Alignment	not modelled	100.0	20 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
42	d1juba_	Alignment	not modelled	100.0	14 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
43	d1f76a_	Alignment	not modelled	100.0	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
44	c3oixA_	Alignment	not modelled	100.0	18 PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
45	d2b4qa1	Alignment	not modelled	100.0	18 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	c4rnvD_	Alignment	not modelled	99.9	23 PDB header: oxidoreductase/inhibitor Chain: D: PDB Molecule: nadh dehydrogenase 1; PDBTitle: g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
47	d1d3ga_	Alignment	not modelled	99.9	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
48	c4xq6A_	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
49	c2htmB_	Alignment	not modelled	99.9	15 PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
50	c4rnxA_	Alignment	not modelled	99.9	17 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme
51	c2fptA_	Alignment	not modelled	99.9	19 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
52	d1tv5a1	Alignment	not modelled	99.9	15 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
53	c1tv5A_	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
54	c1gthD_	Alignment	not modelled	99.9	18 PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
55	c5z9yB_	Alignment	not modelled	99.9	19 PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole

						synthase2 (thig) complexed with dxp
56	d1uuma_	Alignment	not modelled	99.9	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	c2z6jB_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
58	c3gyeA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major
59	c6b8sB_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of putative nitroalkan dehydrogenase from helicobacter2 pylori with bound fmn
60	c4n6eA_	Alignment	not modelled	99.9	17	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
61	c3bo9B_	Alignment	not modelled	99.9	17	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
62	c2rdtA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
63	d1tb3a1	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	d1xm3a_	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
65	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
66	c2a7nA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: (+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
67	d1goxa_	Alignment	not modelled	99.8	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	c5lsmF_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
69	c2cdh1_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
70	d1vrda1	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
71	d1p4ca_	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	c4iqjB_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn
73	c4q33F_	Alignment	not modelled	99.8	15	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
74	c2gjlA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
75	c3ffsC_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
76	c3r2gA_	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 from2 legionella pneumophila
77	c4ff0B_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
78	c3khjE_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
79	c4mjmD_	Alignment	not modelled	99.8	13	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
						Fold: TIM beta/alpha-barrel

80	d1jr1a1	Alignment	not modelled	99.8	15	Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
81	c5upxA	Alignment	not modelled	99.8	14	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
82	c6a0gA	Alignment	not modelled	99.8	22	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
83	c4xtiA	Alignment	not modelled	99.8	15	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
84	c4zqrD	Alignment	not modelled	99.8	18	PDB header: oxidoreductase 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
85	c4n02A	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
86	d1eepea	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
87	d1jcna1	Alignment	not modelled	99.8	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
88	c1ypfB	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
89	c2e77B	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
90	d1vcfa1	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
91	d1p0ka	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	d1pvna1	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
93	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
94	c2zrvC	Alignment	not modelled	99.8	14	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.
95	c1vrda	Alignment	not modelled	99.8	18	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
96	c3sr7C	Alignment	not modelled	99.8	13	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
97	c2rduA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
98	d1kbia1	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
99	c3bw2A	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
100	c1kbiB	Alignment	not modelled	99.7	15	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
101	c4af0B	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
102	c6dvhF	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
103	c1me9A	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound

104	c6bkaA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
105	c1jcnA	Alignment	not modelled	99.7	14	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
106	c6gk9C	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
107	c4utwB	Alignment	not modelled	99.7	23	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
108	d1zfja1	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
109	c3tdmD	Alignment	not modelled	99.6	22	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
110	d1yxa1	Alignment	not modelled	99.6	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
111	c1fcbA	Alignment	not modelled	99.6	15	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
112	c2cu0B	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
113	d2cu0a1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
114	d1wv2a	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
115	c2a7rD	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
116	c2qr6A	Alignment	not modelled	99.5	14	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
117	c3tsdA	Alignment	not modelled	99.5	18	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
118	c2y85D	Alignment	not modelled	99.5	18	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
119	c4axkB	Alignment	not modelled	99.5	18	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
120	c3tdnB	Alignment	not modelled	99.5	22	PDB header: de novo protein Chain: B: PDB Molecule: flr symmetric alpha-beta tim barrel; PDBTitle: computationally designed two-fold symmetric tim-barrel protein, flr