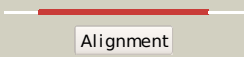
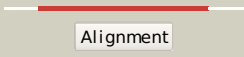
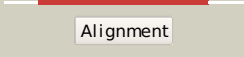
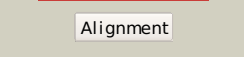
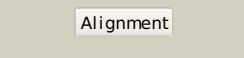
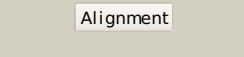
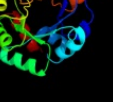
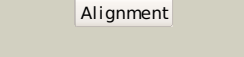
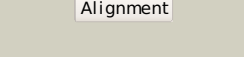
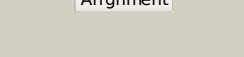
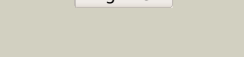
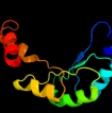
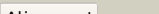
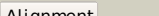
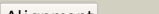
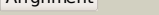
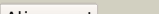
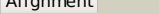
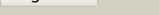
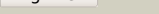
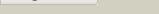
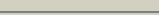


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l6wa_	 Alignment		100.0	70	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
2	c3s1vD_	 Alignment		100.0	33	PDB header: transferase Chain: D: PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
3	d1vpxa_	 Alignment		100.0	37	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
4	d1wx0a1	 Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
5	d1onra_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
6	c3cq0B_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: putative transaldolase ygr043c; PDBTitle: crystal structure of tal2_yeast
7	d1f05a_	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
8	c3m16A_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: transaldolase; PDBTitle: structure of a transaldolase from oleispira antarctica
9	d2e1da1	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
10	c3igxA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: transaldolase; PDBTitle: 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
11	c3hjzA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: transaldolase b; PDBTitle: the structure of an aldolase from prochlorococcus marinus

12	c3clmA	Alignment		100.0	31	PDB header: lyase Chain: A: PDB Molecule: transaldolase; PDBTitle: crystal structure of transaldolase (yp_208650.1) from neisseria2 gonorrhoeae fa 1090 at 1.14 a resolution
13	d1xm3a	Alignment		97.8	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
14	c1kbiB	Alignment		97.6	20	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
15	c2htmB	Alignment		97.6	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
16	c3ffsC	Alignment		97.4	12	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
17	d1kbia1	Alignment		97.4	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
18	d1tb3a1	Alignment		97.2	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
19	d1goxa	Alignment		97.1	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
20	c1zfjA	Alignment		97.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
21	c2a7nA	Alignment	not modelled	97.0	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
22	c3q58A	Alignment	not modelled	96.9	14	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
23	d1ea0a2	Alignment	not modelled	96.9	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
24	d1p0ka	Alignment	not modelled	96.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
25	d1wv2a	Alignment	not modelled	96.8	21	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
26	c3qc3B	Alignment	not modelled	96.8	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
27	d1wbha1	Alignment	not modelled	96.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
28	d1wa3a1	Alignment	not modelled	96.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: structural genomics, unknown function

29	c3labA	Alignment	not modelled	96.6	22	Chain: A: PDB Molecule: putative kdp _g (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdp _g (2-keto-3-deoxy-6-2-phosphogluconate) aldolase from oleispira antarctica
30	c2v82A	Alignment	not modelled	96.6	20	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdp _{gal} complexed to kdp _{gal}
31	dlp4ca	Alignment	not modelled	96.6	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
32	c2e77B	Alignment	not modelled	96.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
33	dlvrda1	Alignment	not modelled	96.4	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
34	dlofd2	Alignment	not modelled	96.4	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
35	dleepa	Alignment	not modelled	96.4	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
36	clme9A	Alignment	not modelled	96.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (im _{pdh}) from2 tritrichomonas foetus with im _p bound
37	c2rduA	Alignment	not modelled	96.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
38	clvrda	Alignment	not modelled	96.1	17	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
39	dlzfja1	Alignment	not modelled	96.0	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
40	dljr1a1	Alignment	not modelled	96.0	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
41	clx1oC	Alignment	not modelled	96.0	17	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
42	dlvhca	Alignment	not modelled	95.9	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
43	c3igsB	Alignment	not modelled	95.9	15	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
44	dlxi3a	Alignment	not modelled	95.9	19	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
45	c2yw3E	Alignment	not modelled	95.7	24	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
46	c2jbmA	Alignment	not modelled	95.6	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
47	c3inpA	Alignment	not modelled	95.6	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.
48	c2gjlA	Alignment	not modelled	95.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
49	cl04uA	Alignment	not modelled	95.5	16	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
50	dl04ua1	Alignment	not modelled	95.5	13	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
51	c2b7pA	Alignment	not modelled	95.5	16	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
52	cljcnA	Alignment	not modelled	95.4	15	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
53	c2p10D_	Alignment	not modelled	95.4	19 PDB header: hydrolase Chain: D: PDB Molecule: ml19387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
54	d1mxsa_	Alignment	not modelled	95.4	15 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
55	d2flia1	Alignment	not modelled	95.3	12 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
56	d1y0ea_	Alignment	not modelled	95.3	8 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
57	d1pvna1	Alignment	not modelled	95.2	13 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
58	d1juba_	Alignment	not modelled	95.2	13 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	c2vdcF_	Alignment	not modelled	95.1	20 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.
60	c3r2gA_	Alignment	not modelled	95.1	17 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
61	c3paiA_	Alignment	not modelled	95.1	17 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
62	d1yxva1	Alignment	not modelled	95.1	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
63	c3oa3A_	Alignment	not modelled	95.0	19 PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
64	c3khjE_	Alignment	not modelled	94.8	15 PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
65	d1mzha_	Alignment	not modelled	94.8	21 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
66	d1rpxa_	Alignment	not modelled	94.7	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
67	c1lm1A_	Alignment	not modelled	94.7	21 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
68	d1tqja_	Alignment	not modelled	94.6	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
69	d1xcfa_	Alignment	not modelled	94.4	17 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
70	c1qpoA_	Alignment	not modelled	94.4	13 PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
71	d2tpsa_	Alignment	not modelled	94.2	21 Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
72	c3ng3A_	Alignment	not modelled	94.0	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
73	c2cdh1_	Alignment	not modelled	94.0	15 PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
74	d1rd5a_	Alignment	not modelled	93.9	11 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	d1vc4a_	Alignment	not modelled	93.7	20 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
76	c2cu0B_	Alignment	not modelled	93.6	13 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3

77	c3l0gD_	 Alignment	not modelled	93.3	14	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrllichia chaffeensis at 2.05a resolution
78	d1qopa_	 Alignment	not modelled	92.9	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
79	d2cu0a1	 Alignment	not modelled	92.9	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
80	c1qapA_	 Alignment	not modelled	92.7	12	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
81	c2a7rD_	 Alignment	not modelled	92.6	14	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
82	c1ypfB_	 Alignment	not modelled	92.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
83	d1d3ga_	 Alignment	not modelled	92.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
84	d1vcfa1	 Alignment	not modelled	92.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	d1qpoa1	 Alignment	not modelled	92.4	12	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
86	c2zrvC_	 Alignment	not modelled	92.4	17	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fm.
87	d1jcna1	 Alignment	not modelled	92.3	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
88	c3o63B_	 Alignment	not modelled	92.2	16	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
89	c2c3zA_	 Alignment	not modelled	92.1	11	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
90	c3ct7E_	 Alignment	not modelled	92.1	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
91	c3bw2A_	 Alignment	not modelled	92.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
92	d1o0ya_	 Alignment	not modelled	91.8	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	d1qapa1	 Alignment	not modelled	91.4	11	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
94	c3ngjC_	 Alignment	not modelled	91.0	20	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
95	c3bo9B_	 Alignment	not modelled	90.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkane dioxygenase; PDBTitle: crystal structure of putative nitroalkane dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
96	c2z6jB_	 Alignment	not modelled	89.8	13	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
97	c2qr6A_	 Alignment	not modelled	89.3	12	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
98	d1a53a_	 Alignment	not modelled	89.1	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
99	d1piia2	 Alignment	not modelled	88.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
100	c2oz3F_	 Alignment	not modelled	88.7	14	PDB header: lyase Chain: F: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
101	d1pv8a_	Alignment	not modelled	88.7	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen

						synthase)
102	d1h1ya_	Alignment	not modelled	87.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
103	c2fptA_	Alignment	not modelled	86.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
104	d1vcva1	Alignment	not modelled	84.9	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
105	d1znna1	Alignment	not modelled	83.6	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
106	c1znnF_	Alignment	not modelled	83.5	17	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
107	d1tqxa_	Alignment	not modelled	80.8	7	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
108	c3noyA_	Alignment	not modelled	79.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
109	d1ub3a_	Alignment	not modelled	79.8	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
110	d2p10a1	Alignment	not modelled	79.0	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MII9387-like
111	d1w0ma_	Alignment	not modelled	77.7	16	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
112	c3exsB_	Alignment	not modelled	76.1	15	PDB header: lyase Chain: B: PDB Molecule: rmpp (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
113	c3b0vD_	Alignment	not modelled	75.3	16	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
114	c3tfxB_	Alignment	not modelled	75.2	15	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
115	c2bdqA_	Alignment	not modelled	74.7	12	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 structural genomics target sar15.
116	c1vadD_	Alignment	not modelled	73.4	17	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
117	c3cxoA_	Alignment	not modelled	73.2	15	PDB header: lyase Chain: A: PDB Molecule: putative galactonate dehydratase; PDBTitle: crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate
118	d1nu5a1	Alignment	not modelled	72.3	19	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
119	c3oixA_	Alignment	not modelled	72.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
120	c3px5A_	Alignment	not modelled	72.2	12	PDB header: metal binding protein Chain: A: PDB Molecule: enzyme of enolase superfamily; PDBTitle: structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure