Phyre^2

Email	l.a.kelley@imperial.ac.uk
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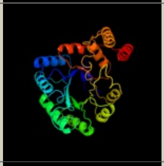
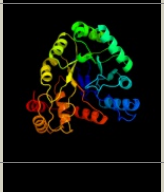
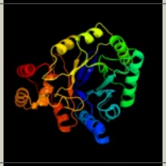
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lqaa_	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
2	d1pyfa_	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
3	c3n2tA_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
4	d1pz1a_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
5	c3erpA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
6	d3eaua1	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
7	c3lutA_	Alignment		100.0	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
8	c3n6qF_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
9	d1ur3m_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
10	d1gvea_	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
11	c1ynpA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)

12	c2bp1C_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph
13	d1q5ma_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
14	d1j96a_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	c3h7uA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
16	d1qwka_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
17	d1afsa_	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
18	c3up8B_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
19	d1frba_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
20	c3f7jB_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
21	d1mi3a_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
22	d1us0a_	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
23	d1hqta_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
24	d1s1pa_	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
25	c3h7rA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
26	c3buvB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxo-5-beta-steroid 4-dehydrogenase; **PDBTitle:** crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
27	c2wztA_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
28	c3o0kB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
29	d1ah4a_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)

30	c1zgdB_	Alignment	not modelled	100.0	23	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
31	d2alra_	Alignment	not modelled	100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
32	d1mzra_	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
33	d1c9wa_	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	d1vp5a_	Alignment	not modelled	100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
35	c3b3dA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
36	c2bgsA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
37	d1hw6a_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
38	c1vbjB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
39	c3krbB_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
40	c3ln3A_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
41	d1jpma1	Alignment	not modelled	93.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
42	c3ktcB_	Alignment	not modelled	80.1	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
43	c1jpmB_	Alignment	not modelled	67.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ala-d/l-glu epimerase; **PDBTitle:** l-ala-d/l-glu epimerase
44	c3l23A_	Alignment	not modelled	66.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
45	c3g8rA_	Alignment	not modelled	62.8	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
46	c3msyC_	Alignment	not modelled	59.4	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
47	d2gdqa1	Alignment	not modelled	57.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
48	c3ik4A_	Alignment	not modelled	56.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
49	c3es8D_	Alignment	not modelled	54.8	11	**PDB header:**isomerase, lyase **Chain:** D: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of divergent enolase from oceanobacillus2 iheyensis complexed with mg and l-malate.
50	c3hf3A_	Alignment	not modelled	48.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
51	c1ps9A_	Alignment	not modelled	44.8	20	**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
52	c3dx5A_	Alignment	not modelled	43.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
53	d3bofa2	Alignment	not modelled	42.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
54	d1xkya1	Alignment	not modelled	41.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase

55	d1r0ma1	Alignment	not modelled	41.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
56	d1ps9a1	Alignment	not modelled	38.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
57	c3dg7B_	Alignment	not modelled	38.1	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of muconate lactonizing enzyme from mucobacterium2 smegmatis complexed with muconolactone
58	d1nu5a1	Alignment	not modelled	36.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
59	d1sjda1	Alignment	not modelled	32.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
60	c2qdeA_	Alignment	not modelled	32.3	12	**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
61	c3smaD_	Alignment	not modelled	32.2	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
62	c2qgyA_	Alignment	not modelled	29.6	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
63	d1yeya1	Alignment	not modelled	29.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
64	d1wuea1	Alignment	not modelled	29.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
65	c1nu5A_	Alignment	not modelled	28.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
66	d1x87a_	Alignment	not modelled	28.3	22	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
67	c2chrA_	Alignment	not modelled	27.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** a re-evaluation of the crystal structure of chloromuconate2 cycloisomerase
68	d1rioa_	Alignment	not modelled	26.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
69	c2nqlB_	Alignment	not modelled	26.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
70	d1a0ea_	Alignment	not modelled	26.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
71	c3bdkB_	Alignment	not modelled	26.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
72	d1a0ca_	Alignment	not modelled	25.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
73	c2fknC_	Alignment	not modelled	25.3	28	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
74	c3bolB_	Alignment	not modelled	24.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
75	d1vlia2	Alignment	not modelled	24.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
76	c3pueA_	Alignment	not modelled	24.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
77	c3noeA_	Alignment	not modelled	24.3	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
78	c1vliA_	Alignment	not modelled	24.3	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
79	c3e4fB_	Alignment	not modelled	23.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
80	c2oz8B_	Alignment	not modelled	23.7	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mll7089 protein;

80	c2oz8B_	Alignment	not modelled	23.7	16	**PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti
81	d1uwka_	Alignment	not modelled	23.6	22	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
82	d2chra1	Alignment	not modelled	22.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
83	c2rfgB_	Alignment	not modelled	22.4	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
84	c2k6xA_	Alignment	not modelled	21.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
85	d1f6ya_	Alignment	not modelled	21.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
86	c3daqB_	Alignment	not modelled	20.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
87	c2ps2A_	Alignment	not modelled	19.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of putative mandelate racemase/muconate2 lactonizing enzyme from aspergillus oryzae
88	d1lmb3_	Alignment	not modelled	19.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
89	d1vjia_	Alignment	not modelled	19.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
90	c3px5A_	Alignment	not modelled	19.1	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**enzyme of enolase superfamily; **PDBTitle:** structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
91	c1sjaA_	Alignment	not modelled	18.8	14	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**n-acylamino acid racemase; **PDBTitle:** x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetylmethionine
92	d1olta_	Alignment	not modelled	18.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
93	d1vcva1	Alignment	not modelled	18.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
94	d2nyga1	Alignment	not modelled	18.0	16	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
95	c2zvrA_	Alignment	not modelled	17.7	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
96	c1wueA_	Alignment	not modelled	17.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of protein gi:29375081, unknown member of enolase2 superfamily from enterococcus faecalis v583
97	c3dfyJ_	Alignment	not modelled	17.5	13	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of apo dipeptide epimerase from2 thermotoga maritima
98	c3ju2A_	Alignment	not modelled	17.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
99	d1qbaa3	Alignment	not modelled	16.8	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain