Phyre^2

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Description	P77258
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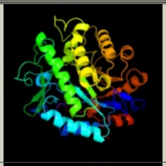
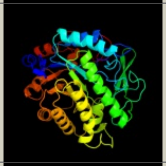
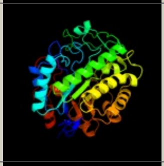
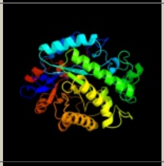
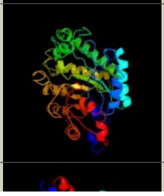
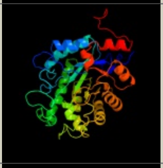
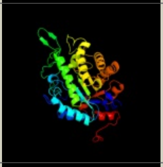
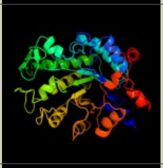
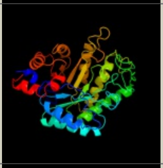
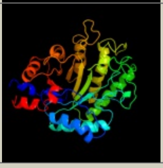
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vyra_	Alignment		100.0	88	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
2	d1gwja_	Alignment		100.0	51	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
3	c2gq8A_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
4	c3atyA_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prostaglandin f2a synthase; **PDBTitle:** crystal structure of tcoye
5	c3gkaB_	Alignment		100.0	49	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
6	d1icpa_	Alignment		100.0	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
7	d1vjia_	Alignment		100.0	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
8	d1oyaa_	Alignment		100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
9	d1q45a_	Alignment		100.0	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
10	c1ps9A_	Alignment		100.0	30	**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
11	c3k30B_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex

12	c1djnB_	Alignment		100.0	25	**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)
13	d1z41a1	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
14	c3hf3A_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
15	c2h90A_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
16	c3l5aA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
17	d1ps9a1	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
18	c3kruC_	Alignment		100.0	35	**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
19	c3gr7A_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
20	d1djqa1	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
21	d1gtea2	Alignment	not modelled	100.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
22	d1ep3a_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
23	d1vhna_	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
24	c3b0vD_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
25	d1f76a_	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
26	d2b4ga1	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
27	c3oixA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
28	d1juba_	Alignment	not modelled	99.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
29	d1d3ga_	Alignment	not modelled	99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases

						Family:FMN-linked oxidoreductases
30	c2fptA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial; **PDBTitle:** dual binding mode of a novel series of dhodh inhibitors
31	d2gl5a1	Alignment	not modelled	99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
32	c1tv5A_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
33	d1tv5a1	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
34	d1uuma_	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
35	c1gthD_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
36	c2htmB_	Alignment	not modelled	99.4	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
37	d1vrda1	Alignment	not modelled	99.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
38	c2gl5A_	Alignment	not modelled	99.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase protein; **PDBTitle:** crystal structure of putative dehydratase from salmonella thyphimurium
39	c3tdmD_	Alignment	not modelled	99.1	22	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
40	c3r2gA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
41	c3gyeA_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, putative; **PDBTitle:** didydroorotate dehydrogenase from leishmania major
42	d1jpma1	Alignment	not modelled	99.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
43	c1kbiB_	Alignment	not modelled	99.0	12	**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
44	c2z6jB_	Alignment	not modelled	99.0	22	**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
45	d1goxa_	Alignment	not modelled	99.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
46	c1zfjA_	Alignment	not modelled	99.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
47	d1tb3a1	Alignment	not modelled	99.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
48	d1pvna1	Alignment	not modelled	99.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
49	d1zfja1	Alignment	not modelled	98.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
50	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
51	d1geqa_	Alignment	not modelled	98.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
52	c1jcnA_	Alignment	not modelled	98.9	19	**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
53	d1kbia1	Alignment	not modelled	98.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
54	c2o56D_	Alignment	not modelled	98.9	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative mandelate racemase; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 salmonella typhimurium
						PDB header:oxidoreductase

55	c2a7nA_	Alignment	not modelled	98.9	19	**Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
56	d1jr1a1	Alignment	not modelled	98.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
57	c2e77B_	Alignment	not modelled	98.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
58	d1p4ca_	Alignment	not modelled	98.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
59	d1wv2a_	Alignment	not modelled	98.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
60	c2oo6A_	Alignment	not modelled	98.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative l-alanine-dl-glutamate epimerase; **PDBTitle:** crystal structure of putative l-alanine-dl-glutamate epimerase from2 burkholderia xenovorans strain lb400
61	d1p0ka_	Alignment	not modelled	98.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
62	c1vrdA_	Alignment	not modelled	98.8	21	**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
63	d1qopa_	Alignment	not modelled	98.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
64	c3ffsC_	Alignment	not modelled	98.7	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
65	c2qq6B_	Alignment	not modelled	98.7	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme- **PDBTitle:** crystal structure of mandelate racemase/muconate2 lactonizing enzyme-like protein from rubrobacter3 xylanophilus dsm 9941
66	c2ox4E_	Alignment	not modelled	98.7	14	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**putative mandelate racemase; **PDBTitle:** crystal structure of putative dehydratase from zymomonas mobilis zm4
67	c2cdh1_	Alignment	not modelled	98.7	19	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
68	d1rd5a_	Alignment	not modelled	98.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
69	d1jcna1	Alignment	not modelled	98.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
70	c2zrvC_	Alignment	not modelled	98.7	17	**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.
71	d1xcfa_	Alignment	not modelled	98.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
72	c3bo9B_	Alignment	not modelled	98.6	22	**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
73	c3khjE_	Alignment	not modelled	98.6	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
74	d1eepa_	Alignment	not modelled	98.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
75	c3rcyC_	Alignment	not modelled	98.6	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme-2 like protein from roseovarius sp. tm1035
76	d1y0ea_	Alignment	not modelled	98.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
77	c3thuC_	Alignment	not modelled	98.6	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**mandelate racemase / muconate lactonizing enzyme family **PDBTitle:** crystal structure of an enolase from sphingomonas sp. ska58 (efi2 target efi-501683) with bound mg
78	c3tjiA_	Alignment	not modelled	98.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, n-terminal **PDBTitle:** crystal structure of an enolase from enterobacter sp. 638 (efi target2 efi-501662) with bound mg

79	d1yxya1	Alignment	not modelled	98.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
80	c2qjjC_	Alignment	not modelled	98.5	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
81	d1xi3a_	Alignment	not modelled	98.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
82	c1me9A_	Alignment	not modelled	98.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
83	c2a7rD_	Alignment	not modelled	98.5	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
84	c3sqsA_	Alignment	not modelled	98.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
85	d1ka9f_	Alignment	not modelled	98.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
86	c3q58A_	Alignment	not modelled	98.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
87	c3bsmD_	Alignment	not modelled	98.4	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
88	d1rvka1	Alignment	not modelled	98.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
89	c3navB_	Alignment	not modelled	98.4	15	**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
90	c3igsB_	Alignment	not modelled	98.4	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
91	c2c3zA_	Alignment	not modelled	98.4	14	**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
92	c2gjlA_	Alignment	not modelled	98.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
93	c3t8qA_	Alignment	not modelled	98.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica
94	c2ekcA_	Alignment	not modelled	98.4	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
95	d1yeya1	Alignment	not modelled	98.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
96	d1xm3a_	Alignment	not modelled	98.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
97	c3dfhC_	Alignment	not modelled	98.4	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibrionales bacterium swat-3
98	c1jvnB_	Alignment	not modelled	98.3	19	**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
99	d1nu5a1	Alignment	not modelled	98.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
100	c3t6cB_	Alignment	not modelled	98.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative mand family dehydratase; **PDBTitle:** crystal structure of an enolase from pantoea ananatis (efi target efi-2 501676) with bound d-gluconate and mg
101	d1thfd_	Alignment	not modelled	98.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
102	d2mnra1	Alignment	not modelled	98.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like

103	d1o0ya_	Alignment	not modelled	98.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
104	c2oz8B_	Alignment	not modelled	98.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mll7089 protein; **PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti
105	c2podA_	Alignment	not modelled	98.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mandelate racemase / muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from burkholderia2 pseudomallei k96243
106	d1vcfa1	Alignment	not modelled	98.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
107	d1mzha_	Alignment	not modelled	98.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
108	c3dipA_	Alignment	not modelled	98.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of an enolase protein from the2 environmental genome shotgun sequencing of the sargasso sea
109	c3tj4B_	Alignment	not modelled	98.2	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
110	d2cu0a1	Alignment	not modelled	98.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
111	d2tpsa_	Alignment	not modelled	98.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
112	d1ub3a_	Alignment	not modelled	98.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
113	c2qgyA_	Alignment	not modelled	98.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
114	d1ofda2	Alignment	not modelled	98.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
115	c2rduA_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
116	d1vzwa1	Alignment	not modelled	98.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
117	c2qdeA_	Alignment	not modelled	98.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
118	c1f9cA_	Alignment	not modelled	98.2	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein (muconate cycloisomerase i); **PDBTitle:** crystal structure of mle d178n variant
119	c2pp1C_	Alignment	not modelled	98.2	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-talarate/galactarate dehydratase; **PDBTitle:** crystal structure of l-talarate/galactarate dehydratase from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate
120	c2pozA_	Alignment	not modelled	98.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase; **PDBTitle:** crystal structure of a putative dehydratase from mesorhizobium loti