Phyre^2

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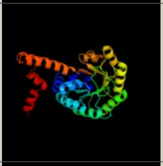
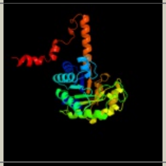
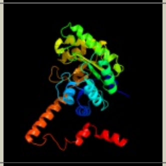
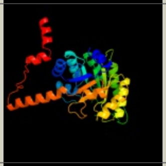
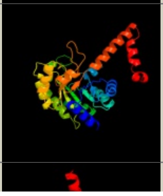
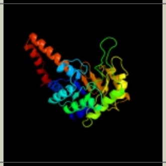
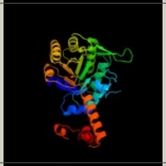
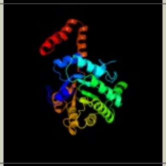
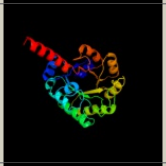
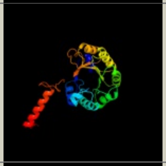
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1muma_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
2	c3eooL_	Alignment		100.0	64	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
3	c3ih1A_	Alignment		100.0	43	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
4	c1zlpA_	Alignment		100.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
5	d1ujqa_	Alignment		100.0	92	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
6	c3b8iF_	Alignment		100.0	29	**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+.
7	c2hjpA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
8	c3fa4D_	Alignment		100.0	32	**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
9	c3lyeA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
10	d1s2wa_	Alignment		100.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
11	c2ze3A_	Alignment		100.0	24	**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
						

12	c2qiwA_	Alignment		100.0	24	**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
13	d1f61a_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
14	c3e5bB_	Alignment		100.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
15	d1igwa_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
16	d1m3ua_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
17	d1dqua_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
18	c3ez4B_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
19	d1oy0a_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
20	d1o66a_	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
21	c2p10D_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
22	d1xcfa_	Alignment	not modelled	98.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
23	d1gvfa_	Alignment	not modelled	98.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
24	c3lerA_	Alignment	not modelled	98.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
25	c3b0vD_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
26	d2p10a1	Alignment	not modelled	98.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
27	d1qopa_	Alignment	not modelled	98.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
28	c3navB_	Alignment	not modelled	98.4	18	**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
						Fold:TIM beta/alpha-barrel

29	d1rd5a_	Alignment	not modelled	98.4	18	**Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
30	c3s5oA_	Alignment	not modelled	98.3	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
31	c2r8wB_	Alignment	not modelled	98.3	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
32	c2nuxB_	Alignment	not modelled	98.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
33	c3igsB_	Alignment	not modelled	98.3	13	**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
34	d1xkya1	Alignment	not modelled	98.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	c2yxgD_	Alignment	not modelled	98.3	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
36	c3fkkA_	Alignment	not modelled	98.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
37	c3daqB_	Alignment	not modelled	98.3	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
38	d1xxxa1	Alignment	not modelled	98.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
39	c3cprB_	Alignment	not modelled	98.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
40	c2c3zA_	Alignment	not modelled	98.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
41	c2r94B_	Alignment	not modelled	98.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
42	c2v9dB_	Alignment	not modelled	98.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
43	d1hl2a_	Alignment	not modelled	98.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	c3na8A_	Alignment	not modelled	98.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
45	d1o5ka_	Alignment	not modelled	98.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
46	c3dz1A_	Alignment	not modelled	98.2	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
47	c3lciA_	Alignment	not modelled	98.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
48	c3si9B_	Alignment	not modelled	98.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
49	c2rfgB_	Alignment	not modelled	98.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
50	c3n2xB_	Alignment	not modelled	98.1	20	**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
51	c3e96B_	Alignment	not modelled	98.1	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
52	c3pueA_	Alignment	not modelled	98.1	18	**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
53	d1w3ia_	Alignment	not modelled	98.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
54	c3noeA	Alignment	not modelled	98.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;

54	[illegible]	Alignment	not modelled	98.1	10	**PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
55	c3eb2A_	Alignment	not modelled	98.1	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
56	c3fluD_	Alignment	not modelled	98.1	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
57	c3bi8A_	Alignment	not modelled	98.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
58	d2a6na1	Alignment	not modelled	98.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	c2vc6A_	Alignment	not modelled	98.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
60	c2ehhE_	Alignment	not modelled	98.1	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
61	c2ekcA_	Alignment	not modelled	98.1	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
62	d1f74a_	Alignment	not modelled	98.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
63	d1h5ya_	Alignment	not modelled	98.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
64	c3g0sA_	Alignment	not modelled	98.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
65	d1gtea2	Alignment	not modelled	98.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
66	c3hf3A_	Alignment	not modelled	98.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
67	c3qfeB_	Alignment	not modelled	98.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
68	c3h5dD_	Alignment	not modelled	98.0	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
69	c3b4uB_	Alignment	not modelled	98.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
70	c3d0cB_	Alignment	not modelled	98.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
71	d1y0ea_	Alignment	not modelled	97.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
72	c3q94B_	Alignment	not modelled	97.9	21	**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'
73	d1vzwa1	Alignment	not modelled	97.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
74	d1jpma1	Alignment	not modelled	97.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
75	d1j5ta_	Alignment	not modelled	97.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
76	c2hmcA_	Alignment	not modelled	97.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
77	c2y85D_	Alignment	not modelled	97.8	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
78	d1yxya1	Alignment	not modelled	97.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
79	c3pm6B_	Alignment	not modelled	97.8	16	**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
80	d1ka9f_	Alignment	not modelled	97.7	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes

81	c2h90A_	Alignment	not modelled	97.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
82	c3gr7A_	Alignment	not modelled	97.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
83	c3q58A_	Alignment	not modelled	97.7	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
84	d1vhna_	Alignment	not modelled	97.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
85	c2iswB_	Alignment	not modelled	97.6	16	**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
86	c3qjaA_	Alignment	not modelled	97.6	16	**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
87	c3qm3C_	Alignment	not modelled	97.6	12	**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
88	d1thfd_	Alignment	not modelled	97.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
89	d1ojxa_	Alignment	not modelled	97.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
90	c3bolB_	Alignment	not modelled	97.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
91	c2w6rA_	Alignment	not modelled	97.4	21	**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
92	d1xm3a_	Alignment	not modelled	97.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
93	d1ps9a1	Alignment	not modelled	97.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	d1geqa_	Alignment	not modelled	97.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
95	c2htmB_	Alignment	not modelled	97.3	22	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
96	c3oixA_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
97	d1vyra_	Alignment	not modelled	97.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	c1znnF_	Alignment	not modelled	97.3	15	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
99	d1rvka1	Alignment	not modelled	97.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
100	c2qjhH_	Alignment	not modelled	97.3	14	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
101	d1znna1	Alignment	not modelled	97.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
102	d1rvga_	Alignment	not modelled	97.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
103	c2z6jB_	Alignment	not modelled	97.2	18	**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
104	c3qz6A_	Alignment	not modelled	97.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
105	c3stgA_	Alignment	not modelled	97.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis

106	d1dxea_	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
107	d1ujpa_	Alignment	not modelled	97.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
108	c1ps9A_	Alignment	not modelled	97.2	23	**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
109	c1jvnB_	Alignment	not modelled	97.1	21	**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
110	c3dfyJ_	Alignment	not modelled	97.1	14	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of apo dipeptide epimerase from2 thermotoga maritima
111	d1gwja_	Alignment	not modelled	97.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
112	d1jvna1	Alignment	not modelled	97.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
113	c2v5jB_	Alignment	not modelled	97.1	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
114	d1juba_	Alignment	not modelled	97.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
115	c1zcoA_	Alignment	not modelled	97.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
116	c2oz8B_	Alignment	not modelled	97.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mll7089 protein; **PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti
117	d8ruca1	Alignment	not modelled	97.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
118	d1dosa_	Alignment	not modelled	97.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
119	d1z41a1	Alignment	not modelled	96.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
120	c3gkaB_	Alignment	not modelled	96.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei