







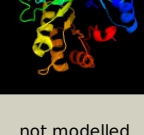


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0478_(deoC)_567225_567899
Date	Tue Jul 23 14:50:56 BST 2019
Unique Job ID	e540c10f699a7136

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ng3A_	Alignment		100.0	82	PDB header: lyase Chain: A; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
2	d1o0ya_	Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
3	c3oa3A_	Alignment		100.0	41	PDB header: lyase Chain: A; PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
4	c3ngjC_	Alignment		100.0	45	PDB header: lyase Chain: C; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
5	d1mzha_	Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
6	c4xlsA_	Alignment		100.0	47	PDB header: lyase Chain: A; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
7	c5dbul_	Alignment		100.0	49	PDB header: lyase Chain: I; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
8	d1ub3a_	Alignment		100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	c3qyaC_	Alignment		100.0	29	PDB header: lyase Chain: C; PDB Molecule: deoxyribose-phosphate aldolase, putative; PDBTitle: 1.8 angstrom resolution crystal structure of a putative deoxyribose-2 phosphate aldolase from toxoplasma gondii me49
10	d2a4aa1	Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
11	d1p1xa_	Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

12	d1vcva1	Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
13	c2a4aB_	Alignment		100.0	28	PDB header: lyase Chain: B: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: deoxyribose-phosphate aldolase from p. yoelii
14	c5c2xB_	Alignment		100.0	33	PDB header: lyase Chain: B: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from colwellia2 psychrerythraea (tetragonal form)
15	c5c6mD_	Alignment		100.0	36	PDB header: lyase Chain: D: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from shewanella2 halifaxensis
16	d1n7ka_	Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
17	c3gndC_	Alignment		99.9	16	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrif; PDBTitle: crystal structure of e. coli lsrif in complex with ribulose-5-phosphate
18	c2qjhH_	Alignment		99.8	21	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
19	c4mozC_	Alignment		99.7	19	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
20	d1ojxa_	Alignment		99.7	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
21	d1to3a_	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
22	c3fokH_	Alignment	not modelled	99.4	16	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
23	c3jrkG_	Alignment	not modelled	99.3	14	PDB header: lyase Chain: G: PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
24	d1yxya1	Alignment	not modelled	99.2	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
25	c3w9zA_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
26	c3q58A_	Alignment	not modelled	99.1	20	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
27	c4utwB_	Alignment	not modelled	99.0	14	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
						PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-

28	c5zknA	Alignment	not modelled	99.0	17	phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
29	c5zjnB	Alignment	not modelled	99.0	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
30	d1d3ga	Alignment	not modelled	99.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
31	c3igsB	Alignment	not modelled	98.9	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
32	c5ocsB	Alignment	not modelled	98.9	24	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
33	d1y0ea	Alignment	not modelled	98.9	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
34	c6bmaA	Alignment	not modelled	98.9	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
35	c4xq6A	Alignment	not modelled	98.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
36	c3tsmB	Alignment	not modelled	98.9	17	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
37	c2fptA	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
38	d1vhna	Alignment	not modelled	98.8	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
39	c3gr7A	Alignment	not modelled	98.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
40	c3hf3A	Alignment	not modelled	98.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
41	c6ei9A	Alignment	not modelled	98.8	25	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
42	d1uuma	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
43	c3qjaA	Alignment	not modelled	98.8	19	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
44	c2h90A	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
45	d1ps9a1	Alignment	not modelled	98.7	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	c3kruC	Alignment	not modelled	98.7	19	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
47	d1f76a	Alignment	not modelled	98.7	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
48	d1a53a	Alignment	not modelled	98.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
49	d1juba	Alignment	not modelled	98.7	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
50	c3ffsC	Alignment	not modelled	98.7	20	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
51	c5z9yB	Alignment	not modelled	98.6	19	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
52	c4ot7A	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
53	c1ps9A	Alignment	not modelled	98.6	20	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
54	c2c3zA_	Alignment	not modelled	98.6	13	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
55	c6b8sB_	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
56	c5x8oA_	Alignment	not modelled	98.6	27	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
57	c3r2gA_	Alignment	not modelled	98.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
58	c4zqrD_	Alignment	not modelled	98.6	26	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
59	d1z41a1	Alignment	not modelled	98.6	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	c3sr7C_	Alignment	not modelled	98.6	22	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
61	c3b0vD_	Alignment	not modelled	98.6	23	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
62	c1tv5A_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
63	d1tv5a1	Alignment	not modelled	98.6	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c1djnB_	Alignment	not modelled	98.6	15	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)
65	c4qccA_	Alignment	not modelled	98.6	25	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
66	d1vyra_	Alignment	not modelled	98.5	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	c4q33F_	Alignment	not modelled	98.5	27	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
68	c5upxA_	Alignment	not modelled	98.5	19	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
69	d1xcfa_	Alignment	not modelled	98.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
70	c2v82A_	Alignment	not modelled	98.5	24	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
71	c4avfD_	Alignment	not modelled	98.5	26	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
72	c4xp7A_	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
73	c4af0B_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
74	c3khjE_	Alignment	not modelled	98.5	23	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
75	d1p0ka_	Alignment	not modelled	98.5	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	c4mz1A_	Alignment	not modelled	98.5	25	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
77	c4xtiA_	Alignment	not modelled	98.5	20	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
78	c6gk9C_	Alignment	not modelled	98.5	26	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
79	c2htmB_	Alignment	not modelled	98.5	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
80	d1goxa_	Alignment	not modelled	98.5	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	d1wbha1	Alignment	not modelled	98.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
82	d1jr1a1	Alignment	not modelled	98.5	23	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
83	c4ff0B_	Alignment	not modelled	98.5	27	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
84	d1djqa1	Alignment	not modelled	98.4	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	c2rdtA_	Alignment	not modelled	98.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
86	c1zfjA_	Alignment	not modelled	98.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
87	c4e38A_	Alignment	not modelled	98.4	18	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
88	c4mjmD_	Alignment	not modelled	98.4	22	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
89	d1qopa_	Alignment	not modelled	98.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
90	d1lepa_	Alignment	not modelled	98.4	22	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
91	d1vrda1	Alignment	not modelled	98.4	26	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
92	c4fxsA_	Alignment	not modelled	98.4	28	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
93	c6a0gA_	Alignment	not modelled	98.4	24	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
94	d1gtea2	Alignment	not modelled	98.4	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
95	c6qkgB_	Alignment	not modelled	98.4	13	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
96	c4bk9B_	Alignment	not modelled	98.4	20	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
97	c2cdh1_	Alignment	not modelled	98.4	25	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
98	d1zfja1	Alignment	not modelled	98.4	30	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
99	c4n02A_	Alignment	not modelled	98.4	18	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
100	d1vhca_	Alignment	not modelled	98.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: oxidoreductase

101	c4jicB_	Alignment	not modelled	98.4	11	Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
102	c6oviA_	Alignment	not modelled	98.4	11	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with 2 pyruvate captured at low ph as a covalent carbinolamine intermediate
103	c1jcnA_	Alignment	not modelled	98.4	24	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
104	c4a3uB_	Alignment	not modelled	98.3	19	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)
105	c3oixA_	Alignment	not modelled	98.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from 2 streptococcus mutans
106	c3tsdA_	Alignment	not modelled	98.3	29	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from 2 bacillus anthracis str. ames complexed with xmp
107	c5kzmA_	Alignment	not modelled	98.3	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from 2 francisella tularensis
108	c3atyA_	Alignment	not modelled	98.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
109	d1jcnA1	Alignment	not modelled	98.3	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
110	c6mywA_	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
111	c1vrDA_	Alignment	not modelled	98.3	27	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
112	c4z87B_	Alignment	not modelled	98.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
113	d1rd5a_	Alignment	not modelled	98.3	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
114	d1kbia1	Alignment	not modelled	98.3	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
115	d1pvna1	Alignment	not modelled	98.3	27	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
116	c2zrvC_	Alignment	not modelled	98.3	20	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.
117	c2e77B_	Alignment	not modelled	98.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
118	c1fcbA_	Alignment	not modelled	98.2	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
119	c4n6eA_	Alignment	not modelled	98.2	18	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
120	d1tb3a1	Alignment	not modelled	98.2	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases