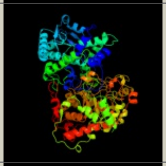
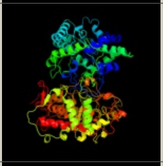
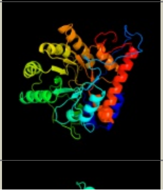
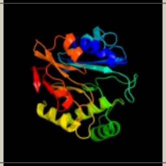
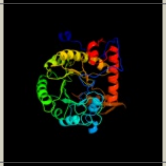
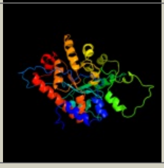
Email	l.a.kelley@imperial.ac.uk
Description	P09831
Date	Wed Jan 25 15:20:14 GMT 2012
Unique Job ID	722e2134c401d045

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vdcF_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
2	c1lm1A_	Alignment		100.0	47	**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
3	d1ofda2	Alignment		100.0	48	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
4	d1ea0a2	Alignment		100.0	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
5	d1ea0a3	Alignment		100.0	43	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
6	d1ofda3	Alignment		100.0	43	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
7	d1ea0a1	Alignment		100.0	45	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Alpha subunit of glutamate synthase, C-terminal domain **Family:**Alpha subunit of glutamate synthase, C-terminal domain
8	d1ofda1	Alignment		100.0	49	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Alpha subunit of glutamate synthase, C-terminal domain **Family:**Alpha subunit of glutamate synthase, C-terminal domain
9	d1p0ka_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
10	c1ecjB_	Alignment		99.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
11	d1tb3a1	Alignment		99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases

12	c1gph1_	Alignment		99.9	29	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
13	c2e77B_	Alignment		99.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
14	d1ecfa2	Alignment		99.8	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
15	d1vrda1	Alignment		99.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
16	c2rduA_	Alignment		99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
17	d1goxa_	Alignment		99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
18	d2cu0a1	Alignment		99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
19	d1p4ca_	Alignment		99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
20	d1kbia1	Alignment		99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
21	d1gph12	Alignment	not modelled	99.8	27	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
22	c2cu0B_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
23	d1eepa_	Alignment	not modelled	99.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
24	c1vrdA_	Alignment	not modelled	99.8	20	**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
25	d1xffa_	Alignment	not modelled	99.8	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
26	d1pvna1	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
27	c1ypfB_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
28	c2a7nA_	Alignment	not modelled	99.7	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
29	c2zrvC_	Alignment	not modelled	99.7	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
30	c3r2gA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
31	c3khjE_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
32	d1jr1a1	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
33	c3ffsC_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
34	d1vcfa1	Alignment	not modelled	99.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
35	c1kbiB_	Alignment	not modelled	99.7	22	**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
36	c1me9A_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
37	c2a7rD_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
38	c1jxaA_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
39	d1zfja1	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
40	c2cdh1_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
41	c1jcnA_	Alignment	not modelled	99.5	20	**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
42	d1juba_	Alignment	not modelled	99.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
43	c2qr6A_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase; **PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
44	d1jcna1	Alignment	not modelled	99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
45	c3oixA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
46	c2fptA_	Alignment	not modelled	99.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial; **PDBTitle:** dual binding mode of a novel series of dhodh inhibitors
47	c3bw2A_	Alignment	not modelled	98.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
48	d1d3ga_	Alignment	not modelled	98.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
49	d1uuma_	Alignment	not modelled	98.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
50	d1te5a_	Alignment	not modelled	98.8	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
51	c3mdnD_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamine aminotransferase class-ii domain protein; **PDBTitle:** structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog,

52	c1tv5A_	Alignment	not modelled	98.7	21	mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
53	d1tv5a1	Alignment	not modelled	98.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
54	c1zfjA_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
55	d1ct9a2	Alignment	not modelled	98.6	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
56	d2b4ga1	Alignment	not modelled	98.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
57	c3gyeA_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, putative; **PDBTitle:** didydroorotate dehydrogenase from leishmania major
58	d1ep3a_	Alignment	not modelled	98.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
59	c2z6jB_	Alignment	not modelled	98.6	19	**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
60	c2gjlA_	Alignment	not modelled	98.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
61	c1ct9D_	Alignment	not modelled	98.5	23	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
62	c3bo9B_	Alignment	not modelled	98.2	24	**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
63	d1jgta2	Alignment	not modelled	97.7	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
64	d1f76a_	Alignment	not modelled	97.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
65	d1gtea2	Alignment	not modelled	97.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
66	c2htmB_	Alignment	not modelled	97.5	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
67	d1wv2a_	Alignment	not modelled	97.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
68	c1m1zB_	Alignment	not modelled	97.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
69	c1gthD_	Alignment	not modelled	96.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
70	d1vhna_	Alignment	not modelled	96.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
71	c2c3zA_	Alignment	not modelled	96.7	19	**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
72	d1l6wa_	Alignment	not modelled	96.7	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
73	d1n7ka_	Alignment	not modelled	96.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
74	d1yxya1	Alignment	not modelled	96.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
75	d1o0ya_	Alignment	not modelled	96.4	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
76	d1y0ea_	Alignment	not modelled	96.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
77	d1xm3a_	Alignment	not modelled	96.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
78	c3qjaA_	Alignment	not modelled	96.1	22	**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

79	d1mzha_	Alignment	not modelled	96.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
80	d1ub3a_	Alignment	not modelled	95.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
81	c2h90A_	Alignment	not modelled	95.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
82	c3oa3A_	Alignment	not modelled	95.9	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
83	c3gr7A_	Alignment	not modelled	95.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
84	d1a53a_	Alignment	not modelled	95.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
85	c3hf3A_	Alignment	not modelled	95.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
86	d1p1xa_	Alignment	not modelled	95.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
87	c3ng3A_	Alignment	not modelled	95.7	26	**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
88	d1geqa_	Alignment	not modelled	95.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
89	c1q15A_	Alignment	not modelled	95.5	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
90	d1qopa_	Alignment	not modelled	95.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
91	c3q58A_	Alignment	not modelled	95.4	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
92	c3b0vD_	Alignment	not modelled	95.3	8	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
93	c3ngjC_	Alignment	not modelled	95.2	29	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
94	d1rd5a_	Alignment	not modelled	95.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
95	c1djnB_	Alignment	not modelled	95.1	17	**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)
96	d1ps9a1	Alignment	not modelled	94.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
97	c3igsB_	Alignment	not modelled	94.7	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
98	c1ps9A_	Alignment	not modelled	94.4	11	**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
99	d1z41a1	Alignment	not modelled	94.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
100	d1djqa1	Alignment	not modelled	94.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
101	c3pajA_	Alignment	not modelled	94.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
102	d1vyra_	Alignment	not modelled	94.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
103	d1wx0a1	Alignment	not modelled	94.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**nadh:flavin oxidoreductase/nadh

104	c3kruC_	Alignment	not modelled	94.0	22	oxidase; **PDBTitle:** crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
105	d1q15a2	Alignment	not modelled	93.3	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
106	c3tdmD_	Alignment	not modelled	93.2	23	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
107	d1w0ma_	Alignment	not modelled	93.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
108	d1qapa1	Alignment	not modelled	93.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
109	c3qyqC_	Alignment	not modelled	93.0	18	**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
110	d1vcva1	Alignment	not modelled	93.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
111	d1hg3a_	Alignment	not modelled	92.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
112	d2a4aa1	Alignment	not modelled	92.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
113	c3s1vD_	Alignment	not modelled	92.4	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable transaldolase; **PDBTitle:** transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
114	c2a4aB_	Alignment	not modelled	92.1	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** deoxyribose-phosphate aldolase from p. yoelii
115	d1qe5a_	Alignment	not modelled	92.1	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
116	c3k30B_	Alignment	not modelled	91.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
117	d1tqxa_	Alignment	not modelled	91.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
118	d1j5ta_	Alignment	not modelled	91.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
119	d1vpxa_	Alignment	not modelled	90.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
120	c1x1oC_	Alignment	not modelled	90.6	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8