







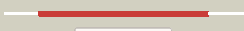












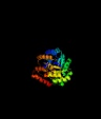



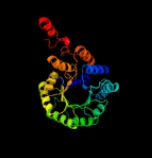


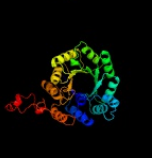




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3469c_(mhpE)_3886252_3887262
Date	Fri Aug 9 18:20:14 BST 2019
Unique Job ID	a00e0c01bf19c5c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nvmG_	 Alignment		100.0	28	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
2	c4jn6C_	 Alignment		100.0	31	PDB header: lyase/oxidoreductase Chain: C; PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
3	c4lrtC_	 Alignment		100.0	30	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
4	c2nx9B_	 Alignment		100.0	19	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
5	c1rr2A_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
6	c5ks8D_	 Alignment		100.0	20	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
7	c3dxiB_	 Alignment		100.0	22	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
8	d1nvma2	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
9	c4qslE_	 Alignment		100.0	16	PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
10	c3bg3A_	 Alignment		100.0	17	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)
11	c3bg5C_	 Alignment		100.0	17	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase

12	c3bg3B_	Alignment		100.0	18	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)
13	c3ivuB_	Alignment		100.0	22	PDB header: transferase Chain: B; PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
14	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
15	c1sr9A_	Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
16	c3rmjB_	Alignment		100.0	24	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
17	c2ftpA_	Alignment		100.0	22	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
18	c4ov9A_	Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
19	c3a9iA_	Alignment		100.0	21	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
20	c3bleA_	Alignment		100.0	21	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
21	c4qslC_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
22	c2zyfA_	Alignment	not modelled	100.0	21	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
23	c1ydnA_	Alignment	not modelled	100.0	20	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.
24	c5ks8F_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: F; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
25	c2cw6B_	Alignment	not modelled	100.0	22	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
26	d1rqba2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
27	c3hpxB_	Alignment	not modelled	100.0	19	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)
						PDB header: lyase

28	c1ydoC_	Alignment	not modelled	100.0	20	Chain: C; PDB Molecule: nmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
29	c3ewbX_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: X; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
30	d1sr9a2	Alignment	not modelled	100.0	18	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	c2qf7A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
33	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
34	c4hnbV_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
35	c5vz0D_	Alignment	not modelled	100.0	16	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
36	c3bg5B_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
37	c3tw6B_	Alignment	not modelled	100.0	19	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	c2ekcA_	Alignment	not modelled	98.6	15	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
40	c3vndD_	Alignment	not modelled	98.5	17	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
41	d1xcfa_	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
42	c5kzmA_	Alignment	not modelled	98.5	16	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
43	c3thaB_	Alignment	not modelled	98.5	14	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
44	c3navB_	Alignment	not modelled	98.4	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
45	d1qopa_	Alignment	not modelled	98.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	c5n2pA_	Alignment	not modelled	98.2	14	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
47	c5k9xA_	Alignment	not modelled	98.2	14	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
48	c3t7vA_	Alignment	not modelled	98.2	15	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
49	d1rd5a_	Alignment	not modelled	98.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
50	c5tchG_	Alignment	not modelled	98.2	18	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
51	c5kinC_	Alignment	not modelled	98.1	17	PDB header: lyase Chain: C; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
52	c4wxcC_	Alignment	not modelled	97.9	13	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fef]-hydrogenase
53	d1geqa_	Alignment	not modelled	97.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
54	c5ey5A_	Alignment	not modelled	97.9	19	PDB header: lyase Chain: A; PDB Molecule: ilbcats-a;

						PDBTitle: lbcats
55	c3cixA	Alignment	not modelled	97.9	11	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from <i>Thermotoga maritima</i> in complex with thiocyanate
56	d1ujpa	Alignment	not modelled	97.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
57	c5exkG	Alignment	not modelled	97.7	14	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
58	d1rvga	Alignment	not modelled	97.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
59	c5u4nA	Alignment	not modelled	97.5	16	PDB header: lyase Chain: A: PDB Molecule: fructose-1; PDBTitle: crystal structure of a fructose-bisphosphate aldolase from <i>Neisseria gonorrhoeae</i>
60	c4nu7C	Alignment	not modelled	97.5	13	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from <i>Toxoplasma gondii</i> .
61	c1r30A	Alignment	not modelled	97.5	15	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
62	d1r30a	Alignment	not modelled	97.5	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
63	d1nvma1	Alignment	not modelled	97.5	18	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
64	d1tqxa	Alignment	not modelled	97.4	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
65	c3ajxA	Alignment	not modelled	97.4	17	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
66	c3f4wA	Alignment	not modelled	97.4	13	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 <i>Salmonella typhimurium</i>
67	c3c52B	Alignment	not modelled	97.3	12	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from <i>Helicobacter pylori</i> 2 in complex with phosphoglycolhydroxamic acid, a competitive3 inhibitor
68	c6ncsB	Alignment	not modelled	97.3	13	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 <i>Leptospira borgpetersenii</i> serovar hardjo-bovis in complex with3 citrate
69	c3nvtA	Alignment	not modelled	97.3	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 <i>Listeria monocytogenes</i> egd-e
70	c5b69A	Alignment	not modelled	96.9	16	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from <i>Thermoplasma acidophilum</i>
71	c4e38A	Alignment	not modelled	96.9	18	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from <i>Vibrionales bacterium swat-3</i> (target efi-502156)
72	d1q6oa	Alignment	not modelled	96.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
73	c3jr2D	Alignment	not modelled	96.8	14	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 <i>Vibrio cholerae</i> o1 biovar el tor str. n16961
74	c2iswB	Alignment	not modelled	96.7	14	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of <i>Giardia</i> fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolhydroxamate
75	c3pg8B	Alignment	not modelled	96.6	11	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 <i>Thermotoga maritima</i>
76	c4lu0A	Alignment	not modelled	96.6	11	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from <i>Pseudomonas aeruginosa</i> .
77	d1h1ya	Alignment	not modelled	96.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase

78	c6oviA	Alignment	not modelled	96.5	12	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with 2 pyruvate captured at low ph as a covalent carbinolamine intermediate
79	d1vr6a1	Alignment	not modelled	96.4	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
80	d1ka9f	Alignment	not modelled	96.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
81	c3inpA	Alignment	not modelled	96.4	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.
82	c3qc3B	Alignment	not modelled	96.4	11	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
83	d1thfd	Alignment	not modelled	96.4	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
84	d2zdra2	Alignment	not modelled	96.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
85	d1gvfa	Alignment	not modelled	96.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
86	c3pm6B	Alignment	not modelled	96.3	16	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from 2 coccidioides immitis solved by combined sad mr
87	d1vhca	Alignment	not modelled	96.2	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
88	c1vliA	Alignment	not modelled	96.2	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein 2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
89	c2ou4C	Alignment	not modelled	96.2	16	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from 2 pseudomonas cichorii
90	d1mxsa	Alignment	not modelled	96.2	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c4rtbA	Alignment	not modelled	96.2	14	PDB header: lyase Chain: A: PDB Molecule: hydG protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydG from 2 carboxydotherrmus hydrogenoformans
92	c6nkeA	Alignment	not modelled	96.1	13	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
93	d1tqja	Alignment	not modelled	96.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
94	d1wbha1	Alignment	not modelled	95.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d1vliA2	Alignment	not modelled	95.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
96	c4ml9A	Alignment	not modelled	95.9	22	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 seabaldella termitidis
97	c3exsB	Alignment	not modelled	95.8	14	PDB header: lyase Chain: B: PDB Molecule: rmppd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in 2 complex with d-r5p
98	c3vylB	Alignment	not modelled	95.8	18	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
99	c1zcoA	Alignment	not modelled	95.7	17	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphoheptonate aldolase; PDBTitle: crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
100	c3w9zA	Alignment	not modelled	95.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
101	d2flia1	Alignment	not modelled	95.7	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
102	c1tx2A	Alignment	not modelled	95.6	15	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus 2 anthracis
103	d1tx2a	Alignment	not modelled	95.6	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase

104	c3ct7E_	 Alignment	not modelled	95.6	11	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
105	c1xuzA_	 Alignment	not modelled	95.5	16	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
106	c5d88A_	 Alignment	not modelled	95.5	25	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
107	c3vkbA_	 Alignment	not modelled	95.4	12	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
108	c3elfA_	 Alignment	not modelled	95.3	15	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
109	c3sz8D_	 Alignment	not modelled	95.3	14	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
110	d1d9ea_	 Alignment	not modelled	95.2	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
111	c5tnvA_	 Alignment	not modelled	95.1	16	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
112	c2h9aB_	 Alignment	not modelled	95.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
113	c2c3zA_	 Alignment	not modelled	95.0	15	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
114	d1qwga_	 Alignment	not modelled	95.0	16	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
115	c1gthD_	 Alignment	not modelled	94.9	14	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
116	d1tv8a_	 Alignment	not modelled	94.9	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
117	c4mwaA_	 Alignment	not modelled	94.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
118	c4u0pB_	 Alignment	not modelled	94.9	11	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
119	c3bolB_	 Alignment	not modelled	94.8	14	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
120	c3l23A_	 Alignment	not modelled	94.8	11	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution