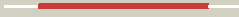





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3534c (-) _3972731_3973771
Date	Fri Aug 9 18:20:21 BST 2019
Unique Job ID	c160e92b86f0910a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4jn6C_	 Alignment		100.0	100	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
2	c4lrtC_	 Alignment		100.0	62	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
3	c1nvmG_	 Alignment		100.0	48	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
4	c3ivuB_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
5	c6e1jB_	 Alignment		100.0	23	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
6	c3a9iA_	 Alignment		100.0	20	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
7	c4ov9A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
8	c1sr9A_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
9	c2zyfA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
10	d1nvm2	 Alignment		100.0	49	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
11	c1rr2A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid

12	c3hpxB_	Alignment		100.0	16	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644)
13	c3rmjB_	Alignment		100.0	26	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
14	c2nx9B_	Alignment		100.0	18	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
15	c3bg3A_	Alignment		100.0	14	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
16	c3bleA_	Alignment		100.0	25	PDB header: transferase Chain: A; PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
17	c5ks8D_	Alignment		100.0	19	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
18	c4qslE_	Alignment		100.0	16	PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
19	c3bg5C_	Alignment		100.0	15	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
20	d1rqba2	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
21	c3dxiB_	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvj_2661) from bacteroides vulgatus
22	c3bg3B_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
23	c2ftpA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
24	c1ydoC_	Alignment	not modelled	100.0	22	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.
25	c5ks8F_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: F; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
26	c2cw6B_	Alignment	not modelled	100.0	21	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
27	c1ydnA_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
28	c3pwhY_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: X; PDB Molecule: 2-isopropylmalate synthase;

28	c3ewbA	Alignment	not modelled	100.0	23	PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes PDB header: ligase
29	c4qslC	Alignment	not modelled	100.0	16	Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
30	d1sr9a2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
31	c3eegB	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
32	c4hnbV	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
33	c2qf7A	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
34	c4qskB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
35	c3bg5B	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
36	c5vz0D	Alignment	not modelled	100.0	15	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
37	c3tw6B	Alignment	not modelled	100.0	16	PDB header: ligase/activator Chain: B; PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
38	c3hblA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
39	d1xcfa	Alignment	not modelled	98.6	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
40	c2ekcA	Alignment	not modelled	98.4	11	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
41	c3t7vA	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
42	c3vndD	Alignment	not modelled	98.4	16	PDB header: lyase Chain: D; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
43	c3thaB	Alignment	not modelled	98.3	14	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
44	c5kzmA	Alignment	not modelled	98.3	17	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
45	c5n2pA	Alignment	not modelled	98.3	13	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
46	c1r30A	Alignment	not modelled	98.2	11	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
47	d1r30a	Alignment	not modelled	98.2	11	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
48	c3navB	Alignment	not modelled	98.2	22	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
49	d1qopa	Alignment	not modelled	98.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
50	c3cixA	Alignment	not modelled	98.1	17	PDB header: adomet binding protein Chain: A; PDB Molecule: fe-fe-hydrogenase maturase; PDBTitle: x-ray structure of the [fe-fe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
51	d1rd5a	Alignment	not modelled	98.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
52	c4e38A	Alignment	not modelled	98.1	15	PDB header: lyase Chain: A; PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
53	c5tchG	Alignment	not modelled	98.1	22	PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
54	c5oxkG	Alignment	not modelled	98.1	13	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase;

54	c5xkg	Alignment	not modelled	98.1	13	PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate PDB header: lyase
55	c5k9xA	Alignment	not modelled	98.1	14	Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
56	c6oviA	Alignment	not modelled	98.0	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
57	c6ncsB	Alignment	not modelled	98.0	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
58	c4nu7C	Alignment	not modelled	97.9	15	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
59	d2zdra2	Alignment	not modelled	97.8	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
60	d1wbha1	Alignment	not modelled	97.8	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
61	c3f4wA	Alignment	not modelled	97.8	18	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
62	c4wxcC	Alignment	not modelled	97.8	14	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
63	c3ajxA	Alignment	not modelled	97.8	17	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
64	d1geqa	Alignment	not modelled	97.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
65	d1vlia2	Alignment	not modelled	97.7	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
66	c5ey5A	Alignment	not modelled	97.7	19	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
67	d1nvma1	Alignment	not modelled	97.7	40	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
68	c1tx2A	Alignment	not modelled	97.6	14	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
69	d1tx2a	Alignment	not modelled	97.6	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
70	d1tqxA	Alignment	not modelled	97.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
71	d1rvga	Alignment	not modelled	97.6	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
72	d1q6oa	Alignment	not modelled	97.6	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
73	d1thfd	Alignment	not modelled	97.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
74	d1vhca	Alignment	not modelled	97.5	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
75	c5kinC	Alignment	not modelled	97.5	15	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
76	d1mxsa	Alignment	not modelled	97.5	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
77	c1xuzA	Alignment	not modelled	97.5	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siaC; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
78	c3qc3B	Alignment	not modelled	97.4	15	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
79	d1ad1a	Alignment	not modelled	97.4	13	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase

80	d1ajza_	Alignment	not modelled	97.4	18	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
81	c1vliA_	Alignment	not modelled	97.4	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
82	d1ujpa_	Alignment	not modelled	97.3	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
83	c3exsB_	Alignment	not modelled	97.3	16	PDB header: lyase Chain: B: PDB Molecule: rmppd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
84	c3jr2D_	Alignment	not modelled	97.3	18	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
85	d1h1ya_	Alignment	not modelled	97.2	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
86	c3pg8B_	Alignment	not modelled	97.2	17	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
87	c5u4nA_	Alignment	not modelled	97.2	18	PDB header: lyase Chain: A: PDB Molecule: fructose-1; PDBTitle: crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
88	c6omzA_	Alignment	not modelled	97.0	17	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
89	c4bk9B_	Alignment	not modelled	97.0	15	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
90	c3nvtA_	Alignment	not modelled	96.9	15	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
91	c4rtbA_	Alignment	not modelled	96.9	14	PDB header: lyase Chain: A: PDB Molecule: hydgc protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydgc from2 carboxydotherrmus hydrogenoformans
92	d1wa3a1	Alignment	not modelled	96.9	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	c3c52B_	Alignment	not modelled	96.9	13	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
94	d1tqja_	Alignment	not modelled	96.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
95	c4u0pB_	Alignment	not modelled	96.8	11	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
96	c4qccA_	Alignment	not modelled	96.7	24	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
97	c3vylB_	Alignment	not modelled	96.7	19	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
98	c3l2iB_	Alignment	not modelled	96.7	17	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
99	c2yw3E_	Alignment	not modelled	96.7	11	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
100	d1rpxa_	Alignment	not modelled	96.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
101	c3w9zA_	Alignment	not modelled	96.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
102	d1j5ta_	Alignment	not modelled	96.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
103	c3tr9A_	Alignment	not modelled	96.4	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex

						with pteroiC2 acid from coxiella burnetii
104	c3d0cB_	Alignment	not modelled	96.3	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
105	c5b69A_	Alignment	not modelled	96.3	21	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: crystal structure of geranylgeranyl glyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
106	c5z79F_	Alignment	not modelled	96.3	17	PDB header: transferase Chain: F: PDB Molecule: hydroxymethyl dihydropterin pyrophosphokinase- PDBTitle: crystal structure analysis of the hppk-dhps in complex with substrates
107	c2v82A_	Alignment	not modelled	96.3	18	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
108	c2vp8A_	Alignment	not modelled	96.3	21	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
109	d1vc4a_	Alignment	not modelled	96.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
110	c2c3zA_	Alignment	not modelled	96.2	11	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
111	c6daqA_	Alignment	not modelled	96.2	19	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
112	c3inpA_	Alignment	not modelled	96.2	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.
113	c3stgA_	Alignment	not modelled	96.2	12	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
114	c6cluC_	Alignment	not modelled	96.1	16	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
115	c5uurA_	Alignment	not modelled	96.1	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
116	d1gqna_	Alignment	not modelled	96.1	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
117	d1vr6a1	Alignment	not modelled	96.1	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
118	c2h9aB_	Alignment	not modelled	96.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
119	d1gvfa_	Alignment	not modelled	96.1	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
120	c3e96B_	Alignment	not modelled	96.1	19	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii