







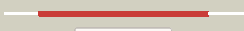










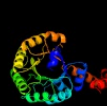




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1998c (-)_2242953_2243729
Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	282be097599114b3

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uncB_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
2	c4lsbA_	 Alignment		100.0	32	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
3	c3ih1A_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
4	c2ze3A_	 Alignment		100.0	37	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
5	d1muma_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
6	c2hjpA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
7	c3b8fF_	 Alignment		100.0	23	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+.
8	c3fa4D_	 Alignment		100.0	22	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
9	c1zlpA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
10	c3eool_	 Alignment		100.0	23	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
11	d1ujqa_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like

12	c3lyeA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
13	c2qiwa_	Alignment		100.0	27	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
14	c4mg4G_	Alignment		100.0	35	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
15	d1s2wa_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
16	c3e5bB_	Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
17	c3i4eA_	Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
18	d1f61a_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
19	d1igwa_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
20	c3eolB_	Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
21	d1m3ua_	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
22	d1oy0a_	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
23	c3ez4B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
24	c5e9fD_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
25	d1dqua_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
26	d1o66a_	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
27	c6g1oA_	Alignment	not modelled	99.9	18	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: structure of pseudomonas aeruginosa isocitrate lyase, icl
28	c2p10D_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphoenolpyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution

29	d2p10a1	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MI9387-like
30	d1rd5a_	Alignment	not modelled	98.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
31	d1xcfa_	Alignment	not modelled	98.5	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
32	d1qopa_	Alignment	not modelled	98.4	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
33	c3navB_	Alignment	not modelled	98.3	15	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from <i>Vibrio cholerae</i> O1 biovar El Tor str. n16961
34	c3vndD_	Alignment	not modelled	98.3	15	PDB header: lyase Chain: D; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of a truncated variant of tryptophan synthase from the <i>Psychrophile Shewanella frigidimarina</i> K14-2
35	c2ekcA_	Alignment	not modelled	98.2	12	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from <i>Aquifex aeolicus</i> vf5
36	c6ofuC_	Alignment	not modelled	98.1	14	PDB header: lyase Chain: C; PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from <i>Escherichia coli</i> K12
37	c5kzmA_	Alignment	not modelled	98.0	13	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from <i>Francisella tularensis</i>
38	c2c3zA_	Alignment	not modelled	98.0	13	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 <i>Sulfolobus solfataricus</i>
39	c3igsB_	Alignment	not modelled	98.0	17	PDB header: isomerase Chain: B; PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the <i>Salmonella enterica</i> n-acetylmannosamine-6-phosphate 2-epimerase
40	c2v5jB_	Alignment	not modelled	98.0	20	PDB header: lyase Chain: B; PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class II aldolase hpch
41	c3daqB_	Alignment	not modelled	97.9	19	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant <i>Staphylococcus aureus</i>
42	c4tv6A_	Alignment	not modelled	97.9	17	PDB header: lyase Chain: A; PDB Molecule: 2-dehydro-3-deoxyglucuronate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
43	c3lerA_	Alignment	not modelled	97.9	17	PDB header: lyase Chain: A; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168
44	d1gvfa_	Alignment	not modelled	97.9	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
45	d1y0ea_	Alignment	not modelled	97.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
46	c3n2xB_	Alignment	not modelled	97.8	22	PDB header: lyase Chain: B; PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from <i>E. coli</i> K12 in complex 3 with pyruvate
47	c3qz6A_	Alignment	not modelled	97.8	14	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from <i>Desulfitobacterium hafniense</i> dcb-2
48	c4ml9A_	Alignment	not modelled	97.8	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized TIM barrel protein with the 2 conserved phosphate binding site from <i>Sebalidella termitidis</i>
49	c4ur7B_	Alignment	not modelled	97.8	16	PDB header: lyase Chain: B; PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase 2 complexed with pyruvate
50	c6daoB_	Alignment	not modelled	97.8	14	PDB header: lyase Chain: B; PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: naive wt selenomethionine
51	d1h5ya_	Alignment	not modelled	97.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
52	c5n2pA_	Alignment	not modelled	97.8	9	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: <i>Sulfolobus solfataricus</i> tryptophan synthase a
53	c2v9dB_	Alignment	not modelled	97.8	22	PDB header: lyase Chain: B; PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from <i>E. coli</i> K12
54	c2qjhH_	Alignment	not modelled	97.8	17	PDB header: lyase Chain: H; PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to 2 dihydroxyacetone phosphate

