Phyre2

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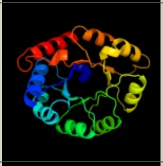
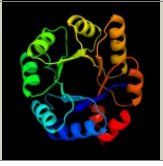
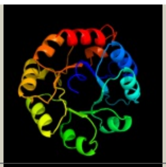
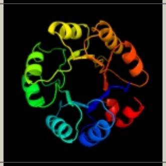
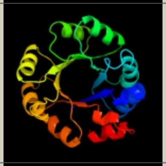
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v82A_	Alignment		100.0	99	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
2	d1vhca_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
3	d1mxsa_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
4	d1wbha1	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
5	d1wa3a1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
6	c3labA_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
7	c2yw3E_	Alignment		100.0	27	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
8	c1yadD_	Alignment		99.9	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
9	c3o63B_	Alignment		99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
10	d2tpsa_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
11	d1vc4a_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes

12	d1xi3a_	Alignment		99.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
13	c3nm3D_	Alignment		99.9	15	**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 biosyhthesis of eukaryotes
14	d1a53a_	Alignment		99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
15	c2c3zA_	Alignment		99.9	16	**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
16	d1piia2	Alignment		99.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
17	c3qjaA_	Alignment		99.9	21	**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	d1i4na_	Alignment		99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
19	c1piiA_	Alignment		99.9	14	**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
20	d1xcfa_	Alignment		99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
21	d1j5ta_	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	c3ceuA_	Alignment	not modelled	99.8	16	**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
23	c3q58A_	Alignment	not modelled	99.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
24	c3igsB_	Alignment	not modelled	99.8	21	**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
25	d1rd5a_	Alignment	not modelled	99.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
26	d1yxya1	Alignment	not modelled	99.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
27	c3qc3B_	Alignment	not modelled	99.8	14	**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
28	d2flia1	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family:D-ribulose-5-phosphate 3-epimerase
29	d1h1ya_	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
30	c3inpA_	Alignment	not modelled	99.8	17	**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.
31	d1qopa_	Alignment	not modelled	99.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
32	d1rpxa_	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
33	d1tqja_	Alignment	not modelled	99.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
34	c3exsB_	Alignment	not modelled	99.7	13	**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
35	c3f4wA_	Alignment	not modelled	99.7	18	**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
36	d1tqxa_	Alignment	not modelled	99.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
37	d1y0ea_	Alignment	not modelled	99.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
38	d1q6oa_	Alignment	not modelled	99.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
39	d1geqa_	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
40	c3navB_	Alignment	not modelled	99.7	21	**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
41	c1gthD_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
42	d1znna1	Alignment	not modelled	99.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
43	c1znnF_	Alignment	not modelled	99.6	19	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
44	c2ekcA_	Alignment	not modelled	99.6	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
45	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
46	c3oixA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
47	d1d3ga_	Alignment	not modelled	99.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
48	c2htmB_	Alignment	not modelled	99.6	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
49	d1h5ya_	Alignment	not modelled	99.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
50	c3jr2D_	Alignment	not modelled	99.6	13	**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
51	d1ka9f_	Alignment	not modelled	99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
52	c2z6jB_	Alignment	not modelled	99.6	17	**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
53	c3ct7E_	Alignment	not modelled	99.6	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
54	c3bo9B_	Alignment	not modelled	99.6	16	**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

55	c2cdh1_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
56	d1wv2a_	Alignment	not modelled	99.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
57	d1juba_	Alignment	not modelled	99.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
58	d1thfd_	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
59	c2fptA_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial; **PDBTitle:** dual binding mode of a novel series of dhodh inhibitors
60	c2gjlA_	Alignment	not modelled	99.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
61	d1uuma_	Alignment	not modelled	99.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
62	d1tv5a1	Alignment	not modelled	99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
63	c1tv5A_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
64	d1w0ma_	Alignment	not modelled	99.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
65	d1vzwa1	Alignment	not modelled	99.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
66	c2e77B_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
67	d1gtea2	Alignment	not modelled	99.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
68	c3thaB_	Alignment	not modelled	99.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
69	d1goxa_	Alignment	not modelled	99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
70	c3bw2A_	Alignment	not modelled	99.4	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
71	d1kbia1	Alignment	not modelled	99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
72	c2y85D_	Alignment	not modelled	99.4	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
73	d1vhna_	Alignment	not modelled	99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
74	d1tb3a1	Alignment	not modelled	99.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
75	d1o4ua1	Alignment	not modelled	99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
76	c3khjE_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
77	d1hg3a_	Alignment	not modelled	99.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
78	c2rduA_	Alignment	not modelled	99.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
79	d2b4ga1	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
80	d1xm3a_	Alignment	not modelled	99.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
81	c2a7pA	Alignment	not modelled	99.4	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase;

81	c2a7nA_	Alignment	not modelled	99.4	10	**PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
82	d2czda1	Alignment	not modelled	99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
83	d1ep3a_	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
84	c3ffsC_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
85	c2h6rG_	Alignment	not modelled	99.4	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
86	d1p4ca_	Alignment	not modelled	99.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
87	c3b0vD_	Alignment	not modelled	99.4	19	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
88	d1f76a_	Alignment	not modelled	99.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
89	d1zfja1	Alignment	not modelled	99.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
90	c3r2gA_	Alignment	not modelled	99.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
91	c1kbiB_	Alignment	not modelled	99.3	13	**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
92	c3cu2A_	Alignment	not modelled	99.3	11	**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
93	c3gyeA_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, putative; **PDBTitle:** didydroorotate dehydrogenase from leishmania major
94	c1zfjA_	Alignment	not modelled	99.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
95	d1qpoa1	Alignment	not modelled	99.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
96	d1pvna1	Alignment	not modelled	99.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
97	c2w6rA_	Alignment	not modelled	99.3	15	**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
98	d1dvja_	Alignment	not modelled	99.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
99	c2zrvC_	Alignment	not modelled	99.2	16	**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.
100	d1vrda1	Alignment	not modelled	99.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
101	d1qapa1	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
102	c1vrdA_	Alignment	not modelled	99.2	22	**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
103	c1me9A_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
104	d1jcna1	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
105	d1eepa_	Alignment	not modelled	99.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)

106	d1ujpa_	Alignment	not modelled	99.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
107	c2a7rD_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
108	c2qr6A_	Alignment	not modelled	99.2	18	**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
109	d1jr1a1	Alignment	not modelled	99.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
110	c1ypfB_	Alignment	not modelled	99.1	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
111	d1vcfa1	Alignment	not modelled	99.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
112	c1jcnA_	Alignment	not modelled	99.1	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
113	d1p0ka_	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
114	c2b7pA_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
115	c2jbmA_	Alignment	not modelled	99.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
116	c2zbtB_	Alignment	not modelled	99.1	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
117	c1x1oC_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
118	c2nv2U_	Alignment	not modelled	99.1	21	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
119	c1o4uA_	Alignment	not modelled	99.1	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
120	c3ru6C_	Alignment	not modelled	99.0	14	**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