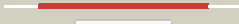



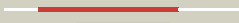















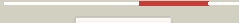












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2868c_(ispG)_3179378_3180541
Date	Wed Aug 7 12:50:54 BST 2019
Unique Job ID	f4fd38e11296dce3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3noyA_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
2	c2y0fD_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
3	c4mwaA_	 Alignment		100.0	49	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
4	c5aopA_	 Alignment		99.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase hemoprotein; PDBTitle: sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
5	c5h92A_	 Alignment		99.4	20	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: sulfite reductase [ferredoxin], chloroplastic; PDBTitle: crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal
6	c1zj8B_	 Alignment		99.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: probable ferredoxin-dependent nitrite reductase nira; PDBTitle: structure of mycobacterium tuberculosis nira protein
7	c3b0nA_	 Alignment		99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: q448k mutant of assimilatory nitrite reductase (nii3) from tobacc02 leaf
8	c2akjA_	 Alignment		99.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nitrite reductase, chloroplast; PDBTitle: structure of spinach nitrite reductase
9	d1aopa4	 Alignment		99.2	28	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
10	d3c7bb3	 Alignment		99.1	20	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
11	c2v4jE_	 Alignment		99.1	23	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration

12	d3c7ba3	Alignment		99.0	21	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
13	d2v4jb3	Alignment		99.0	22	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
14	d2v4ja3	Alignment		99.0	23	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
15	d1zj8a3	Alignment		99.0	23	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
16	d2akja3	Alignment		99.0	29	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
17	d1aopa3	Alignment		98.9	15	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
18	d2akja4	Alignment		98.9	16	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
19	c3c7bA_	Alignment		98.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
20	c3c7bE_	Alignment		98.9	20	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
21	d1zj8a4	Alignment	not modelled	98.8	14	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
22	d1tx2a_	Alignment	not modelled	98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
23	c1tx2A_	Alignment	not modelled	98.6	15	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
24	c5visB_	Alignment	not modelled	98.6	13	PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
25	c2v4jA_	Alignment	not modelled	98.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
26	c5vooB_	Alignment	not modelled	98.6	22	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8
27	c3tr9A_	Alignment	not modelled	98.5	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteric2 acid from coxiella burnetii
						Fold: TIM beta/alpha-barrel

28	d1eyea_	Alignment	not modelled	98.5	18	Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
29	c2y5sA_	Alignment	not modelled	98.4	19	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
30	c3k13A_	Alignment	not modelled	98.4	20	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
31	c2yciX_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
32	d1ad1a_	Alignment	not modelled	98.4	17	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
33	c4o1fB_	Alignment	not modelled	98.4	13	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
34	c3pg8B_	Alignment	not modelled	98.3	15	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
35	d1ajza_	Alignment	not modelled	98.3	17	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
36	c5uswD_	Alignment	not modelled	98.3	14	PDB header: transferase Chain: D: PDB Molecule: dihydropteroate synthase; PDBTitle: the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
37	c6omzA_	Alignment	not modelled	98.3	18	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
38	d1f6ya_	Alignment	not modelled	98.3	13	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
39	d3bofa1	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
40	c5uurA_	Alignment	not modelled	98.2	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
41	c6ncsB_	Alignment	not modelled	98.1	18	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
42	c1vs1B_	Alignment	not modelled	98.1	16	PDB header: transferase Chain: B: PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
43	c4cczA_	Alignment	not modelled	98.1	14	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
44	c3nvtA_	Alignment	not modelled	98.0	24	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
45	c6cluC_	Alignment	not modelled	98.0	18	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sahps) f17l e208k2 double mutant structure
46	d1vr6a1	Alignment	not modelled	97.7	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
47	c2vefB_	Alignment	not modelled	97.6	18	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
48	c2vp8A_	Alignment	not modelled	97.6	13	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
49	c4djeE_	Alignment	not modelled	97.6	16	PDB header: transferase/vitamin-binding protein Chain: E: PDB Molecule: corrinoid/iron-sulfur protein large subunit; PDBTitle: crystal structure of folate-bound corrinoid iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
50	c2h9aA_	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: corrinoid iron-sulfur protein
51	c2dzaA_	Alignment	not modelled	97.5	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from

						thermus2 thermophilus hb8 in complex with 4-aminobenzoate
52	c3fs2A	Alignment	not modelled	97.4	16	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 bruciella melitensis at 1.85a resolution
53	c3bolB	Alignment	not modelled	97.4	13	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
54	c2yr1B	Alignment	not modelled	97.3	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatase dehydratase; PDBTitle: crystal structure of 3-dehydroquinatase dehydratase from geobacillus2 kaustophilus hta426
55	c3t4cD	Alignment	not modelled	97.3	18	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 1; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
56	d2zdra2	Alignment	not modelled	97.3	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
57	c6mdyC	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: C: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a 2-dehydro-3-deoxyphosphooctonate aldolase from2 legionella pneumophila philadelphia 1
58	c2h9aB	Alignment	not modelled	97.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
59	c3js3C	Alignment	not modelled	97.2	20	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinatase dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
60	d1h5ya	Alignment	not modelled	97.2	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
61	c1zcoA	Alignment	not modelled	97.2	13	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
62	c1zfiA	Alignment	not modelled	97.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
63	d1jpmal	Alignment	not modelled	96.9	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
64	c3q45E	Alignment	not modelled	96.8	16	PDB header: isomerase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family; PDBTitle: crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val
65	c4e38A	Alignment	not modelled	96.6	17	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
66	d1nu5a1	Alignment	not modelled	96.5	24	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
67	c3qc3B	Alignment	not modelled	96.5	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
68	c1jpdX	Alignment	not modelled	96.5	19	PDB header: isomerase Chain: X: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
69	d1o60a	Alignment	not modelled	96.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
70	c3ijlA	Alignment	not modelled	96.5	20	PDB header: isomerase Chain: A: PDB Molecule: muconate cycloisomerase; PDBTitle: structure of dipeptide epimerase from bacteroides thetaiotaomicron2 complexed with l-pro-d-glu; nonproductive substrate binding.
71	c4djdD	Alignment	not modelled	96.4	15	PDB header: transferase/vitamin-binding protein Chain: D: PDB Molecule: corrinoid/iron-sulfur protein small subunit; PDBTitle: crystal structure of folate-free corrinoid iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
72	c3ivuB	Alignment	not modelled	96.3	16	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
73	d1tqja	Alignment	not modelled	96.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
74	d1jpdx1	Alignment	not modelled	96.3	19	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
75	c3thaB	Alignment	not modelled	96.2	16	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
						PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate

76	c4lu0A_	Alignment	not modelled	96.2	22	aldolase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.
77	c1jpmB_	Alignment	not modelled	96.2	16	PDB header: isomerase Chain: B: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
78	c2pgwC_	Alignment	not modelled	96.2	20	PDB header: isomerase Chain: C: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of a putative muconate cycloisomerase from2 sinorhizobium meliloti 1021
79	d1rvka1	Alignment	not modelled	96.2	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
80	c1wueA_	Alignment	not modelled	96.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of protein gi:29375081, unknown member of enolase2 superfamily from enterococcus faecalis v583
81	c2bmbA_	Alignment	not modelled	96.0	18	PDB header: transferase Chain: A: PDB Molecule: folic acid synthesis protein fol1; PDBTitle: x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
82	c3q58A_	Alignment	not modelled	96.0	16	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
83	d1d9ea_	Alignment	not modelled	96.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
84	c3qjaA_	Alignment	not modelled	96.0	18	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
85	d1wbha1	Alignment	not modelled	96.0	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	c3px5A_	Alignment	not modelled	95.9	28	PDB header: metal binding protein Chain: A: PDB Molecule: enzyme of enolase superfamily; PDBTitle: structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
87	c2pozA_	Alignment	not modelled	95.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase; PDBTitle: crystal structure of a putative dehydratase from mesorhizobium loti
88	c3i4kA_	Alignment	not modelled	95.8	21	PDB header: isomerase Chain: A: PDB Molecule: muconate lactonizing enzyme; PDBTitle: crystal structure of muconate lactonizing enzyme from corynebacterium2 glutamicum
89	c2fkcC_	Alignment	not modelled	95.8	14	PDB header: isomerase Chain: C: PDB Molecule: n-acylamino acid racemase; PDBTitle: the mutant g127c-t313c of deinococcus radiodurans n-2 acylamino acid racemase
90	c4e4uA_	Alignment	not modelled	95.8	16	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme (target psi-200780) from burkholderia sar-1
91	c3dfyl_	Alignment	not modelled	95.8	20	PDB header: isomerase Chain: J: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of apo dipeptide epimerase from2 thermotoga maritima
92	c2podA_	Alignment	not modelled	95.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mandelate racemase / muconate lactonizing enzyme; PDBTitle: crystal structure of a member of enolase superfamily from burkholderia2 pseudomallei k96243
93	c1xuzA_	Alignment	not modelled	95.8	19	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
94	d1gqna_	Alignment	not modelled	95.8	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	c3mqtv_	Alignment	not modelled	95.8	11	PDB header: isomerase Chain: V: PDB Molecule: PDBTitle: crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from shewanella pealeana
96	c5n2pA_	Alignment	not modelled	95.7	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
97	c1rvkA_	Alignment	not modelled	95.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of enolase agr_l_2751 from agrobacterium tumefaciens
98	c4e5tA_	Alignment	not modelled	95.7	21	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase / muconate lactonizing enzyme, c- PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme (target psi-200750) from labrenzia alexandrii dfl-3 11
99	c3ddmD_	Alignment	not modelled	95.7	19	PDB header: lyase Chain: D: PDB Molecule: putative mandelate racemase/muconate lactonizing

						PDBTitle: crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
100	c4ggbA_	Alignment	not modelled	95.7	18	PDB header: isomerase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a proposed galactarolactone cycloisomerase from2 agrobacterium tumefaciens, target efi-500704, with bound ca,3 disordered loops
101	c2pa6A_	Alignment	not modelled	95.7	18	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of mj0232 from methanococcus jannaschii
102	c3dipA_	Alignment	not modelled	95.7	14	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of an enolase protein from the environmental genome2 shotgun sequencing of the sargasso sea
103	c3stgA_	Alignment	not modelled	95.6	19	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
104	d1h1ya_	Alignment	not modelled	95.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
105	c3l2iB_	Alignment	not modelled	95.6	22	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatate dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinatate dehydratase2 (arod) from salmonella typhimurium lt2.
106	c2qdeA_	Alignment	not modelled	95.6	20	PDB header: lyase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
107	c2p88E_	Alignment	not modelled	95.6	22	PDB header: lyase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme PDBTitle: crystal structure of n-succinyl arg/lys racemase from2 bacillus cereus atcc 14579
108	d1yx1a1	Alignment	not modelled	95.6	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
109	c3mkcA_	Alignment	not modelled	95.5	8	PDB header: isomerase Chain: A: PDB Molecule: racemase; PDBTitle: crystal structure of a putative racemase
110	c5z79F_	Alignment	not modelled	95.5	15	PDB header: transferase Chain: F: PDB Molecule: hydroxymethyldihydropterin pyrophosphokinase- PDBTitle: crystal structure analysis of the hppk-dhps in complex with substrates
111	d1thfd_	Alignment	not modelled	95.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
112	c3sjnB_	Alignment	not modelled	95.5	11	PDB header: lyase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound
113	c6bmaA_	Alignment	not modelled	95.5	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
114	c4ph6A_	Alignment	not modelled	95.4	17	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinatate dehydratase; PDBTitle: structure of 3-dehydroquinatate dehydratase from enterococcus faecalis
115	c3i6tB_	Alignment	not modelled	95.4	15	PDB header: isomerase Chain: B: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of muconate cycloisomerase from jannaschia sp.
116	d1ka9f_	Alignment	not modelled	95.4	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
117	c3msyC_	Alignment	not modelled	95.4	6	PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
118	d2a1a1a1	Alignment	not modelled	95.4	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
119	d1muca1	Alignment	not modelled	95.4	18	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
120	c2ps2A_	Alignment	not modelled	95.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of putative mandelate racemase/muconate lactonizing2 enzyme from aspergillus oryzae