Phyre2

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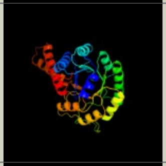
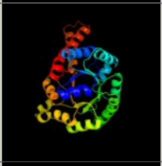
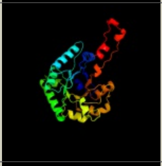
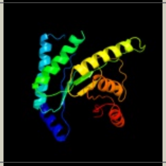
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q94B_	Alignment		100.0	42	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
2	d1gvfa_	Alignment		100.0	55	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
3	d1rvga_	Alignment		100.0	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
4	c3c52B_	Alignment		100.0	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
5	d1dosa_	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
6	c3elfA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
7	c3qm3C_	Alignment		100.0	26	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
8	c2iswB_	Alignment		100.0	41	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
9	c3pm6B_	Alignment		100.0	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
10	d2fiqa1	Alignment		99.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
11	c2qjhH_	Alignment		99.1	17	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate

12	c2c3zA_	Alignment		98.6	12	**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
13	d1thfd_	Alignment		98.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
14	c3gr7A_	Alignment		98.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
15	c2ze3A_	Alignment		98.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
16	d1ps9a1	Alignment		98.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
17	c3gndC_	Alignment		98.4	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
18	d1y0ea_	Alignment		98.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
19	c2h90A_	Alignment		98.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
20	c3eooL_	Alignment		98.3	15	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
21	c3b8iF_	Alignment	not modelled	98.3	16	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
22	d1j5ta_	Alignment	not modelled	98.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
23	c1ps9A_	Alignment	not modelled	98.2	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
24	c3ih1A_	Alignment	not modelled	98.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
25	c3hf3A_	Alignment	not modelled	98.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
26	c3qjaA_	Alignment	not modelled	98.2	15	**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
27	d1muma_	Alignment	not modelled	98.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
28	c3kruC_	Alignment	not modelled	98.2	18	**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
29	d1a53a_	Alignment	not modelled	98.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
30	d1h5ya_	Alignment	not modelled	98.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
31	c3igsB_	Alignment	not modelled	98.1	11	**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
32	d1ujqa_	Alignment	not modelled	98.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
33	d1xcfa_	Alignment	not modelled	98.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
34	d1i4na_	Alignment	not modelled	98.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
35	d1z41a1	Alignment	not modelled	97.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
36	d1tqxa_	Alignment	not modelled	97.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
37	d1yxya1	Alignment	not modelled	97.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
38	c2qiwA_	Alignment	not modelled	97.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
39	c3k30B_	Alignment	not modelled	97.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
40	c3bo9B_	Alignment	not modelled	97.8	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
41	d1vyra_	Alignment	not modelled	97.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
42	d1ka9f_	Alignment	not modelled	97.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
43	d1rd5a_	Alignment	not modelled	97.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
44	c3q58A_	Alignment	not modelled	97.8	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
45	c2z6jB_	Alignment	not modelled	97.7	20	**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
46	c3l5aA_	Alignment	not modelled	97.7	15	**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
47	c2gq8A_	Alignment	not modelled	97.7	16	**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
48	d1h1ya_	Alignment	not modelled	97.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
49	d1qopa_	Alignment	not modelled	97.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
50	d1wbha1	Alignment	not modelled	97.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
51	c3tdmD_	Alignment	not modelled	97.5	16	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
52	c2cw6B_	Alignment	not modelled	97.4	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
53	d1vhca_	Alignment	not modelled	97.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
						Fold:TIM beta/alpha-barrel

54	d1piia2	Alignment	not modelled	97.3	14	**Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
55	c1djnB_	Alignment	not modelled	97.3	15	**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)
56	d1xm3a_	Alignment	not modelled	97.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
57	c3fa4D_	Alignment	not modelled	97.3	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
58	d1ojxa_	Alignment	not modelled	97.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	d1m3ua_	Alignment	not modelled	97.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
60	c1zlpA_	Alignment	not modelled	97.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
61	d1s2wa_	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
62	c2y85D_	Alignment	not modelled	97.2	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
63	c3lyeA_	Alignment	not modelled	97.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
64	d1gwja_	Alignment	not modelled	97.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
65	c3thaB_	Alignment	not modelled	97.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
66	c2w6rA_	Alignment	not modelled	97.2	11	**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
67	c2gjlA_	Alignment	not modelled	97.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
68	d1wa3a1	Alignment	not modelled	97.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
69	c2ftpA_	Alignment	not modelled	97.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
70	d1mxsa_	Alignment	not modelled	97.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
71	d1geqa_	Alignment	not modelled	97.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
72	c3dxiB_	Alignment	not modelled	97.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
73	c3ivuB_	Alignment	not modelled	97.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
74	c1ydoC_	Alignment	not modelled	96.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
75	c3daqB_	Alignment	not modelled	96.8	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
76	d1wv2a_	Alignment	not modelled	96.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
77	c3ajxA_	Alignment	not modelled	96.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hexulose-6-phosphate synthase; **PDBTitle:** crystal structure of 3-hexulose-6-phosphate synthase
78	d1vzwa1	Alignment	not modelled	96.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
79	c2nx9B_	Alignment	not modelled	96.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
80	c3lerA_	Alignment	not modelled	96.6	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;

80	c3ferA_	Alignment	not modelled	96.6	19	**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
81	c3qc3B_	Alignment	not modelled	96.6	11	**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
82	c2zrvC_	Alignment	not modelled	96.6	14	**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.
83	c3pueA_	Alignment	not modelled	96.5	19	**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
84	c3f4wA_	Alignment	not modelled	96.5	16	**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
85	c2rfgB_	Alignment	not modelled	96.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
86	c1ydnA_	Alignment	not modelled	96.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
87	d1rpxa_	Alignment	not modelled	96.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
88	c2hjpA_	Alignment	not modelled	96.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
89	c3inpA_	Alignment	not modelled	96.4	15	**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.
90	d1xkya1	Alignment	not modelled	96.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
91	c3bi8A_	Alignment	not modelled	96.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
92	d2flia1	Alignment	not modelled	96.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
93	c2a7nA_	Alignment	not modelled	96.3	14	**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
94	d1vjia_	Alignment	not modelled	96.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
95	d1djqa1	Alignment	not modelled	96.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
96	d1vc4a_	Alignment	not modelled	96.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
97	d1tb3a1	Alignment	not modelled	96.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	c3gkaB_	Alignment	not modelled	96.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
99	d2a6na1	Alignment	not modelled	96.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
100	c3labA_	Alignment	not modelled	96.1	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
101	d1p0ka_	Alignment	not modelled	96.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
102	d1p4ca_	Alignment	not modelled	96.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
103	c3noeA_	Alignment	not modelled	96.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
104	d1xi3a_	Alignment	not modelled	96.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
105	d1icpa_	Alignment	not modelled	95.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
						Fold:TIM beta/alpha-barrel

106	d1tqja_	Alignment	not modelled	95.8	18	**Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
107	c2vc6A_	Alignment	not modelled	95.8	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
108	c3fluD_	Alignment	not modelled	95.8	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
109	d1qo2a_	Alignment	not modelled	95.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
110	d2mnra1	Alignment	not modelled	95.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
111	d1xxxa1	Alignment	not modelled	95.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
112	d1goxa_	Alignment	not modelled	95.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
113	d1o5ka_	Alignment	not modelled	95.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
114	d1w0ma_	Alignment	not modelled	95.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
115	c3g0sA_	Alignment	not modelled	95.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
116	d1oyaa_	Alignment	not modelled	95.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
117	c2r8wB_	Alignment	not modelled	95.6	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
118	c3jrkG_	Alignment	not modelled	95.6	21	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
119	c3lciA_	Alignment	not modelled	95.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
120	c3n2xB_	Alignment	not modelled	95.4	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate