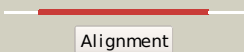
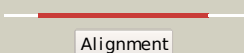
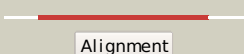
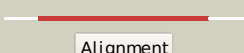
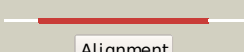
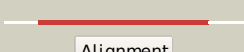
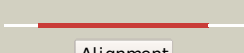
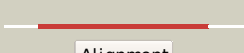


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gvfa_	 Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
2	c3q94B_	 Alignment		100.0	42	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
3	d1rvga_	 Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
4	c3c52B_	 Alignment		100.0	36	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolhydroxamic acid, a competitive inhibitor
5	d1dosa_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
6	c3elfA_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
7	c3qm3C_	 Alignment		100.0	28	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
8	c2iswB_	 Alignment		100.0	37	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 phosphoglycolhydroxamate
9	c3pm6B_	 Alignment		100.0	34	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-bisphosphate aldolase from2 coccidioides immitis solved by combined sad mr
10	d2fiqa1	 Alignment		99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
11	c2qjhH_	 Alignment		99.1	17	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate

12	d1thfd_	Alignment		98.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
13	c3gr7A_	Alignment		98.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
14	c2c3zA_	Alignment		98.5	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
15	c2ze3A_	Alignment		98.5	15	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
16	d1ps9a1	Alignment		98.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
17	c2h90A_	Alignment		98.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
18	d1j5ta_	Alignment		98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
19	d1a53a_	Alignment		98.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
20	d1y0ea_	Alignment		98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
21	c1ps9A_	Alignment	not modelled	98.2	17	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
22	c3qjaA_	Alignment	not modelled	98.2	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
23	c3igsB_	Alignment	not modelled	98.2	15	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
24	c3kruC_	Alignment	not modelled	98.1	14	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
25	c3gndC_	Alignment	not modelled	98.1	19	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
26	c3eo0L_	Alignment	not modelled	98.1	17	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
27	c3b8iF_	Alignment	not modelled	98.1	18	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+.
						PDB header: oxidoreductase

28	c3hf3A_	Alignment	not modelled	98.1	18	Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
29	d1ujqa_	Alignment	not modelled	98.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
30	d1muma_	Alignment	not modelled	98.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
31	c3l5aA_	Alignment	not modelled	98.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
32	c3q58A_	Alignment	not modelled	98.0	16	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
33	d1i4na_	Alignment	not modelled	98.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
34	d1ka9f_	Alignment	not modelled	97.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
35	c2gq8A_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
36	d1tqxa_	Alignment	not modelled	97.8	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
37	d1yxya1	Alignment	not modelled	97.8	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
38	c2z6jB_	Alignment	not modelled	97.8	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
39	c3k30B_	Alignment	not modelled	97.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioodes simplex
40	d1vyra_	Alignment	not modelled	97.8	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
41	d1wbha1	Alignment	not modelled	97.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
42	d1vhca_	Alignment	not modelled	97.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
43	d1xcfa_	Alignment	not modelled	97.7	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c2cw6B_	Alignment	not modelled	97.7	18	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
45	c3ih1A_	Alignment	not modelled	97.6	12	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
46	d1piia2	Alignment	not modelled	97.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
47	d1z41a1	Alignment	not modelled	97.6	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
48	c3tdmD_	Alignment	not modelled	97.6	20	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
49	d1qopa_	Alignment	not modelled	97.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
50	c2ftpA_	Alignment	not modelled	97.6	17	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
51	c3bo9B_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
52	c2qiwa_	Alignment	not modelled	97.5	17	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
53	d1h5ya_	Alignment	not modelled	97.4	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes

54	dlgwja_	Alignment	not modelled	97.4	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
55	dlxm3a_	Alignment	not modelled	97.4	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
56	dlwa3a1	Alignment	not modelled	97.3	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
57	dlh1ya_	Alignment	not modelled	97.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
58	c2w6rA_	Alignment	not modelled	97.3	13	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
59	dlrd5a_	Alignment	not modelled	97.3	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
60	clzlpA_	Alignment	not modelled	97.2	14	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
61	c3dxiB_	Alignment	not modelled	97.2	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bv_u_2661) from bacteroides vulgatus
62	c2y85D_	Alignment	not modelled	97.2	16	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
63	clydoC_	Alignment	not modelled	97.0	17	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
64	dlm3ua_	Alignment	not modelled	97.0	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
65	c3ajxA_	Alignment	not modelled	97.0	17	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
66	c3thaB_	Alignment	not modelled	97.0	13	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
67	dlvzwa1	Alignment	not modelled	97.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
68	clydnA_	Alignment	not modelled	96.9	15	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.
69	cldjnB_	Alignment	not modelled	96.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: tri methylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
70	c3qc3B_	Alignment	not modelled	96.9	12	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
71	dlvjia_	Alignment	not modelled	96.9	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	dloyaA_	Alignment	not modelled	96.8	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	dlS2wa_	Alignment	not modelled	96.8	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
74	dlvc4a_	Alignment	not modelled	96.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	c3daqB_	Alignment	not modelled	96.8	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
76	c2rfgB_	Alignment	not modelled	96.8	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
77	c3ivuB_	Alignment	not modelled	96.7	17	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
78	dlxi3a_	Alignment	not modelled	96.7	19	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
79	c2nx9B_	Alignment	not modelled	96.6	22	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae PDB header: transferase

80	c2cdh1	Alignment	not modelled	96.6	17	Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
81	d1wv2a	Alignment	not modelled	96.6	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
82	c3fa4D	Alignment	not modelled	96.6	16	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
83	c3lerA	Alignment	not modelled	96.5	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
84	d1ojxa	Alignment	not modelled	96.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	c2gjlA	Alignment	not modelled	96.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
86	c2zrvC	Alignment	not modelled	96.4	21	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fm. n.
87	d1rpxa	Alignment	not modelled	96.4	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
88	d1icpa	Alignment	not modelled	96.4	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	d1xkya1	Alignment	not modelled	96.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
90	d1geqa	Alignment	not modelled	96.3	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
91	c3pueA	Alignment	not modelled	96.3	20	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
92	d2flia1	Alignment	not modelled	96.3	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
93	c3jrkG	Alignment	not modelled	96.3	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
94	d1qo2a	Alignment	not modelled	96.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
95	d2mnra1	Alignment	not modelled	96.1	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
96	c3f4wA	Alignment	not modelled	96.1	14	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
97	c2vc6A	Alignment	not modelled	96.0	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
98	c2p10D	Alignment	not modelled	96.0	15	PDB header: hydrolase Chain: D: PDB Molecule: ml19387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
99	c3gkaB	Alignment	not modelled	96.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
100	c3iwpK	Alignment	not modelled	96.0	13	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
101	c3bi8A	Alignment	not modelled	96.0	21	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
102	d1p0ka	Alignment	not modelled	95.9	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
103	c1f9cA	Alignment	not modelled	95.9	19	PDB header: isomerase Chain: A: PDB Molecule: protein (muconate cycloisomerase i); PDBTitle: crystal structure of mle d178n variant
104	c3noeA	Alignment	not modelled	95.9	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
105	c3fluD	Alignment	not modelled	95.9	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis

106	d1djqa1	Alignment	not modelled	95.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
107	c3fkkA	Alignment	not modelled	95.7	15	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
108	c3lyeA	Alignment	not modelled	95.7	13	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
109	c2a7nA	Alignment	not modelled	95.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
110	c3n2xB	Alignment	not modelled	95.7	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
111	d1tqja	Alignment	not modelled	95.7	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
112	d1tb3a1	Alignment	not modelled	95.7	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
113	d2a6na1	Alignment	not modelled	95.6	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
114	c3inpA	Alignment	not modelled	95.6	11	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
115	d1o5ka	Alignment	not modelled	95.6	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
116	c3bw2A	Alignment	not modelled	95.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
117	d1e0ta2	Alignment	not modelled	95.6	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
118	d1hg3a	Alignment	not modelled	95.5	23	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
119	c3navB	Alignment	not modelled	95.4	16	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
120	c3e96B	Alignment	not modelled	95.4	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii