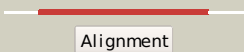

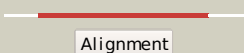

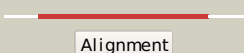

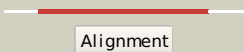

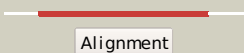

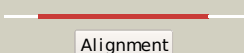

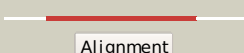

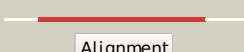

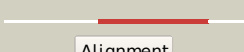

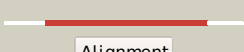

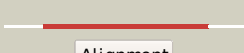







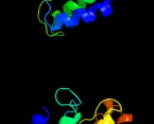
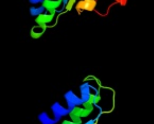

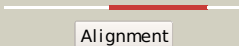
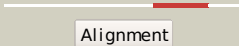






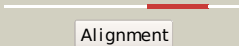

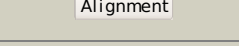


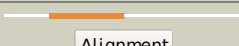
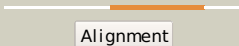

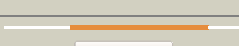



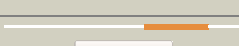
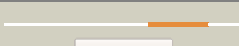




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l6sa_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
2	d2c1ha1	 Alignment		100.0	47	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
3	c3obkH_	 Alignment		100.0	43	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
4	d1gzga_	 Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
5	d1h7na_	 Alignment		100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
6	d1pv8a_	 Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
7	d1ps9a1	 Alignment		97.4	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
8	d1wbha1	 Alignment		97.2	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	d1svda1	 Alignment		96.9	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
10	c2h90A_	 Alignment		96.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
11	c3thaB_	 Alignment		96.7	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.

12	c2qygC	Alignment		96.6	21	PDB header: unknown function Chain: C: PDB Molecule: ribulose biphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
13	d1ykwa1	Alignment		96.6	21	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
14	c1ps9A	Alignment		96.6	24	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
15	c3eooL	Alignment		96.5	21	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
16	c3nwrA	Alignment		96.4	21	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
17	c1telA	Alignment		96.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
18	c3qfwB	Alignment		96.4	23	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
19	c1rldB	Alignment		96.3	17	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
20	c1rcxH	Alignment		96.2	17	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose biphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
21	d1ej7I1	Alignment	not modelled	96.2	19	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
22	d1mxsa	Alignment	not modelled	96.2	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
23	d5ruba1	Alignment	not modelled	96.0	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
24	c3fk4A	Alignment	not modelled	96.0	25	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
25	d1geha1	Alignment	not modelled	96.0	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
26	d1bxna1	Alignment	not modelled	95.9	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
27	d2d69a1	Alignment	not modelled	95.9	19	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
28	c2zviB	Alignment	not modelled	95.8	25	PDB header: isomerase 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 PDB header: isomerase Chain: D: PDB Molecule: 228aa long hvpothetical hvdantoin

29	c2eq5D_	Alignment	not modelled	95.8	21	racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
30	d1rblal	Alignment	not modelled	95.8	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
31	c1gehE_	Alignment	not modelled	95.7	17	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)
32	c2ze3A_	Alignment	not modelled	95.7	22	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
33	c2d69B_	Alignment	not modelled	95.7	19	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)
34	c3labA_	Alignment	not modelled	95.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpq (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdpq (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
35	c2oemA_	Alignment	not modelled	95.6	26	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-diketohehexane 1-phosphate
36	d1muma_	Alignment	not modelled	95.6	26	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
37	d1wddal	Alignment	not modelled	95.4	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
38	d1oy0a_	Alignment	not modelled	95.3	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
39	c3fa4D_	Alignment	not modelled	95.2	15	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
40	c3gr7A_	Alignment	not modelled	95.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
41	d8ruca1	Alignment	not modelled	95.0	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
42	d1djqa1	Alignment	not modelled	94.8	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
43	c3ez4B_	Alignment	not modelled	94.7	19	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
44	c3hf3A_	Alignment	not modelled	94.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
45	c1zlpA_	Alignment	not modelled	94.5	25	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
46	d1gk8a1	Alignment	not modelled	94.5	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
47	c2rusB_	Alignment	not modelled	94.4	17	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: rubisco (ribulose-1,5-bisphosphate PDBTitle: crystal structure of the ternary complex of ribulose-1,5-2 bisphosphate carboxylase, mg(ii), and activator co2 at 2.3-3 angstroms resolution
48	d1vjia_	Alignment	not modelled	94.4	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
49	d1vhca_	Alignment	not modelled	94.2	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
50	d1bwva1	Alignment	not modelled	94.1	21	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
51	d1rd5a_	Alignment	not modelled	94.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
52	c1djnb_	Alignment	not modelled	93.9	17	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)
53	d1m3ua_	Alignment	not modelled	93.5	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain

						Family: Ketopantoate hydroxymethyltransferase PanB
54	c9rubB_	 Alignment	not modelled	93.2	18	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate2 carboxylase complexed with its substrate, ribulose-1,5-3 bisphosphate
55	c1yadD_	 Alignment	not modelled	92.5	30	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
56	c1bwvA_	 Alignment	not modelled	92.3	22	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
57	c3kruC_	 Alignment	not modelled	92.2	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
58	d1wa3a1	 Alignment	not modelled	91.9	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
59	c2qjH_	 Alignment	not modelled	91.3	18	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
60	c3k30B_	 Alignment	not modelled	91.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioles simplex
61	c2qiW_	 Alignment	not modelled	91.0	22	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
62	d2czda1	 Alignment	not modelled	91.0	29	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
63	c2vlbC_	 Alignment	not modelled	90.7	22	PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase
64	d1ujqa_	 Alignment	not modelled	90.6	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
65	d1xcfa_	 Alignment	not modelled	90.5	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
66	c3gkaB_	 Alignment	not modelled	90.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
67	d1s2wa_	 Alignment	not modelled	89.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
68	c1zfjA_	 Alignment	not modelled	88.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
69	c3lerA_	 Alignment	not modelled	87.9	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
70	c2y7eA_	 Alignment	not modelled	87.7	22	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminoheptanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminoheptanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
71	d3bofa2	 Alignment	not modelled	87.6	20	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
72	c3chvA_	 Alignment	not modelled	86.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
73	c3cixA_	 Alignment	not modelled	86.9	17	PDB header: adomet binding protein Chain: A: PDB Molecule: fe(II)-hydrogenase maturase; PDBTitle: x-ray structure of the [fe(II)]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
74	c3bolB_	 Alignment	not modelled	84.8	19	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	d1h5ya_	 Alignment	not modelled	84.8	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
76	c3js3C_	 Alignment	not modelled	84.6	21	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
77	c3lyeA_	 Alignment	not modelled	84.5	11	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase;

						PDBTitle: crystal structure of oxaloacetate acetylhydrolase
78	c1ydoC	Alignment	not modelled	84.2	23	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.
79	c2hjpA	Alignment	not modelled	84.1	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
80	c3s5oA	Alignment	not modelled	83.7	17	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
81	d2a6na1	Alignment	not modelled	83.6	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
82	c3q58A	Alignment	not modelled	82.9	22	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
83	d1gqna	Alignment	not modelled	81.4	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
84	c3no5C	Alignment	not modelled	80.9	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
85	c3ih1A	Alignment	not modelled	80.5	19	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
86	d1vyra	Alignment	not modelled	79.4	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	c2ekcA	Alignment	not modelled	79.0	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
88	d1z41a1	Alignment	not modelled	78.9	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c3eb2A	Alignment	not modelled	78.7	22	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
90	c2infB	Alignment	not modelled	78.7	14	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
91	c1rr2A	Alignment	not modelled	76.9	25	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
92	c3s1vD	Alignment	not modelled	76.4	32	PDB header: transferase Chain: D: PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
93	c1ydnA	Alignment	not modelled	76.1	21	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.
94	d1km4a	Alignment	not modelled	76.0	29	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
95	d1xxa1	Alignment	not modelled	76.0	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
96	c3o63B	Alignment	not modelled	75.2	30	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
97	d1gwja	Alignment	not modelled	75.1	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	d1o5ka	Alignment	not modelled	72.5	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	d1lt7a	Alignment	not modelled	71.8	20	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
100	c3dz1A	Alignment	not modelled	71.8	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
101	c3b8fF	Alignment	not modelled	70.9	20	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+.
102	c3na8A	Alignment	not modelled	70.9	21	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate

						synthetase from2 pseudomonas aeruginosa
103	c3e96B_	 Alignment	not modelled	70.1	25	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
104	c1x1oC_	 Alignment	not modelled	69.5	23	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
105	c3d0cB_	 Alignment	not modelled	69.5	23	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
106	c3qfeB_	 Alignment	not modelled	68.7	19	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
107	d1qopa_	 Alignment	not modelled	67.5	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
108	d1umya_	 Alignment	not modelled	67.4	20	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
109	d1l6wa_	 Alignment	not modelled	66.6	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
110	d1dvja_	 Alignment	not modelled	66.4	37	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
111	c3c6cA_	 Alignment	not modelled	66.4	12	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
112	d1ajza_	 Alignment	not modelled	66.2	24	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
113	c2ehhE_	 Alignment	not modelled	66.0	23	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
114	c2yr1B_	 Alignment	not modelled	65.9	19	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
115	c2v9dB_	 Alignment	not modelled	65.5	21	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
116	c3ct7E_	 Alignment	not modelled	64.8	17	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
117	c2yw3E_	 Alignment	not modelled	64.8	24	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
118	d1q45a_	 Alignment	not modelled	64.6	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
119	d1f74a_	 Alignment	not modelled	64.2	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
120	d1icpa_	 Alignment	not modelled	64.1	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases