

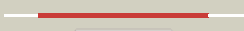






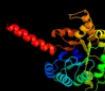



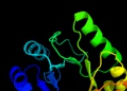





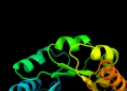

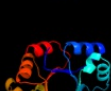












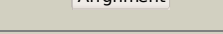
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vwtA_	 Alignment		100.0	100	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
2	c2v5jB_	 Alignment		100.0	55	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
3	d1dxea_	 Alignment		100.0	44	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
4	clizcA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
5	d1izcA_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
6	c3qz6A_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
7	c1sgjB_	 Alignment		100.0	24	PDB header: lyase Chain: B: PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
8	d1sgja_	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
9	c1u5vA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
10	d1u5ha_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
11	d1e0ta2	 Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase

12	c3qqwC_	Alignment		99.9	14	PDB header: lyase Chain: C: PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
13	c2hwgA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
14	c2hroA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
15	c2bg5C_	Alignment		99.9	21	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
16	c3r4iB_	Alignment		99.9	14	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
17	d1vbga1	Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
18	d1h6za1	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
19	c1h6zA_	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
20	d1liua2	Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
21	d1kbla1	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
22	d1a3xa2	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
23	d1pkla2	Alignment	not modelled	99.9	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
24	c1kbla_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
25	c1vbhA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
26	c2olsA_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
27	c3puga_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
28	d2g50a2	Alignment	not modelled	99.8	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
						PDB header: transferase Chain: A: PDB Molecule: malate synthase a;

29	c3cuzA_	Alignment	not modelled	99.8	17	PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
30	c3cuxA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
31	c3khdC_	Alignment	not modelled	99.5	19	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
32	c1e0tD_	Alignment	not modelled	99.4	18	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
33	c1t5aB_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
34	c3e0vB_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
35	c1aqfB_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
36	c1pklB_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
37	c2vgbB_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
38	c3t07D_	Alignment	not modelled	99.3	17	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
39	c2e28A_	Alignment	not modelled	99.3	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
40	c1a3wB_	Alignment	not modelled	99.3	22	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
41	c3eoeC_	Alignment	not modelled	99.2	20	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
42	c3ma8A_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
43	d1qopa_	Alignment	not modelled	98.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
44	d1rd5a_	Alignment	not modelled	98.4	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
45	c3odmE_	Alignment	not modelled	98.3	23	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
46	d1rpxa_	Alignment	not modelled	98.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
47	d1xcfa_	Alignment	not modelled	98.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
48	c2ekcA_	Alignment	not modelled	98.1	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
49	d2tpsa_	Alignment	not modelled	98.1	17	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
50	d1vhca_	Alignment	not modelled	98.1	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
51	c3navB_	Alignment	not modelled	98.0	17	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
52	d2flia1	Alignment	not modelled	98.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
53	d1tqxa_	Alignment	not modelled	98.0	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
54	d1d8ca_	Alignment	not modelled	97.9	16	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
55	d1h1ya_	Alignment	not modelled	97.8	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase

56	c2qiWA	Alignment	not modelled	97.8	19	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
57	d1xi3a	Alignment	not modelled	97.8	17	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
58	d1tqja	Alignment	not modelled	97.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
59	c3qjaA	Alignment	not modelled	97.7	19	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
60	c3igsB	Alignment	not modelled	97.6	16	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
61	d1n8ia	Alignment	not modelled	97.6	14	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
62	c3inpA	Alignment	not modelled	97.6	14	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
63	c2c3zA	Alignment	not modelled	97.6	17	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
64	c3qc3B	Alignment	not modelled	97.6	16	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
65	c2hjpA	Alignment	not modelled	97.5	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
66	c1zfjA	Alignment	not modelled	97.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (imph; ec 1.1.1.205) from2 streptococcus pyogenes
67	c3ct7E	Alignment	not modelled	97.5	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
68	d1mxsa	Alignment	not modelled	97.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
69	d1wa3a1	Alignment	not modelled	97.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
70	c3o63B	Alignment	not modelled	97.4	18	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
71	d1wbha1	Alignment	not modelled	97.3	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c1zlpA	Alignment	not modelled	97.3	17	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
73	d1i4na	Alignment	not modelled	97.1	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
74	d1j5ta	Alignment	not modelled	97.1	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	c3b8iF	Alignment	not modelled	97.1	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+.
76	c3q58A	Alignment	not modelled	97.0	15	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
77	d1muma	Alignment	not modelled	97.0	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
78	d1ujqa	Alignment	not modelled	96.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
79	c1yadD	Alignment	not modelled	96.9	17	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
80	c2ze3A	Alignment	not modelled	96.9	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

81	dlvc4a_	Alignment	not modelled	96.9	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
82	c3fa4D_	Alignment	not modelled	96.9	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	c3lyeA_	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
84	c3ih1A_	Alignment	not modelled	96.6	19	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
85	dljqna_	Alignment	not modelled	96.6	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
86	c3thaB_	Alignment	not modelled	96.6	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
87	dls2wa_	Alignment	not modelled	96.3	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
88	dlujpa_	Alignment	not modelled	96.2	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
89	dla53a_	Alignment	not modelled	96.2	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
90	c2v82A_	Alignment	not modelled	96.1	18	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
91	dlgvfa_	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
92	c3eo0L_	Alignment	not modelled	96.1	12	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
93	cljqoA_	Alignment	not modelled	96.0	16	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
94	dljqoa_	Alignment	not modelled	96.0	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
95	c2yw3E_	Alignment	not modelled	95.8	17	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
96	dlgeqa_	Alignment	not modelled	95.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
97	c2p10D_	Alignment	not modelled	95.6	16	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
98	c2z6jB_	Alignment	not modelled	95.5	14	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
99	c3q94B_	Alignment	not modelled	95.5	15	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'
100	c3pm6B_	Alignment	not modelled	95.3	13	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
101	c2bdqA_	Alignment	not modelled	95.1	12	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 structural genomics target sar15.
102	c3cu2A_	Alignment	not modelled	94.7	10	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
103	dlpiia2	Alignment	not modelled	94.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
104	c3labA_	Alignment	not modelled	94.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpG (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdpG (2-keto-3-deoxy-6-2-phosphogluconate) aldolase from oleispira antarctica
105	c3bo9B_	Alignment	not modelled	94.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkane dioxygenase; PDBTitle: crystal structure of putative nitroalkane dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution

106	c2iswB_	 Alignment	not modelled	94.4	14	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
107	d1zfja1	 Alignment	not modelled	94.4	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
108	d1mvoa_	 Alignment	not modelled	94.4	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	d1w0ma_	 Alignment	not modelled	94.3	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
110	d1y0ea_	 Alignment	not modelled	94.1	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
111	c3nm3D_	 Alignment	not modelled	94.1	18	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
112	d1dz3a_	 Alignment	not modelled	94.1	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
113	d1o4ua1	 Alignment	not modelled	94.1	20	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
114	d1q6oa_	 Alignment	not modelled	93.9	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
115	d1yxya1	 Alignment	not modelled	93.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
116	c1znnF_	 Alignment	not modelled	93.7	13	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
117	d2p10a1	 Alignment	not modelled	93.3	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MII9387-like
118	c3ez4B_	 Alignment	not modelled	93.0	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
119	d1h5ya_	 Alignment	not modelled	93.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
120	d1a2oa1	 Alignment	not modelled	92.6	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related