55	c3s5oA	Alignment	not modelled	97.8	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
56	c6b8sB	Alignment	not modelled	97.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
57	d1xxxa1	Alignment	not modelled	97.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c3noeA	Alignment	not modelled	97.7	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
59	c3tsmB	Alignment	not modelled	97.7	16	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
60	c3e96B	Alignment	not modelled	97.7	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
61	c3cprB	Alignment	not modelled	97.7	20	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
62	c4nq1B	Alignment	not modelled	97.7	15	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
63	c4x2rA	Alignment	not modelled	97.7	17	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
64	c2r8wB	Alignment	not modelled	97.7	15	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
65	c5zknA	Alignment	not modelled	97.7	18	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
66	d1o5ka	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	d1dxea	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
68	c3w9zA	Alignment	not modelled	97.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
69	c4uxdC	Alignment	not modelled	97.6	6	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
70	d1ojxa	Alignment	not modelled	97.6	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	c4xkyC	Alignment	not modelled	97.6	15	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
72	c2yxgD	Alignment	not modelled	97.6	21	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
73	c3fkkA	Alignment	not modelled	97.6	21	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
74	c2ehhE	Alignment	not modelled	97.6	16	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
75	c6mqhA	Alignment	not modelled	97.6	17	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
76	c3qfeB	Alignment	not modelled	97.6	22	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
77	c6h4eB	Alignment	not modelled	97.6	11	PDB header: lyase Chain: B: PDB Molecule: putative n-acetylneuraminate lyase; PDBTitle: proteus mirabilis n-acetylneuraminate lyase
78	c3lciA	Alignment	not modelled	97.6	16	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
79	c3eb2A	Alignment	not modelled	97.6	23	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution

80	d1xkya1	Alignment	not modelled	97.6	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
81	c3fluD_	Alignment	not modelled	97.6	21	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
82	c3qjaA_	Alignment	not modelled	97.6	17	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
83	c5ud6B_	Alignment	not modelled	97.6	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
84	c4i7vD_	Alignment	not modelled	97.6	19	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhds with pyruvate
85	c5ey5A_	Alignment	not modelled	97.6	15	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
86	c3d0cB_	Alignment	not modelled	97.6	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
87	c4mf4F_	Alignment	not modelled	97.5	16	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
88	c3bi8A_	Alignment	not modelled	97.5	22	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
89	c3g0sA_	Alignment	not modelled	97.5	18	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
90	d1vzwa1	Alignment	not modelled	97.5	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
91	c2rfgB_	Alignment	not modelled	97.5	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
92	c6daqA_	Alignment	not modelled	97.5	18	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
93	c5kinC_	Alignment	not modelled	97.5	14	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
94	c4n4qD_	Alignment	not modelled	97.5	17	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
95	c3thaB_	Alignment	not modelled	97.5	10	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
96	c5afdA_	Alignment	not modelled	97.5	13	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: native structure of n-acetylneuraminate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
97	c4ah7C_	Alignment	not modelled	97.5	18	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
98	c3q94B_	Alignment	not modelled	97.5	13	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
99	c3dz1A_	Alignment	not modelled	97.4	20	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
100	d1hl2a_	Alignment	not modelled	97.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
101	c3si9B_	Alignment	not modelled	97.4	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
102	c4icnB_	Alignment	not modelled	97.4	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
103	d2a6na1	Alignment	not modelled	97.4	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
104	c2vc6A_	Alignment	not modelled	97.4	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
105	c1ps9A_	Alignment	not modelled	97.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase PDB header: lyase

106	c2vwtA_	Alignment	not modelled	97.4	17	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
107	d1rvga_	Alignment	not modelled	97.4	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
108	d1geqa_	Alignment	not modelled	97.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
109	c3na8A_	Alignment	not modelled	97.3	17	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
110	c4n6eA_	Alignment	not modelled	97.3	17	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
111	c4xq6A_	Alignment	not modelled	97.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
112	c2nuxB_	Alignment	not modelled	97.3	11	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 sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
113	c4utwB_	Alignment	not modelled	97.3	18	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
114	c4ot7A_	Alignment	not modelled	97.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
115	c2r94B_	Alignment	not modelled	97.3	14	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
116	c2htmB_	Alignment	not modelled	97.3	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
117	c6r62A_	Alignment	not modelled	97.2	18	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
118	c3pm6B_	Alignment	not modelled	97.2	11	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
119	c5c54D_	Alignment	not modelled	97.2	23	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminase lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
120	c5zjnB_	Alignment	not modelled	97.2	20	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate