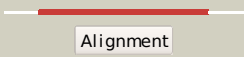
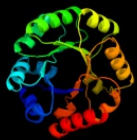
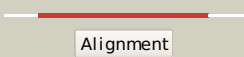

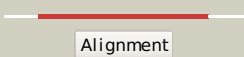

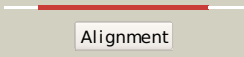

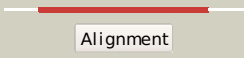
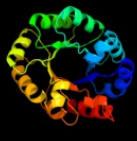
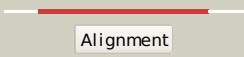

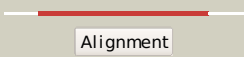

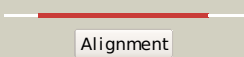

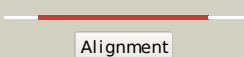

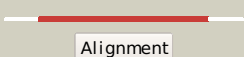

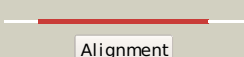



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q6oa_	 Alignment		100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
2	c3jr2D_	 Alignment		100.0	47	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbl; 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
3	c3exsB_	 Alignment		100.0	45	PDB header: lyase Chain: B: PDB Molecule: rmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
4	c3ajxA_	 Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
5	c3f4wA_	 Alignment		100.0	28	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
6	c3ru6C_	 Alignment		100.0	18	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
7	c3tr2A_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii
8	d1eixa_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
9	d1dbta_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
10	c3tfxB_	 Alignment		100.0	18	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
11	d1km4a_	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase

12	c3ldvB_	Alignment		100.0	17	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
13	d1dvja_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
14	c2yytA_	Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
15	c2qcnA_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: uridine 5'-monophosphate synthase; PDBTitle: covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump
16	c3bvjA_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: uridine 5'-monophosphate synthase; PDBTitle: crystal structure of human orotidine 5'-monophosphate decarboxylase2 complexed with xmp
17	d2czda1	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
18	d1dqwa_	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
19	c3qw3B_	Alignment		100.0	19	PDB header: transferase, lyase Chain: B: PDB Molecule: orotidine-5-phosphate decarboxylase/orotate PDBTitle: structure of leishmania donovani omp decarboxylase
20	d1vqta1	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
21	c3ct7E_	Alignment	not modelled	100.0	17	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
22	d1losc_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
23	c3qc3B_	Alignment	not modelled	100.0	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
24	d1tqxa_	Alignment	not modelled	100.0	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
25	d1h1ya_	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
26	c3cu2A_	Alignment	not modelled	100.0	14	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
27	d1qopa_	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
28	c3qw4B_	Alignment	not modelled	100.0	22	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
29	c3innA_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase;

29	c3mpa_	Alignment	not modelled	99.9	20	PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
30	d1rpxa_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
31	c3thaB_	Alignment	not modelled	99.9	11	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
32	c3navB_	Alignment	not modelled	99.9	18	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
33	d2flia1	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
34	c3l52A_	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of putative orotidine 5'-phosphate2 decarboxylase from streptomyces avermitilis ma-4680
35	d1rd5a_	Alignment	not modelled	99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
36	d2q8za1	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
37	d2ffca1	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
38	c2ekcA_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
39	c3r89A_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
40	d1ujpa_	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
41	d1geqa_	Alignment	not modelled	99.9	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
42	c2fdsA_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine-monophosphate-decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-2 monophosphate decarboxylase (ortholog of plasmodium3 falciparum pf10_0225)
43	d2fdsa1	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
44	d1tqja_	Alignment	not modelled	99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
45	d1xcfa_	Alignment	not modelled	99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	c2v82A_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
47	c3gndC_	Alignment	not modelled	99.7	13	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrif; PDBTitle: crystal structure of e. coli lsrif in complex with ribulose-5-phosphate
48	d1wbha1	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
49	d1j5ta_	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
50	d1ojxa_	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
51	d1wa3a1	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
52	d1piia2	Alignment	not modelled	99.7	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
53	c3igsB_	Alignment	not modelled	99.7	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
54	d2tpsa_	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
55	d1vhca_	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

56	d1xi3a_	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
57	c3qjaA_	Alignment	not modelled	99.7	15	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	c3q58A_	Alignment	not modelled	99.7	17	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
59	c1yadD_	Alignment	not modelled	99.7	13	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
60	c2c3zA_	Alignment	not modelled	99.7	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
61	d1i4na_	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
62	d1a53a_	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
63	c2qjhH_	Alignment	not modelled	99.6	11	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
64	d1vc4a_	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
65	c3labA_	Alignment	not modelled	99.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpd (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdpd (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
66	d1mxsa_	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	d1y0ea_	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
68	c3o63B_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
69	d1yxya1	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
70	d1w0ma_	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
71	c3nm3D_	Alignment	not modelled	99.5	13	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
72	d1wv2a_	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
73	d1hg3a_	Alignment	not modelled	99.5	10	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
74	c2yw3E_	Alignment	not modelled	99.5	20	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
75	c1piiA_	Alignment	not modelled	99.4	12	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
76	c2htmB_	Alignment	not modelled	99.4	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
77	d2f6ua1	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	d1viza_	Alignment	not modelled	99.3	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
79	d1xm3a_	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
						Fold: TIM beta/alpha-barrel

80	dlh5ya_	Alignment	not modelled	99.3	15	Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
81	d1ka9f_	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
82	d1thfd_	Alignment	not modelled	99.2	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
83	c2bdqA_	Alignment	not modelled	99.2	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.
84	c2h6rG_	Alignment	not modelled	99.2	14	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
85	d1znnal	Alignment	not modelled	99.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
86	c1znnF_	Alignment	not modelled	99.1	14	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
87	c2y85D_	Alignment	not modelled	99.1	12	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
88	c3ceuA_	Alignment	not modelled	99.1	11	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
89	d1zfja1	Alignment	not modelled	99.0	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
90	d1o4ua1	Alignment	not modelled	98.9	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
91	c2z6jB_	Alignment	not modelled	98.9	14	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
92	c2gjlA_	Alignment	not modelled	98.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
93	d1vzwa1	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
94	c2cdh1_	Alignment	not modelled	98.8	17	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
95	d1vrda1	Alignment	not modelled	98.8	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
96	c3bo9B_	Alignment	not modelled	98.8	14	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
97	c1zfjA_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
98	c3khjE_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
99	c3ffsC_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
100	d1eepa_	Alignment	not modelled	98.7	12	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
101	d1p0ka_	Alignment	not modelled	98.7	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
102	c3r2gA_	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
103	d1gtea2	Alignment	not modelled	98.6	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	d1jcna1	Alignment	not modelled	98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
105	c1jcna_	Alignment	not modelled	98.6	14	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	dlqpoa1	Alignment	not modelled	98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
107	dlqapa1	Alignment	not modelled	98.5	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
108	dljr1a1	Alignment	not modelled	98.5	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
109	c3gr7A_	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
110	c3ivuB_	Alignment	not modelled	98.5	13	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
111	dlgoxa_	Alignment	not modelled	98.5	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	c2a7rD_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
113	clvrda_	Alignment	not modelled	98.5	14	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
114	c2zyfa_	Alignment	not modelled	98.5	10	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
115	dltb3a1	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
116	c2zrvC_	Alignment	not modelled	98.5	13	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.
117	c2w6rA_	Alignment	not modelled	98.5	12	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
118	dlto3a_	Alignment	not modelled	98.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
119	clypfB_	Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
120	dlz41a1	Alignment	not modelled	98.4	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases