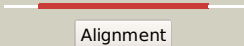

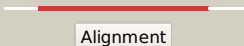

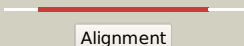







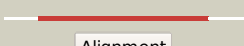











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1872c_(lldD2)_2121914_2123158
Date	Fri Aug 2 13:30:48 BST 2019
Unique Job ID	ab24142e1572ecc1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dvhF_			100.0	30	PDB header: oxidoreductase Chain: F; PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
2	c1fcbA_			100.0	34	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
3	c2a7nA_			100.0	37	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
4	c2e77B_			100.0	28	PDB header: oxidoreductase Chain: B; PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
5	d1kbia1			100.0	33	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
6	c1kbiB_			100.0	33	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
7	d1p4ca_			100.0	38	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
8	d1goxa_			100.0	38	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
9	c2rduA_			100.0	33	PDB header: oxidoreductase Chain: A; PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
10	d1tb3a1			100.0	37	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
11	c2rdtA_			100.0	36	PDB header: oxidoreductase Chain: A; PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst

12	c6a0gA_	Alignment		100.0	40	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
13	c2zrvC_	Alignment		100.0	16	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
14	c4n02A_	Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
15	c1jcnA_	Alignment		100.0	16	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
16	c3sr7C_	Alignment		100.0	21	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
17	d1p0ka_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
18	d1vcfa1	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
19	c6gk9C_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
20	d1jcna1	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
21	c4zqrD_	Alignment	not modelled	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
22	c4mjmD_	Alignment	not modelled	100.0	17	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
23	c2cdh1_	Alignment	not modelled	100.0	42	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
24	c3khjE_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
25	d1eepa_	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
26	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
27	c4avfD_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase PDB header: oxidoreductase

28	c3ffsC_	Alignment	not modelled	100.0	23	Chain: C; PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
29	d1vrda1	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
30	c1vrda_	Alignment	not modelled	100.0	22	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	c2qr6A_	Alignment	not modelled	100.0	19	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
32	c4q33F_	Alignment	not modelled	100.0	24	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
33	c4ff0B_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
34	c4mz1A_	Alignment	not modelled	100.0	22	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
35	c2a7rD_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D; PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
36	d1jrla1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
37	d1uuma_	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
38	d2cu0a1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
39	c1me9A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
40	c4af0B_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
41	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
42	c3r2gA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
43	c2cu0B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
44	c4xtiA_	Alignment	not modelled	100.0	21	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
45	c5upxA_	Alignment	not modelled	100.0	21	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
46	c2fptA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
47	c4dqwb_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
48	d1pvna1	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
49	c6b8sB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B; PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
						Fold: TIM beta/alpha-barrel

50	d1d3ga_	Alignment	not modelled	100.0	14	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
51	c1tv5A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
52	d1tv5a1	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
53	d1zfja1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
54	c4xq6A_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
55	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
56	d1juba_	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	c3tsdA_	Alignment	not modelled	100.0	19	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
58	c3oixA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
59	d1f76a_	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	d2b4ga1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
61	c3gyeA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major
62	c5x8oA_	Alignment	not modelled	100.0	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
63	d1ea0a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	d1ep3a_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	d1ofda2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
66	c1zfa_	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
67	d1gtea2	Alignment	not modelled	99.9	27	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	c6bkaA_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
69	c1lm1A_	Alignment	not modelled	99.9	17	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
70	c2gjlA_	Alignment	not modelled	99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
71	c2vdcF_	Alignment	not modelled	99.9	18	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.
72	c5ismF_	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
73	c3bw2A_	Alignment	not modelled	99.9	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
74	c1gthD_	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dph) from pig, ternary complex with2 nadph and 5-iodouracil PDB header: oxidoreductase

75	c3bo9B_	Alignment	not modelled	99.9	20	Chain: B; PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
76	c4iqiB_	Alignment	not modelled	99.9	20	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
77	c2z6jB_	Alignment	not modelled	99.9	16	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
78	c5n2pA_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
79	c2htmB_	Alignment	not modelled	99.8	20	PDB header: biosynthetic protein Chain: B; PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
80	c6ei9A_	Alignment	not modelled	99.7	14	PDB header: flavoprotein Chain: A; PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
81	c5z9yB_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: B; PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
82	c5zknA_	Alignment	not modelled	99.7	15	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	c2w6rA_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A; PDB Molecule: imidazole glycerol phosphate synthase subunit PDBTitle: crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
84	c4n6eA_	Alignment	not modelled	99.7	14	PDB header: lyase/biosynthetic protein Chain: A; PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
85	c4z38B_	Alignment	not modelled	99.6	13	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
86	c6bmaA_	Alignment	not modelled	99.6	14	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
87	d1y0ea_	Alignment	not modelled	99.6	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
88	c3w9zA_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: A; PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
89	d1vhna_	Alignment	not modelled	99.6	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
90	d1yxya1	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
91	c3qjaA_	Alignment	not modelled	99.5	18	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
92	c3gr7A_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
93	c4z9rA_	Alignment	not modelled	99.5	16	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.
94	c4xp7A_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A; PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)-like]; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
95	c3b0vD_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase/rna Chain: D; PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
96	c3tsmB_	Alignment	not modelled	99.4	16	PDB header: lyase Chain: B; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
97	c3q58A_	Alignment	not modelled	99.4	15	PDB header: isomerase Chain: A; PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
98	c3igsB_	Alignment	not modelled	99.3	19	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
99	c3hf3A_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A; PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01

100	d1xm3a_	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
101	d1rd5a_	Alignment	not modelled	99.3	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
102	c5zjnB_	Alignment	not modelled	99.3	15	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
103	d1z41a1	Alignment	not modelled	99.3	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	d1geqa_	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
105	c4utwB_	Alignment	not modelled	99.3	17	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
106	c2c3zA_	Alignment	not modelled	99.3	12	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
107	d1ps9a1	Alignment	not modelled	99.3	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
108	c3kruC_	Alignment	not modelled	99.2	12	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
109	d1a53a_	Alignment	not modelled	99.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
110	c2h90A_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
111	c2v82A_	Alignment	not modelled	99.2	11	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
112	d1wa3a1	Alignment	not modelled	99.2	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
113	d1wv2a_	Alignment	not modelled	99.2	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
114	c4ot7A_	Alignment	not modelled	99.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
115	d1djqa1	Alignment	not modelled	99.1	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
116	c5ocsB_	Alignment	not modelled	99.1	12	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
117	d1vc4a_	Alignment	not modelled	99.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
118	d1ka9f_	Alignment	not modelled	99.1	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
119	c6qkgB_	Alignment	not modelled	99.1	15	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
120	c4cw5B_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens