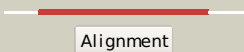
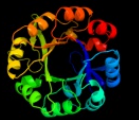
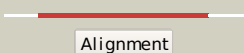

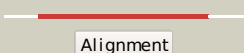

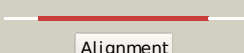



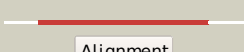

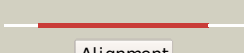

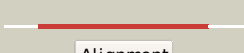


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlqo2a_</a>	 Alignment		100.0	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
2	<a href="#">dljvna1</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
3	<a href="#">cljvnB_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
4	<a href="#">dlh5ya_</a>	 Alignment		100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
5	<a href="#">c2y85D_</a>	 Alignment		100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
6	<a href="#">dlthfd_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
7	<a href="#">dlka9f_</a>	 Alignment		100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
8	<a href="#">c2agkA_</a>	 Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) <b>PDBTitle:</b> structure of s. cerevisiae his6 protein
9	<a href="#">c2w6rA_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit <b>PDBTitle:</b> crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
10	<a href="#">dlvzwa1</a>	 Alignment		100.0	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
11	<a href="#">clznnF_</a>	 Alignment		100.0	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> plp synthase; <b>PDBTitle:</b> structure of the synthase subunit of plp synthase

12	<a href="#">dlznnal</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> PdxS-like
13	<a href="#">c3qjaA</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
14	<a href="#">dlvc4a</a>	Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
15	<a href="#">dla53a</a>	Alignment		99.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
16	<a href="#">c2c3zA</a>	Alignment		99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
17	<a href="#">c1piiA</a>	Alignment		99.9	15	<b>PDB header:</b> bifunctional(isomerase and synthase) <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
18	<a href="#">dli4na</a>	Alignment		99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
19	<a href="#">d1pii2</a>	Alignment		99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
20	<a href="#">d1j5ta</a>	Alignment		99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
21	<a href="#">c3igsB</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2; <b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
22	<a href="#">c3q58A</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
23	<a href="#">c3tdmD</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> computationally designed two-fold symmetric tim-barrel <b>PDBTitle:</b> computationally designed tim-barrel protein, halfllr
24	<a href="#">d1tqja</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
25	<a href="#">d1y0ea</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
26	<a href="#">d1h1ya</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
27	<a href="#">d2flia1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
28	<a href="#">d1yxa1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like

29	<a href="#">dlrpxa_</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
30	<a href="#">c3inpA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
31	<a href="#">c3qc3B_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
32	<a href="#">dlqopa_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
33	<a href="#">dlrd5a_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
34	<a href="#">dlxm3a_</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
35	<a href="#">dltxa_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
36	<a href="#">c3ct7E_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
37	<a href="#">c3navB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
38	<a href="#">dlwbha1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
39	<a href="#">dlxcfa_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
40	<a href="#">dlgeqa_</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
41	<a href="#">dlwa3a1</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
42	<a href="#">c3cwoX_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> de novo protein <b>Chain:</b> X: <b>PDB Molecule:</b> beta/alpha-barrel protein based on 1thf and 1tny; <b>PDBTitle:</b> a beta/alpha-barrel built by the combination of fragments2 from different folds
43	<a href="#">c3cu2A_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose-5-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
44	<a href="#">c2ekcA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
45	<a href="#">c3thaB_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
46	<a href="#">c2v82A_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
47	<a href="#">dlvhca_</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
48	<a href="#">dlw0ma_</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
49	<a href="#">dlmxsa_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
50	<a href="#">dlviza_</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
51	<a href="#">d2tpsa_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
52	<a href="#">dlhg3a_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
53	<a href="#">clzfjA_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
54	<a href="#">dlxi3a_</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
55	<a href="#">dlujpa_</a>	Alianment	not modelled	99.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel

					<b>Family:</b> Tryptophan biosynthesis enzymes
56	<a href="#">c3labA_</a>	Alignment	not modelled	99.3	20 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpG (2-keto-3-deoxy-6-phosphogluconate) <b>PDBTitle:</b> crystal structure of a putative kdpG (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
57	<a href="#">c3gr7A_</a>	Alignment	not modelled	99.3	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
58	<a href="#">c3f4wA_</a>	Alignment	not modelled	99.3	14 <b>PDB header:</b> synthase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase; <b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
59	<a href="#">c2h6rG_</a>	Alignment	not modelled	99.3	17 <b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
60	<a href="#">d2f6ua1</a>	Alignment	not modelled	99.3	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
61	<a href="#">c3b0vD_</a>	Alignment	not modelled	99.2	20 <b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
62	<a href="#">c3o63B_</a>	Alignment	not modelled	99.2	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiamine-phosphate pyrophosphorylase; <b>PDBTitle:</b> crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
63	<a href="#">d1vhna_</a>	Alignment	not modelled	99.2	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
64	<a href="#">c2htmB_</a>	Alignment	not modelled	99.2	17 <b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole biosynthesis protein thig; <b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8
65	<a href="#">c3ajxA_</a>	Alignment	not modelled	99.2	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hexulose-6-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3-hexulose-6-phosphate synthase
66	<a href="#">c2zrvC_</a>	Alignment	not modelled	99.2	17 <b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase; <b>PDBTitle:</b> crystal structure of sulfobolus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmN.
67	<a href="#">d1wv2a_</a>	Alignment	not modelled	99.1	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
68	<a href="#">d1jcna1</a>	Alignment	not modelled	99.1	26 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
69	<a href="#">c3khjE_</a>	Alignment	not modelled	99.1	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
70	<a href="#">c3ffsC_</a>	Alignment	not modelled	99.1	27 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
71	<a href="#">c1jcna_</a>	Alignment	not modelled	99.1	21 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase i; <b>PDBTitle:</b> binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
72	<a href="#">d1vrda1</a>	Alignment	not modelled	99.1	27 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
73	<a href="#">c2yw3E_</a>	Alignment	not modelled	99.1	24 <b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
74	<a href="#">d1eepa_</a>	Alignment	not modelled	99.1	20 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
75	<a href="#">c2z6jB_</a>	Alignment	not modelled	99.1	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acp reductase ii; <b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
76	<a href="#">c3exsB_</a>	Alignment	not modelled	99.1	14 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rmpp (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
77	<a href="#">c1yadD_</a>	Alignment	not modelled	99.1	19 <b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
78	<a href="#">c3r2gA_</a>	Alignment	not modelled	99.1	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine 5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
79	<a href="#">c3hf3A_</a>	Alignment	not modelled	99.1	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01

80	<a href="#">c2qr6A_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imp dehydrogenase/gmp reductase; <b>PDBTitle:</b> crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
81	<a href="#">dljr1a1</a>	Alignment	not modelled	99.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
82	<a href="#">clvrdA_</a>	Alignment	not modelled	99.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
83	<a href="#">dltb3a1</a>	Alignment	not modelled	99.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
84	<a href="#">dlzfja1</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
85	<a href="#">dlz41a1</a>	Alignment	not modelled	99.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
86	<a href="#">dlgoxa_</a>	Alignment	not modelled	99.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
87	<a href="#">dlp4ca_</a>	Alignment	not modelled	99.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
88	<a href="#">dlq6oa_</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
89	<a href="#">dlkbia1</a>	Alignment	not modelled	99.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
90	<a href="#">c2a7nA_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> il(+)-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
91	<a href="#">c2gj1A_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1024; <b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase
92	<a href="#">dlpvna1</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
93	<a href="#">c2bdqA_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 structural genomics target sar15.
94	<a href="#">c3bo9B_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroalkan dioxygenase; <b>PDBTitle:</b> crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
95	<a href="#">c2h90A_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
96	<a href="#">clme9A_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
97	<a href="#">dltwda_</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> CutC-like <b>Family:</b> CutC-like
98	<a href="#">dlp0ka_</a>	Alignment	not modelled	98.9	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
99	<a href="#">dlgtea2</a>	Alignment	not modelled	98.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
100	<a href="#">c2cdh1_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> enoyl reductase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
101	<a href="#">c2a7rD_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> gmp reductase 2; <b>PDBTitle:</b> crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
102	<a href="#">dltv5a1</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
103	<a href="#">cltv5A_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotate dehydrogenase homolog, mitochondrial; <b>PDBTitle:</b> plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
104	<a href="#">dlps9a1</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
						<b>PDB header:</b> oxidoreductase

105	<a href="#">c3bw2A_</a>	Alignment	not modelled	98.9	20	<b>Chain:</b> A: <b>PDB Molecule:</b> 2-nitropropane dioxygenase; <b>PDBTitle:</b> crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
106	<a href="#">c3jr2D_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> hexulose-6-phosphate synthase sgbh; <b>PDBTitle:</b> x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
107	<a href="#">c1ps9A_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
108	<a href="#">c2cu0B_</a>	Alignment	not modelled	98.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
109	<a href="#">c2e77B_</a>	Alignment	not modelled	98.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate oxidase; <b>PDBTitle:</b> crystal structure of l-lactate oxidase with pyruvate complex
110	<a href="#">c1ypfB_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp reductase; <b>PDBTitle:</b> crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
111	<a href="#">c2rduA_</a>	Alignment	not modelled	98.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyacid oxidase 1; <b>PDBTitle:</b> crystal structure of human glycolate oxidase in complex with2 glyoxylate
112	<a href="#">c1kbiB_</a>	Alignment	not modelled	98.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b2; <b>PDBTitle:</b> crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
113	<a href="#">c3ru6C_</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
114	<a href="#">c1djnB_</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
115	<a href="#">d1d3ga_</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
116	<a href="#">d1vyra_</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
117	<a href="#">c3iwpK_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> copper homeostasis protein cutc homolog; <b>PDBTitle:</b> crystal structure of human copper homeostasis protein cutc
118	<a href="#">c3kruC_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
119	<a href="#">d2cu0a1</a>	Alignment	not modelled	98.8	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
120	<a href="#">d2b4ga1</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases