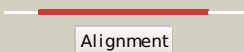
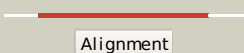
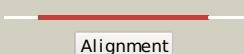
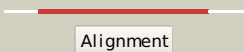
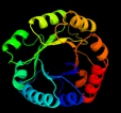
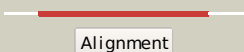
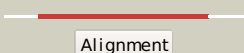
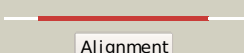
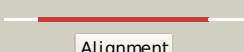
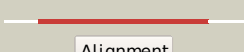
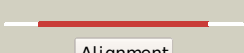
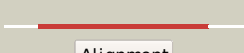


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nm3D_	 Alignment		100.0	28	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
2	d2tpsa_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
3	c3o63B_	 Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
4	d1xi3a_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
5	c1yadD_	 Alignment		100.0	23	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
6	c3ceuA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: thiamine phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
7	c2v82A_	 Alignment		99.9	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
8	d1wa3a1	 Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	d1mxsa_	 Alignment		99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
10	c3labA_	 Alignment		99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdp (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdp (2-keto-3-deoxy-6-2-phosphogluconate) aldolase from oleispira antarctica
11	c2yw3E_	 Alignment		99.9	16	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 thb1

12	dlvhca_	Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
13	dlwbha1	Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
14	dlvc4a_	Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
15	c3qc3B_	Alignment		99.9	16	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
16	dl1tqa_	Alignment		99.9	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
17	c3qjaA_	Alignment		99.9	19	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
18	dla53a_	Alignment		99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
19	dlpiia2	Alignment		99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
20	dlwv2a_	Alignment		99.8	13	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
21	c3inpA_	Alignment	not modelled	99.8	12	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.
22	d2flia1	Alignment	not modelled	99.8	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
23	dli4na_	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
24	dlrd5a_	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
25	dlh1ya_	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
26	c2c3zA_	Alignment	not modelled	99.8	15	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
27	dl1tja_	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
28	dlrpxa_	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
29	dlj5ta_	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

					Family: Tryptophan biosynthesis enzymes
30	dlqopa_	Alignment	not modelled	99.7	16 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
31	dlyxya1	Alignment	not modelled	99.7	15 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
32	c3igsB_	Alignment	not modelled	99.7	17 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
33	dly0ea_	Alignment	not modelled	99.7	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
34	c1piiA_	Alignment	not modelled	99.7	13 PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'-phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
35	dlo4ua1	Alignment	not modelled	99.7	16 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
36	c3q58A_	Alignment	not modelled	99.6	15 PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
37	c3f4wA_	Alignment	not modelled	99.6	19 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
38	d1xcfa_	Alignment	not modelled	99.6	17 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
39	c3ajxA_	Alignment	not modelled	99.6	20 PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
40	d1h5ya_	Alignment	not modelled	99.6	13 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
41	d1q6oa_	Alignment	not modelled	99.5	13 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
42	d1ka9f_	Alignment	not modelled	99.5	17 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
43	d1qpoa1	Alignment	not modelled	99.5	24 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
44	c3navB_	Alignment	not modelled	99.5	16 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
45	c3exsB_	Alignment	not modelled	99.4	12 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
46	d1w0ma_	Alignment	not modelled	99.4	19 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
47	d1hg3a_	Alignment	not modelled	99.4	17 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
48	d1thfd_	Alignment	not modelled	99.4	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
49	d1qapa1	Alignment	not modelled	99.4	17 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
50	d1geqa_	Alignment	not modelled	99.3	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
51	c1x1oC_	Alignment	not modelled	99.3	31 PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
52	d1znna1	Alignment	not modelled	99.3	13 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
53	c2b7pA_	Alignment	not modelled	99.3	23 PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
54	c1znnF_	Alignment	not modelled	99.3	13 PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase;

						PDBTitle: structure of the synthase subunit of plp synthase
55	c2h6rG	Alignment	not modelled	99.3	18	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
56	c2ekcA	Alignment	not modelled	99.3	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
57	c2y85D	Alignment	not modelled	99.3	19	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
58	c3jr2D	Alignment	not modelled	99.3	9	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
59	c2jbmA	Alignment	not modelled	99.3	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
60	c3ct7E	Alignment	not modelled	99.2	16	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
61	c3gndC	Alignment	not modelled	99.2	15	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
62	c3thaB	Alignment	not modelled	99.2	15	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
63	c2w6rA	Alignment	not modelled	99.2	14	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
64	d1xm3a	Alignment	not modelled	99.2	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
65	c1o4uA	Alignment	not modelled	99.2	15	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
66	c2z6jB	Alignment	not modelled	99.2	15	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
67	c2qjhH	Alignment	not modelled	99.1	18	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
68	c2htmB	Alignment	not modelled	99.1	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
69	d1ojxa	Alignment	not modelled	99.1	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
70	c3l0gD	Alignment	not modelled	99.0	13	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlchia chaffeensis at 2.05a resolution
71	c3bo9B	Alignment	not modelled	99.0	10	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
72	c2gjlA	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
73	c1qapA	Alignment	not modelled	99.0	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
74	c3tqvA	Alignment	not modelled	99.0	20	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
75	d1ujpa	Alignment	not modelled	99.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
76	c3bw2A	Alignment	not modelled	99.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
77	d2czda1	Alignment	not modelled	99.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
78	c3pajA	Alignment	not modelled	98.9	22	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
79	dljvna1	Alignment	not modelled	98.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
80	c1qpoA	Alignment	not modelled	98.9	26	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
81	c2bdqA	Alignment	not modelled	98.9	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 strucural genomics target sar15.
82	c1jvnB	Alignment	not modelled	98.8	14	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
83	d1vzwa1	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
84	c3cu2A	Alignment	not modelled	98.8	13	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
85	c3ru6C	Alignment	not modelled	98.8	13	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
86	c2h90A	Alignment	not modelled	98.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
87	d1vqta1	Alignment	not modelled	98.8	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
88	c3khjE	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
89	d1zfja1	Alignment	not modelled	98.7	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
90	c1djnB	Alignment	not modelled	98.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylphilus methylotrophus (sp.3 w3a1)
91	d1ps9a1	Alignment	not modelled	98.7	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c1ps9A	Alignment	not modelled	98.7	17	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
93	c1zfjA	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
94	c2cdh1	Alignment	not modelled	98.6	14	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
95	c3kruC	Alignment	not modelled	98.5	15	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
96	c3r2gA	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
97	d1qo2a	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
98	d1eepa	Alignment	not modelled	98.4	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
99	d1vrda1	Alignment	not modelled	98.4	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
100	d1djqa1	Alignment	not modelled	98.4	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
101	d1dvja	Alignment	not modelled	98.4	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
102	c3tdmD	Alignment	not modelled	98.4	18	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold

102	c3tmd_	Alignment	not modelled	98.4	10	symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
103	c3hf3A_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
104	c3tr2A_	Alignment	not modelled	98.4	12	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii
105	c1jcnA_	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
106	c3tfxB_	Alignment	not modelled	98.3	20	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
107	d1km4a_	Alignment	not modelled	98.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
108	d1jr1a1	Alignment	not modelled	98.3	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
109	c3ldvB_	Alignment	not modelled	98.3	15	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.77 angstrom resolution crystal structure of orotidine 5'-2 phosphate decarboxylase from vibrio cholerae o1 biovar3 eltor str. n16961
110	d1pvna1	Alignment	not modelled	98.3	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
111	d1viza_	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	d1jcna1	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
113	d1twda_	Alignment	not modelled	98.2	16	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
114	d1v5xa_	Alignment	not modelled	98.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
115	d1to3a_	Alignment	not modelled	98.2	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
116	d1gtea2	Alignment	not modelled	98.2	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
117	d1z41a1	Alignment	not modelled	98.2	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
118	c1vrda_	Alignment	not modelled	98.2	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
119	d1nsja_	Alignment	not modelled	98.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
120	c3gr7A_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form