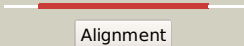

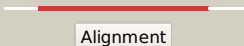

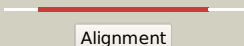







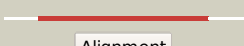














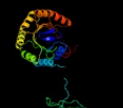





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1533_(-)_1733616_1734743
Date	Fri Aug 2 13:30:12 BST 2019
Unique Job ID	7f8035ab5605d407

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gjlA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
2	c3bo9B_	 Alignment		100.0	35	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
3	c3bw2A_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
4	c4iq1B_	 Alignment		100.0	32	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
5	c6bkaA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
6	c5ismF_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
7	c2z6jB_	 Alignment		100.0	29	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	21	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	25	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	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens
11	c3tsdA_	 Alignment		100.0	22	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

12	c4xtiA_	Alignment		100.0	16	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
13	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
14	c4af0B_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
15	dlzfja1	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
16	c4z87B_	Alignment		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
17	c4fxsA_	Alignment		100.0	19	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
18	c5upxA_	Alignment		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
19	dljcnal	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
20	c6gk9C_	Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
21	c4zqrD_	Alignment	not modelled	100.0	24	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	c4ff0B_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
23	dlvrda1	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
24	dlpvna1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
25	dljr1a1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
26	c4q33F_	Alignment	not modelled	100.0	22	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
27	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
						PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate

28	c3r2gA_	Alignment	not modelled	100.0	18	dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
29	c4mz1A_	Alignment	not modelled	100.0	24	PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from campylobacter jejuni complexed3 with inhibitor compound p12 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
30	c4dqwb_	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
31	d1eepa_	Alignment	not modelled	100.0	18	PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
32	c1vrdA_	Alignment	not modelled	100.0	23	PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase;
33	c4avfD_	Alignment	not modelled	100.0	23	PDBTitle: crystal structure of corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
34	c2qr6A_	Alignment	not modelled	100.0	17	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 Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
35	c4mjmD_	Alignment	not modelled	100.0	21	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
36	d2cu0a1	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
37	c2uval_	Alignment	not modelled	100.0	19	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
38	c2a7rD_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
39	c2vkhH_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
40	c2cdh1_	Alignment	not modelled	100.0	28	PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
41	c1me9A_	Alignment	not modelled	100.0	17	PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3 PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase;
42	c2cu0B_	Alignment	not modelled	100.0	18	PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase;
43	c3ffsC_	Alignment	not modelled	100.0	19	PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid synthase;
44	c6dvhf_	Alignment	not modelled	100.0	22	PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
45	c4b3yB_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase;
46	d1tb3a1	Alignment	not modelled	100.0	18	PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase;
47	c5x8oA_	Alignment	not modelled	100.0	21	PDBTitle: inosine monophosphate dehydrogenase (impdh); ec 1.1.1.205) from2 streptococcus pyogenes PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1;
48	c1zfiA_	Alignment	not modelled	100.0	22	PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase;
49	c2rdtA_	Alignment	not modelled	100.0	22	PDBTitle: crystal structure of l-lactate oxidase with pyruvate PDB header: oxidoreductase
50	c2e77B_	Alignment	not modelled	100.0	15	

						complex
51	d1goxa	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	c6a0gA	Alignment	not modelled	100.0	21	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
53	c1ypfB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
54	c2a7nA	Alignment	not modelled	100.0	18	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
55	c2rduA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
56	c1fcbA	Alignment	not modelled	100.0	14	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
57	d1p4ca	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
58	d1kbia1	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	c1kbiB	Alignment	not modelled	100.0	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
60	c3sr7C	Alignment	not modelled	99.9	18	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
61	c2zrvC	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfobolus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
62	d1p0ka	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
63	c4n02A	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
64	d1vcfa1	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	c2htmB	Alignment	not modelled	99.9	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
66	d1juba	Alignment	not modelled	99.9	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	c5zknA	Alignment	not modelled	99.8	17	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
68	c3oixA	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
69	d1y0ea	Alignment	not modelled	99.8	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
70	c4n6eA	Alignment	not modelled	99.8	14	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
71	d2b4ga1	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	c5z9yB	Alignment	not modelled	99.7	23	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
73	c4xq6A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
74	d1xm3a	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
75	d1tv5a1	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
						PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog,

76	c1tv5A_	Alignment	not modelled	99.7	14	mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
77	d1gtea2	Alignment	not modelled	99.7	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	d1ofda2	Alignment	not modelled	99.7	23	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
79	d1f76a_	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
80	c3gyeA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major
81	c4utwB_	Alignment	not modelled	99.7	24	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
82	d1ea0a2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c2fptA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
84	d1uuma_	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	d1wv2a_	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
86	d1ep3a_	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	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
88	d1d3ga_	Alignment	not modelled	99.7	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c3q58A_	Alignment	not modelled	99.6	19	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
90	c5zjnB_	Alignment	not modelled	99.6	20	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
91	d1wa3a1	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
92	c3igsB_	Alignment	not modelled	99.6	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
93	c2vdcF_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
94	c3w9zA_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
95	d1wbha1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
96	c1lm1A_	Alignment	not modelled	99.6	24	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
97	c5n2pA_	Alignment	not modelled	99.6	11	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
98	d1yxya1	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
99	c6oviA_	Alignment	not modelled	99.5	14	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
100	c3qjaA_	Alignment	not modelled	99.5	15	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 PDB header: lyase

101	c6bmaA_	Alignment	not modelled	99.4	12	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
102	c3tsmB_	Alignment	not modelled	99.4	9	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
103	d1vhca_	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
104	c4e38A_	Alignment	not modelled	99.4	12	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)
105	d1mxsa_	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
106	d1a53a_	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
107	c3vndD_	Alignment	not modelled	99.3	17	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
108	c2w6rA_	Alignment	not modelled	99.3	16	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
109	c2c3zA_	Alignment	not modelled	99.3	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
110	d1vhna_	Alignment	not modelled	99.3	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
111	d1qopa_	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
112	c6ei9A_	Alignment	not modelled	99.3	22	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
113	d1rd5a_	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
114	c4qccA_	Alignment	not modelled	99.3	24	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
115	d1xcfa_	Alignment	not modelled	99.2	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
116	c4bk9B_	Alignment	not modelled	99.2	16	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
117	c3b0vD_	Alignment	not modelled	99.2	19	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
118	d1vc4a_	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
119	c2v82A_	Alignment	not modelled	99.2	20	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
120	d1geqa_	Alignment	not modelled	99.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes