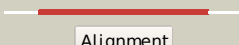
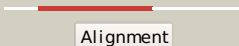
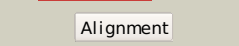
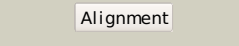
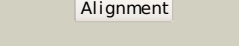
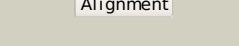
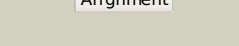
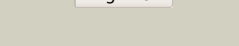
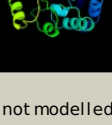


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P00909
Date	Thu Jan 5 10:57:09 GMT 2012
Unique Job ID	9a32d7d1d115eae5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1piiA_	 Alignment		100.0	100	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5' phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylantranilate isomerase:3 indoleglycerol phosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
2	d1piia2	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
3	d1vc4a_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
4	d1i4na_	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
5	d1a53a_	 Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
6	c3qjaA_	 Alignment		100.0	36	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
7	d1piia1	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
8	d1j5ta_	 Alignment		100.0	33	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
9	d1v5xa_	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
10	d1nsja_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
11	c2c3za_	 Alignment		100.0	35	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

12	d1znnal	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
13	c1znnF_	Alignment		100.0	19	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
14	c2kzhA_	Alignment		100.0	99	PDB header: isomerase Chain: A: PDB Molecule: tryptophan biosynthesis protein trpcf; PDBTitle: three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
15	c2h6rG_	Alignment		100.0	16	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
16	d1w0ma_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
17	c3q58A_	Alignment		100.0	16	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
18	d1hg3a_	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
19	c3igsB_	Alignment		100.0	16	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
20	d1yxya1	Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
21	d1rpxa_	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
22	c2v82A_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
23	d1tqja_	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
24	d1h5ya_	Alignment	not modelled	99.9	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
25	d1y0ea_	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
26	d1ka9f_	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
27	d2flia1	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
28	c2y85D_	Alignment	not modelled	99.9	18	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
29	d1thfd_	Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

					Family: Histidine biosynthesis enzymes
30	c3inpA	Alignment	not modelled	99.8	13 PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
31	c3qc3B	Alignment	not modelled	99.8	11 PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
32	d1h1ya	Alignment	not modelled	99.8	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
33	d1wbha1	Alignment	not modelled	99.8	15 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
34	d1vzwa1	Alignment	not modelled	99.8	15 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
35	d1vhca	Alignment	not modelled	99.8	16 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
36	d1wa3a1	Alignment	not modelled	99.8	12 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	d1tqxa	Alignment	not modelled	99.8	11 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
38	d1xi3a	Alignment	not modelled	99.7	20 Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
39	d1mxsa	Alignment	not modelled	99.7	13 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	d2tpsa	Alignment	not modelled	99.7	18 Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
41	d1o4ua1	Alignment	not modelled	99.6	19 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
42	c3o63B	Alignment	not modelled	99.6	17 PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
43	d1qopa	Alignment	not modelled	99.6	17 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
44	c1yadD	Alignment	not modelled	99.6	17 PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
45	d1rd5a	Alignment	not modelled	99.5	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
46	c2w6rA	Alignment	not modelled	99.5	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
47	c3f4wA	Alignment	not modelled	99.4	14 PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
48	c3ajxA	Alignment	not modelled	99.4	18 PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
49	d1q6oa	Alignment	not modelled	99.4	12 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
50	d1geqa	Alignment	not modelled	99.4	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
51	c3labA	Alignment	not modelled	99.3	10 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpq (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdpq (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
52	c2ekcA	Alignment	not modelled	99.3	16 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
53	c1o4uA	Alignment	not modelled	99.2	17 PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
54	c2z6jB	Alignment	not modelled	99.2	12 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
					Fold: TIM beta/alpha-barrel

55	d1ojxa_	Alignment	not modelled	99.2	18	Superfamily: Aldolase Family: Class I aldolase
56	c3khjE_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
57	c3ffsC_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
58	d1xcfa_	Alignment	not modelled	99.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
59	c2htmB_	Alignment	not modelled	99.1	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
60	d1wv2a_	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
61	c3ct7E_	Alignment	not modelled	99.1	19	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
62	d1qapa1	Alignment	not modelled	99.1	21	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
63	d1p0ka_	Alignment	not modelled	99.0	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c1jvnB_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
65	c3navB_	Alignment	not modelled	99.0	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
66	d1xm3a_	Alignment	not modelled	99.0	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
67	c2qj1A_	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
68	c3bo9B_	Alignment	not modelled	98.9	11	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
69	d1ujpa_	Alignment	not modelled	98.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
70	c1zfjA_	Alignment	not modelled	98.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
71	c3thaB_	Alignment	not modelled	98.8	12	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
72	c2yw3E_	Alignment	not modelled	98.8	21	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
73	d1jr1a1	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
74	c3r2gA_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
75	c2qjhH_	Alignment	not modelled	98.8	23	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
76	d1tb3a1	Alignment	not modelled	98.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
77	d1goxa_	Alignment	not modelled	98.8	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	d1d3ga_	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
79	c1vrdA_	Alignment	not modelled	98.8	15	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
80	c2e77B_	Alignment	not modelled	98.8	18 PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
81	d1vrda1	Alignment	not modelled	98.8	17 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
82	c2yztB_	Alignment	not modelled	98.8	16 PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from 2 methanocaldococcus jannaschii
83	d1dvja_	Alignment	not modelled	98.8	19 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
84	c2rduA_	Alignment	not modelled	98.7	17 PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with 2 glyoxylate
85	d1jvna1	Alignment	not modelled	98.7	21 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
86	c1me9A_	Alignment	not modelled	98.7	16 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from 2 tritrichomonas foetus with imp bound
87	c3jr2D_	Alignment	not modelled	98.7	14 PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbb; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate 2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
88	d1eepa_	Alignment	not modelled	98.7	14 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
89	c3exsB_	Alignment	not modelled	98.7	10 PDB header: lyase Chain: B: PDB Molecule: rmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpd from streptococcus mutans in 2 complex with d-r5p
90	c2zrvC_	Alignment	not modelled	98.7	13 PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfobolus shibatae isopentenyl 2 diphosphate isomerase in complex with reduced fmn.
91	c3bw2A_	Alignment	not modelled	98.7	20 PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane 2 oxidase from streptomyces ansochromogenes
92	c2cdh1_	Alignment	not modelled	98.7	16 PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty 2 acid synthase at 5 angstrom resolution.
93	d1jcna1	Alignment	not modelled	98.7	18 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
94	d1kbia1	Alignment	not modelled	98.7	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
95	c2qr6A_	Alignment	not modelled	98.6	21 PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein 2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at 3.150 a resolution
96	d1p4ca_	Alignment	not modelled	98.6	26 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
97	c2fptA_	Alignment	not modelled	98.6	20 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
98	c1jcna_	Alignment	not modelled	98.6	17 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase 2 with 6-cl-imp
99	c2a7rD_	Alignment	not modelled	98.6	13 PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate 2 reductase 2 (gmpr2)
100	d2b4ga1	Alignment	not modelled	98.6	15 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
101	c2a7nA_	Alignment	not modelled	98.6	23 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
102	c2jbmA_	Alignment	not modelled	98.6	20 PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
103	d1juba_	Alignment	not modelled	98.6	16 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	c3femB_	Alignment	not modelled	98.6	15 PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from 2 saccharomyces cerevisiae

105	c2zbtB_	Alignment	not modelled	98.6	18	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
106	d1pvna1	Alignment	not modelled	98.6	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
107	c1ypfB_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
108	d1uuma_	Alignment	not modelled	98.5	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
109	d1qo2a_	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
110	c2nv2U_	Alignment	not modelled	98.5	18	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
111	d1gtea2	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	c3gndC_	Alignment	not modelled	98.5	14	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
113	c1kbiB_	Alignment	not modelled	98.5	16	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
114	d2czda1	Alignment	not modelled	98.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
115	c3ru6C_	Alignment	not modelled	98.5	12	PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
116	c1x1oC_	Alignment	not modelled	98.5	20	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
117	d2cu0a1	Alignment	not modelled	98.4	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
118	d2zdra2	Alignment	not modelled	98.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
119	c2cu0B_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
120	d1qpoa1	Alignment	not modelled	98.4	11	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like