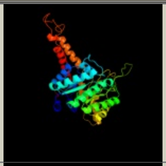
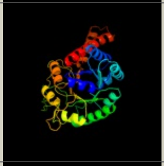
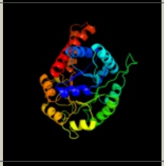
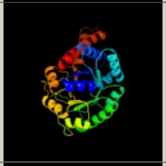
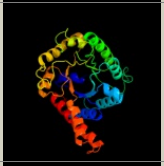
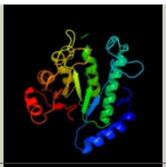
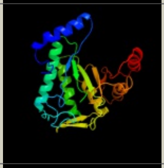
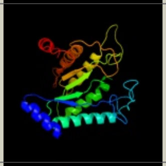
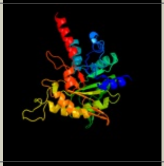
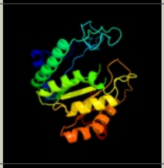
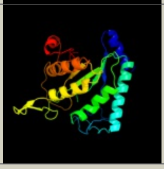
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P0AB71
Date	Thu Jan 5 11:14:46 GMT 2012
Unique Job ID	b6cb5ac53dcbc33a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dosa_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
2	c3qm3C_	Alignment		100.0	59	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
3	c3elfA_	Alignment		100.0	41	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
4	c3q94B_	Alignment		100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
5	d1rvga_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
6	d1gvfa_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
7	c3c52B_	Alignment		100.0	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
8	c2iswB_	Alignment		100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
9	c3pm6B_	Alignment		100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
10	d2fiqa1	Alignment		99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
11	c2qjhH_	Alignment		99.1	18	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate

12	c3gr7A_	Alignment		98.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
13	d1ps9a1	Alignment		98.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
14	c1ps9A_	Alignment		98.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
15	d1z41a1	Alignment		98.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
16	c2ze3A_	Alignment		98.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
17	c3hf3A_	Alignment		98.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
18	c3gndC_	Alignment		98.1	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
19	c3b8iF_	Alignment		98.1	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
20	c3kruC_	Alignment		98.0	10	**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
21	d1ujqa_	Alignment	not modelled	98.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
22	c2qiwA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
23	d1muma_	Alignment	not modelled	97.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
24	d1thfd_	Alignment	not modelled	97.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
25	d1vyra_	Alignment	not modelled	97.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
26	c3l5aA_	Alignment	not modelled	97.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
27	c3k30B_	Alignment	not modelled	97.7	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
28	d1a53a_	Alignment	not modelled	97.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes

29	d1yxya1	Alignment	not modelled	97.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
30	c2h90A_	Alignment	not modelled	97.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
31	c2c3zA_	Alignment	not modelled	97.5	21	**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
32	c1djnB_	Alignment	not modelled	97.5	14	**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)
33	c3igsB_	Alignment	not modelled	97.5	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
34	d1y0ea_	Alignment	not modelled	97.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
35	c3eooL_	Alignment	not modelled	97.4	12	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
36	c3lyeA_	Alignment	not modelled	97.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
37	c3ih1A_	Alignment	not modelled	97.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
38	d1rd5a_	Alignment	not modelled	97.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
39	c3fa4D_	Alignment	not modelled	97.1	8	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
40	c3q58A_	Alignment	not modelled	96.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
41	c2gq8A_	Alignment	not modelled	96.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
42	d1gwja_	Alignment	not modelled	96.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
43	d1j5ta_	Alignment	not modelled	96.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
44	d1ojxa_	Alignment	not modelled	96.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
45	c3jrkG_	Alignment	not modelled	96.7	13	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
46	d1piia2	Alignment	not modelled	96.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
47	d1h5ya_	Alignment	not modelled	96.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
48	c3tdmD_	Alignment	not modelled	96.3	16	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
49	d1i4na_	Alignment	not modelled	96.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
50	d1s2wa_	Alignment	not modelled	96.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
51	d1tqxa_	Alignment	not modelled	96.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
52	d1to3a_	Alignment	not modelled	96.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
53	d1m3ua_	Alignment	not modelled	96.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
54	d1vjia_	Alignment	not modelled	96.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
						PDB header:lyase

55	c2cw6B_	Alignment	not modelled	96.0	18	**Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
56	d1djqa1	Alignment	not modelled	96.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
57	c3qjaA_	Alignment	not modelled	96.0	11	**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
58	d1wbha1	Alignment	not modelled	95.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	d1qopa_	Alignment	not modelled	95.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
60	d1vhca_	Alignment	not modelled	95.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
61	c2hjpA_	Alignment	not modelled	95.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
62	d1xcfa_	Alignment	not modelled	95.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
63	c2cdh1_	Alignment	not modelled	95.5	15	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
64	c1zlpA_	Alignment	not modelled	95.5	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
65	c2vwtA_	Alignment	not modelled	95.4	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
66	c2ftpA_	Alignment	not modelled	95.4	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
67	c3ivuB_	Alignment	not modelled	95.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
68	c3bo9B_	Alignment	not modelled	95.3	12	**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	d1h1ya_	Alignment	not modelled	95.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
70	c3pg8B_	Alignment	not modelled	95.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
71	d1xm3a_	Alignment	not modelled	94.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
72	c2nx9B_	Alignment	not modelled	94.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
73	c2z6jB_	Alignment	not modelled	94.7	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
74	c3inpA_	Alignment	not modelled	94.5	16	**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.
75	c1ydoC_	Alignment	not modelled	94.5	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
76	c3ct7E_	Alignment	not modelled	94.4	15	**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
77	c2w6rA_	Alignment	not modelled	94.4	10	**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
78	c2e77B_	Alignment	not modelled	94.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
79	d1vzwa1	Alignment	not modelled	94.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
80	c2rduA_	Alignment	not modelled	94.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1;

		Alignment				**PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
81	d1tb3a1	Alignment	not modelled	93.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
82	d1xi3a_	Alignment	not modelled	93.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
83	d1vr6a1	Alignment	not modelled	93.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
84	c2y85D_	Alignment	not modelled	93.2	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
85	c1ydnA_	Alignment	not modelled	93.2	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
86	c2a7nA_	Alignment	not modelled	93.1	17	**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
87	d1kbia1	Alignment	not modelled	93.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
88	d1liua2	Alignment	not modelled	92.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
89	c3thaB_	Alignment	not modelled	92.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
90	d1vhna_	Alignment	not modelled	92.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
91	d1p4ca_	Alignment	not modelled	92.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
92	d1ka9f_	Alignment	not modelled	92.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
93	d1oyaa_	Alignment	not modelled	92.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	d1wa3a1	Alignment	not modelled	92.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
95	c1kbiB_	Alignment	not modelled	92.0	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
96	c3gkaB_	Alignment	not modelled	91.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
97	c3bg5C_	Alignment	not modelled	91.8	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
98	c3ez4B_	Alignment	not modelled	91.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
99	d1wv2a_	Alignment	not modelled	91.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
100	d1tqja_	Alignment	not modelled	91.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
101	d1icpa_	Alignment	not modelled	90.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
102	d1q45a_	Alignment	not modelled	90.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
103	c1rr2A_	Alignment	not modelled	90.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
104	d1p0ka_	Alignment	not modelled	90.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
105	c3qc3B_	Alignment	not modelled	90.6	13	**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
106	c3khjE_	Alignment	not modelled	90.6	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound

						by inhibitor c64
107	d1e0ta2	Alignment	not modelled	90.5	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
108	d1vc4a_	Alignment	not modelled	90.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
109	c3bleA_	Alignment	not modelled	90.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
110	c2a7rD_	Alignment	not modelled	89.9	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
111	d1goxa_	Alignment	not modelled	89.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
112	d2zdra2	Alignment	not modelled	89.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
113	d1d9ea_	Alignment	not modelled	89.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
114	d1rpxa_	Alignment	not modelled	88.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
115	d1mxsa_	Alignment	not modelled	87.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
116	c1vs1B_	Alignment	not modelled	87.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase; **PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
117	c3r2gA_	Alignment	not modelled	86.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
118	c2bdqA_	Alignment	not modelled	86.4	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
119	d1m5wa_	Alignment	not modelled	86.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
120	c2rfgB_	Alignment	not modelled	85.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution