Phyre^2

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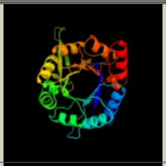
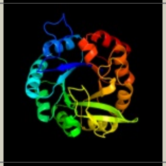
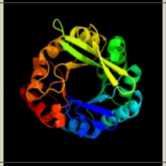
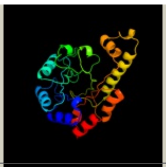
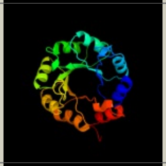
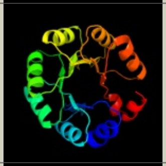
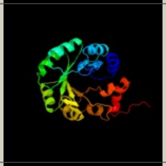
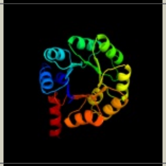
Description	P60664
Date	Thu Jan 5 12:07:01 GMT 2012
Unique Job ID	7c8c2d282f3e13fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jvna1	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
2	c1jvnB_	Alignment		100.0	33	**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
3	d1thfd_	Alignment		100.0	52	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
4	d1qo2a_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
5	d1ka9f_	Alignment		100.0	51	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
6	d1h5ya_	Alignment		100.0	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
7	c2y85D_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
8	c2w6rA_	Alignment		100.0	34	**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
9	c2agkA_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) **PDBTitle:** structure of s. cerevisiae his6 protein
10	d1vzwa1	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
11	d1znna1	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like

12	c1znnF_	Alignment		100.0	17	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
13	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
14	d1vc4a_	Alignment		99.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
15	d1a53a_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
16	c2c3zA_	Alignment		99.9	18	**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
17	c3tdmD_	Alignment		99.9	39	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
18	c1piiA_	Alignment		99.8	18	**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
19	c3igsB_	Alignment		99.8	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
20	c3q58A_	Alignment		99.8	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
21	d1piia2	Alignment	not modelled	99.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	d1i4na_	Alignment	not modelled	99.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
23	d1j5ta_	Alignment	not modelled	99.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
24	d1yxya1	Alignment	not modelled	99.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
25	d1y0ea_	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
26	d1vhna_	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
27	d1xm3a_	Alignment	not modelled	99.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
28	d1h1ya_	Alignment	not modelled	99.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
29	d2flia1	Alignment	not modelled	99.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family:D-ribulose-5-phosphate 3-epimerase
30	d1tqja_	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
31	c3cwoX_	Alignment	not modelled	99.6	37	**PDB header:**de novo protein **Chain:** X: **PDB Molecule:**beta/alpha-barrel protein based on 1thf and 1tmy; **PDBTitle:** a beta/alpha-barrel built by the combination of fragments2 from different folds
32	d1rpxa_	Alignment	not modelled	99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
33	d1qopa_	Alignment	not modelled	99.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
34	d1wbha1	Alignment	not modelled	99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	c3inpA_	Alignment	not modelled	99.5	14	**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.
36	d1rd5a_	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
37	c3b0vD_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
38	d1xcfa_	Alignment	not modelled	99.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
39	c1zfjA_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
40	c3navB_	Alignment	not modelled	99.4	17	**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	d1geqa_	Alignment	not modelled	99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
42	d1vhca_	Alignment	not modelled	99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
43	c2ekcA_	Alignment	not modelled	99.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
44	c2v82A_	Alignment	not modelled	99.4	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
45	d1wa3a1	Alignment	not modelled	99.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
46	d1mxsa_	Alignment	not modelled	99.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
47	c3thaB_	Alignment	not modelled	99.3	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
48	c3labA_	Alignment	not modelled	99.3	16	**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
49	d2tpsa_	Alignment	not modelled	99.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
50	c2z6jB_	Alignment	not modelled	99.3	19	**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
51	c3qc3B_	Alignment	not modelled	99.3	9	**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
52	d1xi3a_	Alignment	not modelled	99.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
53	d1wv2a_	Alignment	not modelled	99.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
54	c2htmB_	Alignment	not modelled	99.2	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
55	d1tqxa_	Alignment	not modelled	99.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase

56	d1zfja1	Alignment	not modelled	99.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
57	c3gr7A_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
58	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
59	c3khjE_	Alignment	not modelled	99.2	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
60	d1w0ma_	Alignment	not modelled	99.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
61	c2gjlA_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
62	d1gtea2	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
63	d1pvna1	Alignment	not modelled	99.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
64	d1hg3a_	Alignment	not modelled	99.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
65	d1ujpa_	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
66	d1jcna1	Alignment	not modelled	99.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
67	c3ffsC_	Alignment	not modelled	99.1	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
68	c3r2gA_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
69	d1jr1a1	Alignment	not modelled	99.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
70	c3o63B_	Alignment	not modelled	99.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
71	c2yw3E_	Alignment	not modelled	99.1	21	**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
72	c2qr6A_	Alignment	not modelled	99.1	19	**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
73	c2zbtB_	Alignment	not modelled	99.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
74	d1d3ga_	Alignment	not modelled	99.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
75	c2nv2U_	Alignment	not modelled	99.0	19	**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
76	c3bo9B_	Alignment	not modelled	99.0	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
77	d1vrda1	Alignment	not modelled	99.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
78	c3f4wA_	Alignment	not modelled	99.0	13	**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
79	c1jcnA_	Alignment	not modelled	99.0	20	**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
						PDB header:isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-

80	c2zrvC_	Alignment	not modelled	99.0	13	isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
81	c3ajxA_	Alignment	not modelled	99.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hexulose-6-phosphate synthase; **PDBTitle:** crystal structure of 3-hexulose-6-phosphate synthase
82	c2yzrB_	Alignment	not modelled	99.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
83	d1eepa_	Alignment	not modelled	99.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
84	d1tv5a1	Alignment	not modelled	99.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
85	c1tv5A_	Alignment	not modelled	99.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
86	c1yadD_	Alignment	not modelled	99.0	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
87	c1vrdA_	Alignment	not modelled	99.0	24	**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
88	c2cdh1_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
89	d1uuma_	Alignment	not modelled	99.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
90	d1f76a_	Alignment	not modelled	99.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
91	c2fptA_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial; **PDBTitle:** dual binding mode of a novel series of dhodh inhibitors
92	d1tb3a1	Alignment	not modelled	98.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
93	c3hf3A_	Alignment	not modelled	98.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
94	c3kruC_	Alignment	not modelled	98.9	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
95	d1ep3a_	Alignment	not modelled	98.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
96	c2h6rG_	Alignment	not modelled	98.9	21	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
97	c3femB_	Alignment	not modelled	98.9	16	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
98	c1ypfB_	Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
99	d1kbia1	Alignment	not modelled	98.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
100	c3bw2A_	Alignment	not modelled	98.9	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
101	d2f6ua1	Alignment	not modelled	98.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
102	c1kbiB_	Alignment	not modelled	98.9	21	**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
103	c2a7rD_	Alignment	not modelled	98.8	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
104	c2cu0B_	Alignment	not modelled	98.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
						PDB header:oxidoreductase

105	c2h90A_	Alignment	not modelled	98.8	12	**Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
106	c1me9A_	Alignment	not modelled	98.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
107	d1ps9a1	Alignment	not modelled	98.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
108	c1djnB_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
109	d1viza_	Alignment	not modelled	98.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
110	d1q6oa_	Alignment	not modelled	98.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
111	d1p4ca_	Alignment	not modelled	98.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
112	c1ps9A_	Alignment	not modelled	98.8	18	**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
113	d2cu0a1	Alignment	not modelled	98.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
114	c2a7nA_	Alignment	not modelled	98.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
115	d1goxa_	Alignment	not modelled	98.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
116	d1juba_	Alignment	not modelled	98.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
117	c3exsB_	Alignment	not modelled	98.7	15	**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
118	d1djqa1	Alignment	not modelled	98.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
119	c2e77B_	Alignment	not modelled	98.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
120	d1z41a1	Alignment	not modelled	98.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases