

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1173_(fbiC)_1302936_1305506
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	02e017f26b80b3e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cixA_	 Alignment		100.0	21	PDB header: adomet binding protein Chain: A; PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
2	c4rtbA_	 Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
3	c3t7vA_	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
4	c4r33A_	 Alignment		100.0	13	PDB header: lyase Chain: A; PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
5	c4wxcC_	 Alignment		100.0	17	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
6	c1r30A_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
7	d1r30a_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
8	c4u0pB_	 Alignment		99.9	16	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
9	c5exkG_	 Alignment		99.9	19	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
10	c5zmyF_	 Alignment		99.9	16	PDB header: hydrolase Chain: F; PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
11	c4jc0B_	 Alignment		99.9	15	PDB header: transferase Chain: B; PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77

12	d1olta_	Alignment		99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
13	c6fd2B_	Alignment		99.8	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative apramycin biosynthetic oxidoreductase 4; PDBTitle: radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
14	c5l7jA_	Alignment		99.7	12	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
15	c2qqgF_	Alignment		99.6	9	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
16	c6qk7C_	Alignment		99.6	9	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
17	d1tv8a_	Alignment		99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
18	c6iazA_	Alignment		99.5	11	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
19	c3rfaB_	Alignment		99.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
20	c5vslB_	Alignment		99.2	16	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
21	c5v1tA_	Alignment	not modelled	99.2	15	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
22	c5ul4A_	Alignment	not modelled	99.2	17	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
23	c6efnA_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
24	c6b4cH_	Alignment	not modelled	99.2	13	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
25	c3rfaA_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
26	c3c8fA_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
27	c6fz6B_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
						PDB header: oxidoreductase

28	c4k39A	Alignment	not modelled	99.0	11	Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
29	c4m7tA	Alignment	not modelled	98.8	10	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
30	c2a5hC	Alignment	not modelled	98.6	13	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from <i>Clostridium subterminale</i> sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
31	c2yx0A	Alignment	not modelled	98.4	12	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
32	c4fheA	Alignment	not modelled	98.4	9	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
33	c5wggA	Alignment	not modelled	98.3	9	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis of lactopeptides
34	c5th5C	Alignment	not modelled	98.1	10	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Bacillus subtilis</i> with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
35	c6c8vA	Alignment	not modelled	98.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from <i>Methylobacterium extorquens</i>
36	c3e02A	Alignment	not modelled	98.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from <i>Burkholderia xenovorans</i> lb400 at 1.90 a resolution
37	c3e49A	Alignment	not modelled	97.8	19	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from <i>Burkholderia xenovorans</i> lb4003 at 1.75 a resolution
38	c3chvA	Alignment	not modelled	97.8	18	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spo_a0042) from <i>Silicibacter pomeroyi</i> dss-3 at 1.45 a3 resolution
39	c3no5C	Alignment	not modelled	97.8	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from <i>Ralstonia eutropha</i> jmp134 at 1.90 a resolution
40	c3c6cA	Alignment	not modelled	97.7	14	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from <i>Ralstonia eutropha</i> jmp134 at 1.72 a3 resolution
41	c2y7eA	Alignment	not modelled	97.7	16	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from <i>Candidatus Cloacamonas acidaminovorans</i> (tetragonal form)
42	c3lotC	Alignment	not modelled	97.6	16	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from <i>Archaeoglobus fulgidus</i> at 1.89 a resolution
43	c1nmvG	Alignment	not modelled	97.5	14	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
44	d1ka9f	Alignment	not modelled	97.2	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
45	c3ivuB	Alignment	not modelled	97.1	11	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
46	c2nx9B	Alignment	not modelled	96.9	13	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the oxaloacetate decarboxylase na+ pump from <i>Vibrio cholerae</i>
47	c4jn6C	Alignment	not modelled	96.8	16	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from <i>Mycobacterium tuberculosis</i> hrv37
48	c2cw6B	Alignment	not modelled	96.8	9	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into 2 catalysis and the molecular basis for 3 hydroxymethylglutaric aciduria
49	c3eegB	Alignment	not modelled	96.8	14	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from <i>Cytophaga hutchinsonii</i>
50	c4njka	Alignment	not modelled	96.6	14	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Burkholderia multivorans</i> in

						complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
51	d1nvma2	Alignment	not modelled	96.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
52	c1rr2A	Alignment	not modelled	96.5	12	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
53	c3canA	Alignment	not modelled	96.5	14	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
54	c3bleA	Alignment	not modelled	96.4	9	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
55	c2ftpA	Alignment	not modelled	96.4	11	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
56	c5ks8D	Alignment	not modelled	96.3	14	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
57	c1ydnA	Alignment	not modelled	96.2	10	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.
58	c3labA	Alignment	not modelled	96.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpk (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpk (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
59	c6e1jB	Alignment	not modelled	96.0	10	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
60	d1thfd	Alignment	not modelled	96.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
61	c3rmjB	Alignment	not modelled	95.9	14	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
62	c3bg3B	Alignment	not modelled	95.8	21	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)
63	c1ydoC	Alignment	not modelled	95.6	9	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.
64	c5kzmA	Alignment	not modelled	95.5	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
65	d1h5ya	Alignment	not modelled	95.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
66	c4nncA	Alignment	not modelled	95.5	20	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate
67	d1wbha1	Alignment	not modelled	95.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
68	d1m5wa	Alignment	not modelled	95.3	18	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
69	c5dlcC	Alignment	not modelled	95.1	19	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
70	c4lrtc	Alignment	not modelled	95.0	16	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
71	c3dxiB	Alignment	not modelled	94.8	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
72	d1rqba2	Alignment	not modelled	94.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
73	d1rvka1	Alignment	not modelled	94.4	10	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
74	c3ewbX	Alignment	not modelled	94.3	14	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
						Fold: TIM beta/alpha-barrel

75	d1tx2a_	Alignment	not modelled	94.2	16	Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
76	c1tx2A_	Alignment	not modelled	94.2	16	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
77	c1vs1B_	Alignment	not modelled	94.0	15	PDB header: transferase Chain: B: PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphatase synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
78	c3gk0H_	Alignment	not modelled	93.8	16	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
79	c5vooB_	Alignment	not modelled	93.6	16	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8
80	c3obkH_	Alignment	not modelled	93.5	17	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
81	c1zcoA_	Alignment	not modelled	93.4	14	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
82	d1mxsa_	Alignment	not modelled	93.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
83	c6oviA_	Alignment	not modelled	92.8	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
84	d1pv8a_	Alignment	not modelled	92.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
85	c3vndD_	Alignment	not modelled	92.6	15	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
86	d2c1ha1	Alignment	not modelled	92.3	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
87	c5visB_	Alignment	not modelled	92.3	21	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.
88	c2vefB_	Alignment	not modelled	92.1	16	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
89	c2z2uA_	Alignment	not modelled	92.1	14	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
90	c3fs2A_	Alignment	not modelled	92.1	12	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 brucella melitensis at 1.85a resolution
91	d1ad1a_	Alignment	not modelled	92.0	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
92	c5ks8F_	Alignment	not modelled	92.0	12	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
93	d2a21a1	Alignment	not modelled	91.9	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
94	c3bg3A_	Alignment	not modelled	91.7	22	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)
95	d1ajza_	Alignment	not modelled	91.4	20	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
96	d1h7na_	Alignment	not modelled	91.3	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
97	c2bdqA_	Alignment	not modelled	91.1	13	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
98	c1sr9A_	Alignment	not modelled	90.9	11	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
99	d1ozza_	Alignment	not modelled	90.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase

99	d1gzya_	Alignment	not modelled	90.7	17	Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
100	d2flia1	Alignment	not modelled	90.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
101	c2zyfA	Alignment	not modelled	90.4	10	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
102	c2v82A	Alignment	not modelled	90.3	16	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
103	c2ekcA	Alignment	not modelled	90.1	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
104	c3w9zA	Alignment	not modelled	90.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
105	d1l6sa_	Alignment	not modelled	89.9	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
106	c6nhlB	Alignment	not modelled	89.8	17	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
107	c4e38A	Alignment	not modelled	89.7	11	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)
108	d1qopa_	Alignment	not modelled	89.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
109	c5umfB	Alignment	not modelled	89.4	11	PDB header: isomerase Chain: B: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
110	c6fnuA	Alignment	not modelled	88.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: methylenetetrahydrofolate reductase 1; PDBTitle: structure of s. cerevisiae methylenetetrahydrofolate reductase 1,2 catalytic domain
111	d1h1ya_	Alignment	not modelled	88.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
112	c5uurA	Alignment	not modelled	88.6	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
113	d1vhca_	Alignment	not modelled	88.4	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
114	d1bqga1	Alignment	not modelled	88.2	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
115	d1ub3a_	Alignment	not modelled	88.2	30	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
116	c4z1bA	Alignment	not modelled	88.0	9	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: structure of h204a mutant kdo8ps from h.pylori
117	c6cluC	Alignment	not modelled	87.9	20	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
118	c3tdmD	Alignment	not modelled	87.9	15	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfllr
119	c4ot7A	Alignment	not modelled	87.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
120	d1jdfa1	Alignment	not modelled	87.1	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like