

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hl2a_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
2	c3lciA_	 Alignment		100.0	100	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
3	c3g0sA_	 Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
4	d1f74a_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
5	d1xkya1	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
6	d1xxxa1	 Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
7	c3fluD_	 Alignment		100.0	27	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
8	d2a6na1	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	c2r8wB_	 Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
10	c3eb2A_	 Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
11	c3bi8A_	 Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum

12	c3pueA	Alignment		100.0	30	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
13	c3noeA	Alignment		100.0	29	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
14	c3si9B	Alignment		100.0	24	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
15	c3na8A	Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
16	c2rfgB	Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
17	c3h5dD	Alignment		100.0	24	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
18	c3cprB	Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
19	c2yxgD	Alignment		100.0	26	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
20	c2ehhE	Alignment		100.0	25	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
21	c3lerA	Alignment	not modelled	100.0	26	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
22	c3s5oA	Alignment	not modelled	100.0	24	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	c2v9dB	Alignment	not modelled	100.0	25	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
24	c2vc6A	Alignment	not modelled	100.0	28	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
25	d1o5ka	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
26	c3daqB	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
27	c3n2xB	Alignment	not modelled	100.0	25	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
28	c3fkkA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
		Alignment				PDB header: lyase

29	c2r94B_	Alignment	not modelled	100.0	23	Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
30	d1w3ia_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
31	c3e96B_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
32	c3dz1A_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
33	c2nuxB_	Alignment	not modelled	100.0	25	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	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
35	c3b4uB_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
36	c2pcqA_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthase; PDBTitle: crystal structure of putative dihydrodipicolinate synthase (ttha0737)2 from thermus thermophilus hb8
37	c2hmcA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
38	c3qfeB_	Alignment	not modelled	100.0	23	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
39	d1muma_	Alignment	not modelled	98.2	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
40	c3lyeA_	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
41	c3eooL_	Alignment	not modelled	97.9	13	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
42	c3fa4D_	Alignment	not modelled	97.9	12	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
43	c2ze3A_	Alignment	not modelled	97.9	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
44	d1ujga_	Alignment	not modelled	97.8	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
45	c1zlpA_	Alignment	not modelled	97.8	16	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
46	c3ih1A_	Alignment	not modelled	97.8	13	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
47	c2qiwa_	Alignment	not modelled	97.6	15	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	c3b8iF_	Alignment	not modelled	97.6	15	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+.
49	d1s2wa_	Alignment	not modelled	97.5	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
50	c2hjpa_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
51	c3gr7A_	Alignment	not modelled	97.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
52	d1rbla1	Alignment	not modelled	97.3	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
53	c2h90A_	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
						PDB header: oxidoreductase

54	c1ps9A	Alignment	not modelled	97.2	21	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
55	dlps9a1	Alignment	not modelled	97.1	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
56	dlxcfa	Alignment	not modelled	97.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
57	dlbxna1	Alignment	not modelled	96.9	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
58	c3hf3A	Alignment	not modelled	96.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
59	dlwdda1	Alignment	not modelled	96.7	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
60	dlgvfa	Alignment	not modelled	96.6	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
61	c3thaB	Alignment	not modelled	96.6	21	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
62	clrldB	Alignment	not modelled	96.6	14	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
63	dloy0a	Alignment	not modelled	96.5	25	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
64	c3nwrA	Alignment	not modelled	96.4	16	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
65	c3qfwB	Alignment	not modelled	96.4	22	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
66	c3ez4B	Alignment	not modelled	96.4	18	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
67	c2d69B	Alignment	not modelled	96.4	16	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)
68	c2e77B	Alignment	not modelled	96.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
69	c2ftpA	Alignment	not modelled	96.3	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
70	dlsvda1	Alignment	not modelled	96.3	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
71	c2cw6B	Alignment	not modelled	96.2	16	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
72	c2cdh1	Alignment	not modelled	96.2	16	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
73	c3k30B	Alignment	not modelled	96.2	21	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex
74	dlz41a1	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
75	dltv5a1	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	c1tv5A	Alignment	not modelled	96.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
77	c3bleA	Alignment	not modelled	96.1	13	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
78	d8ruca1	Alignment	not modelled	96.1	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain

79	c3navB_	Alignment	not modelled	96.1	14	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
80	c3q94B_	Alignment	not modelled	96.0	17	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'
81	d1f61a_	Alignment	not modelled	96.0	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
82	d1ej7l1	Alignment	not modelled	96.0	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
83	c3kruC_	Alignment	not modelled	96.0	11	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
84	c2oemA_	Alignment	not modelled	96.0	17	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
85	c2rduA_	Alignment	not modelled	96.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
86	d1geha1	Alignment	not modelled	96.0	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
87	c3fk4A_	Alignment	not modelled	95.9	19	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
88	d1f76a_	Alignment	not modelled	95.7	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c1rcxH_	Alignment	not modelled	95.7	17	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
90	d2f6ka1	Alignment	not modelled	95.7	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
91	c2qjhH_	Alignment	not modelled	95.7	10	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
92	d1goxa_	Alignment	not modelled	95.6	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
93	c1gthD_	Alignment	not modelled	95.6	20	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
94	d1ykwa1	Alignment	not modelled	95.6	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
95	d1tb3a1	Alignment	not modelled	95.6	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
96	c3tr9A_	Alignment	not modelled	95.5	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteric2 acid from coxiella burnetii
97	c1jcnA_	Alignment	not modelled	95.5	17	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
98	d1qopa_	Alignment	not modelled	95.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
99	c1gehE_	Alignment	not modelled	95.4	11	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)
100	c3gndC_	Alignment	not modelled	95.3	14	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
101	c3bolB_	Alignment	not modelled	95.1	18	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
102	d1d3ga_	Alignment	not modelled	95.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
103	c1djnb_	Alignment	not modelled	95.0	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)
104	d1vhna	Alignment	not modelled	94.9	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c2ekcA	Alignment	not modelled	94.9	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus v5f
106	c2iswB	Alignment	not modelled	94.9	21	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
107	d1rvga	Alignment	not modelled	94.8	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
108	c3nurA	Alignment	not modelled	94.7	7	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
109	c2ejaB	Alignment	not modelled	94.7	18	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
110	d1geqa	Alignment	not modelled	94.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
111	d1bwva1	Alignment	not modelled	94.6	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
112	c3ngjC	Alignment	not modelled	94.6	16	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
113	c1ydoC	Alignment	not modelled	94.6	17	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.
114	c2zviB	Alignment	not modelled	94.6	18	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
115	d1gk8a1	Alignment	not modelled	94.6	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
116	c2htmB	Alignment	not modelled	94.5	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
117	c1telA	Alignment	not modelled	94.5	12	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
118	c3ivuB	Alignment	not modelled	94.4	12	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
119	c1bwvA	Alignment	not modelled	94.3	15	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
120	d1to3a	Alignment	not modelled	94.3	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase