


Phyre2

Email	mdejesus@rockefeller.edu
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Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bw2A_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces anschromogenes
2	c5lsmF_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: F; PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
3	c6bkaA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
4	c3bo9B_	 Alignment		100.0	28	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
5	c2gjlA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
6	c4iqiB_	 Alignment		100.0	31	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
7	c2z6jB_	 Alignment		100.0	28	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
8	c4z9rA_	 Alignment		100.0	19	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.
9	c4z38B_	 Alignment		100.0	18	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
10	c4cw5B_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: B; PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens
11	c4xtiA_	 Alignment		100.0	17	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

12	c4af0B_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
13	c3tsdA_	Alignment		100.0	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
14	d1zfja1	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
15	d1vrda1	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
16	d1jcnal	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
17	c1jcnA_	Alignment		100.0	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
18	c4zqrD_	Alignment		100.0	23	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
19	c5upxA_	Alignment		100.0	17	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
20	c3r2qA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
21	d1jr1a1	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
22	c4q33F_	Alignment	not modelled	100.0	19	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
23	c4ff0B_	Alignment	not modelled	100.0	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
24	c4mz1A_	Alignment	not modelled	100.0	17	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
25	d1pvna1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
26	c1vrda_	Alignment	not modelled	100.0	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
27	c3khjE_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound

						by inhibitor c64
28	c4z87B_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
29	d1eepa_	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
30	c4mjmD_	Alignment	not modelled	100.0	16	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
31	c6gk9C_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
32	c2vkzH_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
33	c2uval_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
34	d2cu0a1	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
35	c4avfD_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
36	c4fxsA_	Alignment	not modelled	100.0	18	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
37	c2qr6A_	Alignment	not modelled	100.0	16	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
38	c2cdh1_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
39	c1me9A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
40	c2cu0B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
41	c4dqwb_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
42	c2a7rD_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
43	c3ffsC_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
44	c4b3yB_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
45	c1ypfB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
46	d1tb3a1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
47	c2rdtA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
48	c6a0gA_	Alignment	not modelled	99.9	24	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
49	c5x8oA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
50	c2e77B_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase;

50	c2e77b	Alignment	not modelled	99.9	10	PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
51	d1goxa	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	c1zfa	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from <i>streptococcus pyogenes</i>
53	c6dvhF	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from <i>mycobacterium smegmatis</i> - c203a mutant
54	d1p4ca	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
55	c2rduA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with 2 glyoxylate
56	c2a7nA	Alignment	not modelled	99.9	19	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
57	c1kbiB	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of 2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
58	c1fcbA	Alignment	not modelled	99.9	16	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
59	d1kbia1	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	c3sr7C	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of <i>s. mutans</i> isopentenyl pyrophosphate isomerase
61	c4n02A	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from <i>s. pneumoniae</i>
62	c2htmB	Alignment	not modelled	99.9	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from <i>thermus thermophilus</i> hb8
63	c2zrvC	Alignment	not modelled	99.9	22	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of <i>sulfolobus shibatae</i> isopentenyl diphosphate2 isomerase in complex with reduced <i>fmn</i> .
64	d1p0ka	Alignment	not modelled	99.9	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	d2b4ga1	Alignment	not modelled	99.8	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
66	c4n6eA	Alignment	not modelled	99.8	23	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of <i>amycolatopsis orientalis</i> bexx/cyso complex
67	d1vcfa1	Alignment	not modelled	99.8	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	d1juba	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
69	d1xm3a	Alignment	not modelled	99.8	12	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
70	d1y0ea	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
71	d1ea0a2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	d1ofda2	Alignment	not modelled	99.8	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	c3gyeA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: dihydroorotate dehydrogenase from <i>leishmania major</i>
74	c5z9yB	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of <i>mycobacterium tuberculosis</i> thiazole synthase2 (thig) complexed with <i>dxp</i>
75	c3w9zA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of <i>dusc</i>
76	d1uuma	Alignment	not modelled	99.8	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases

77	d1d3ga_	Alignment	not modelled	99.8	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	c1tv5A_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
79	d1tv5a1	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
80	c3oixA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
81	c2fptA_	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
82	c5zknA_	Alignment	not modelled	99.8	19	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
83	d1wv2a_	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
84	d1ep3a_	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	c2vdcF_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] 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.
86	d1f76a_	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	c4xq6A_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
88	d1gtea2	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c1lm1A_	Alignment	not modelled	99.7	21	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
90	c4utwB_	Alignment	not modelled	99.7	21	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
91	c6b8sB_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
92	d1vhna_	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
93	c5zjnB_	Alignment	not modelled	99.6	22	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
94	c3b0vD_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
95	c3q58A_	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
96	c3igsB_	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
97	c6ei9A_	Alignment	not modelled	99.6	20	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
98	c4xp7A_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
99	d1yxya1	Alignment	not modelled	99.5	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
100	c5n2pA_	Alignment	not modelled	99.5	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
						Fold: TIM beta/alpha-barrel

101	d1wa3a1	Alignment	not modelled	99.4	18	Superfamily: Aldolase Family: Class I aldolase
102	c1gthD	Alignment	not modelled	99.4	21	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
103	d1rd5a	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
104	d1wbha1	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
105	c3tsmB	Alignment	not modelled	99.3	26	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
106	c6bmaA	Alignment	not modelled	99.3	23	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
107	c3qjaA	Alignment	not modelled	99.3	24	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
108	d1a53a	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
109	d1geqa	Alignment	not modelled	99.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
110	c2c3zA	Alignment	not modelled	99.2	16	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
111	c3gr7A	Alignment	not modelled	99.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
112	d1w0ma	Alignment	not modelled	99.2	22	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
113	c3tdmD	Alignment	not modelled	99.2	19	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
114	d1xcfa	Alignment	not modelled	99.2	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
115	c3vndD	Alignment	not modelled	99.1	20	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
116	d1vhca	Alignment	not modelled	99.1	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
117	c4ot7A	Alignment	not modelled	99.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
118	d1h5ya	Alignment	not modelled	99.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
119	d1ka9f	Alignment	not modelled	99.1	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
120	c2h90A	Alignment	not modelled	99.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin