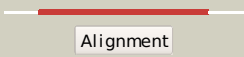
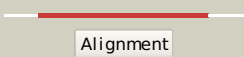
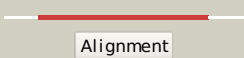
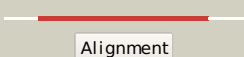
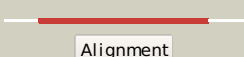
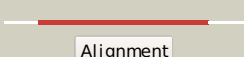
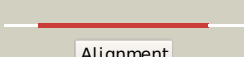
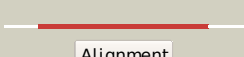
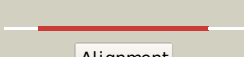
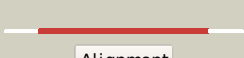


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a6na1	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
2	c3g0sA	 Alignment		100.0	91	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
3	c3fluD	 Alignment		100.0	49	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
4	c3noeA	 Alignment		100.0	57	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
5	c3si9B	 Alignment		100.0	41	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
6	c3bi8A	 Alignment		100.0	42	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
7	c3pueA	 Alignment		100.0	51	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
8	dlxxa1	 Alignment		100.0	33	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	dlxka1	 Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
10	c2ehhE	 Alignment		100.0	46	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
11	c2rfgB	 Alignment		100.0	42	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution

12	c3eb2A_	Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
13	d1o5ka_	Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
14	d1hl2a_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
15	d1f74a_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
16	c2r8wB_	Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
17	c2vc6A_	Alignment		100.0	44	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
18	c2yxqD_	Alignment		100.0	44	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
19	c3cprB_	Alignment		100.0	33	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
20	c2v9dB_	Alignment		100.0	28	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
21	c3lciA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
22	c3s5oA_	Alignment	not modelled	100.0	23	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
23	c3h5dD_	Alignment	not modelled	100.0	37	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
24	c3n2xB_	Alignment	not modelled	100.0	28	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
25	c3lerA_	Alignment	not modelled	100.0	37	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
26	c3na8A_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
27	c3daqB_	Alignment	not modelled	100.0	36	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
28	c3fkka_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase;

					PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
29	c3e96B_	Alignment	not modelled	100.0	23 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
30	c2r94B_	Alignment	not modelled	100.0	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
31	d1w3ia_	Alignment	not modelled	100.0	23 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
32	c3d0cB_	Alignment	not modelled	100.0	24 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
33	c2nuxB_	Alignment	not modelled	100.0	22 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
34	c3dz1A_	Alignment	not modelled	100.0	21 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
35	c3qfeB_	Alignment	not modelled	100.0	20 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
36	c2hmcA_	Alignment	not modelled	100.0	27 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
37	c2pcqA_	Alignment	not modelled	100.0	28 PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthase; PDBTitle: crystal structure of putative dihydrodipicolinate synthase (ttha0737)2 from thermus thermophilus hb8
38	c3b4uB_	Alignment	not modelled	100.0	23 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
39	d1muma_	Alignment	not modelled	98.3	14 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
40	c3lyeA_	Alignment	not modelled	98.2	17 PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
41	c3ih1A_	Alignment	not modelled	98.0	13 PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
42	c2ze3A_	Alignment	not modelled	98.0	18 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
43	d1ujga_	Alignment	not modelled	98.0	14 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
44	c3eooL_	Alignment	not modelled	98.0	13 PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
45	c1zlpA_	Alignment	not modelled	97.9	17 PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
46	d1s2wa_	Alignment	not modelled	97.9	14 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
47	c2qiwa_	Alignment	not modelled	97.8	19 PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
48	c3fa4D_	Alignment	not modelled	97.8	13 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
49	c3b8iF_	Alignment	not modelled	97.8	21 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+.
50	c2hjpA_	Alignment	not modelled	97.8	19 PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
51	c1rcxH_	Alignment	not modelled	97.6	12 PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bispophosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
52	d1xcfa_	Alignment	not modelled	97.6	16 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
					PDB header: isomerase

53	c2zviB_	Alignment	not modelled	97.6	13	Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
54	c3gr7A_	Alignment	not modelled	97.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
55	d8ruca1	Alignment	not modelled	97.4	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
56	d1svda1	Alignment	not modelled	97.3	5	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
57	c1gehE_	Alignment	not modelled	97.3	15	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
58	d1geha1	Alignment	not modelled	97.3	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
59	c1ps9A_	Alignment	not modelled	97.3	14	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
60	d1bxna1	Alignment	not modelled	97.2	9	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
61	d1ps9a1	Alignment	not modelled	97.2	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
62	c3ez4B_	Alignment	not modelled	97.2	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
63	d1rb1a1	Alignment	not modelled	97.2	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
64	c3hf3A_	Alignment	not modelled	97.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
65	c3fk4A_	Alignment	not modelled	97.2	14	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
66	c2oemA_	Alignment	not modelled	97.1	14	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
67	c2h90A_	Alignment	not modelled	97.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
68	d1f61a_	Alignment	not modelled	97.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
69	d1ykwa1	Alignment	not modelled	97.0	8	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
70	c3navB_	Alignment	not modelled	97.0	19	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
71	c2qygC_	Alignment	not modelled	97.0	11	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
72	d1wdda1	Alignment	not modelled	97.0	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
73	c2d69B_	Alignment	not modelled	97.0	12	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
74	d1ej711	Alignment	not modelled	96.9	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
75	d1z41a1	Alignment	not modelled	96.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	d2d69a1	Alignment	not modelled	96.9	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
77	c1telA_	Alignment	not modelled	96.8	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose bisphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum

78	dloy0a_	Alignment	not modelled	96.8	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
79	c3thaB_	Alignment	not modelled	96.8	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
80	c1rldB_	Alignment	not modelled	96.6	12	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
81	c3nwrA_	Alignment	not modelled	96.5	13	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
82	d1f76a_	Alignment	not modelled	96.5	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c1tv5A_	Alignment	not modelled	96.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
84	d1tv5a1	Alignment	not modelled	96.4	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	d1gk8a1	Alignment	not modelled	96.4	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
86	d1qopa_	Alignment	not modelled	96.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
87	d1bwva1	Alignment	not modelled	96.3	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
88	c3kruC_	Alignment	not modelled	96.3	7	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
89	c2rduA_	Alignment	not modelled	96.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
90	d1xya1	Alignment	not modelled	96.3	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
91	d1j5ta_	Alignment	not modelled	96.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
92	c1bwvA_	Alignment	not modelled	96.2	13	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
93	c2e77B_	Alignment	not modelled	96.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
94	d1geqa_	Alignment	not modelled	96.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
95	d1gvfa_	Alignment	not modelled	96.1	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
96	c2qjhH_	Alignment	not modelled	96.1	11	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
97	c3bolB_	Alignment	not modelled	96.1	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+
98	c2cdh1_	Alignment	not modelled	96.1	15	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
99	d1gwja_	Alignment	not modelled	96.0	9	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
100	d1juba_	Alignment	not modelled	96.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
101	c3labA_	Alignment	not modelled	96.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdp (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdp (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
102	d1d3ga_	Alignment	not modelled	95.9	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
						Fold: TIM beta/alpha-barrel

103	d1m3ua_	Alignment	not modelled	95.8	20	Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
104	d1goxa_	Alignment	not modelled	95.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c3qc3B_	Alignment	not modelled	95.7	15	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
106	c3q94B_	Alignment	not modelled	95.7	13	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'
107	c3qfwB_	Alignment	not modelled	95.7	11	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
108	c3k30B_	Alignment	not modelled	95.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioles simplex
109	d2f6ka1	Alignment	not modelled	95.7	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
110	c3oixA_	Alignment	not modelled	95.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
111	c3gndC_	Alignment	not modelled	95.6	17	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
112	d1o0ya_	Alignment	not modelled	95.6	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
113	c3jrkG_	Alignment	not modelled	95.6	16	PDB header: lyase Chain: G: PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
114	d1tb3a1	Alignment	not modelled	95.5	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
115	d1rd5a_	Alignment	not modelled	95.5	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
116	c2ekcA_	Alignment	not modelled	95.5	20	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
117	d1vhna_	Alignment	not modelled	95.5	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
118	c3ivuB_	Alignment	not modelled	95.5	10	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
119	c2iswB_	Alignment	not modelled	95.4	13	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
120	c1jcnA_	Alignment	not modelled	95.4	10	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