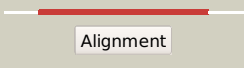

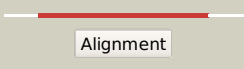

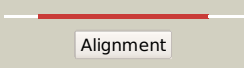

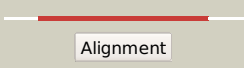

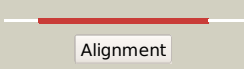

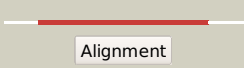

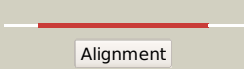

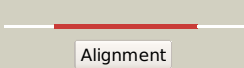

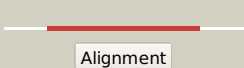

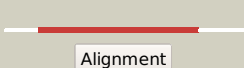

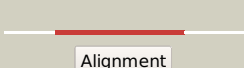





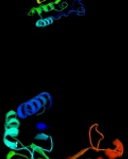
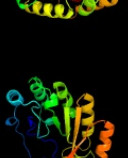


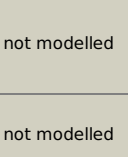


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1589_(bioB)_1790291_1791340
 Date Fri Aug 2 13:30:18 BST 2019
 Unique Job ID 37ba975b5671e3c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cixA_			100.0	21	PDB header: adomet binding protein Chain: A; PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyd from2 thermotoga maritima in complex with thiocyanate
2	c4rtbA_			100.0	21	PDB header: lyase Chain: A; PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
3	c1r30A_			100.0	35	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
4	d1r30a_			100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
5	c3t7vA_			100.0	18	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
6	c4wxcC_			100.0	18	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
7	c4r33A_			100.0	16	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
8	c4jc0B_			100.0	18	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
9	c5exkG_			100.0	17	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
10	c4u0pB_			100.0	19	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
11	c6fd2B_			100.0	20	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

12	d1olta_	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
13	c5l7jA_	Alignment		99.9	15	PDB header: translation Chain: A; PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
14	c6qk7C_	Alignment		99.9	17	PDB header: translation Chain: C; PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
15	c2qgqF_	Alignment		99.9	15	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	c5ul4A_	Alignment		99.9	14	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
17	c6iazA_	Alignment		99.8	16	PDB header: transferase Chain: A; PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
18	d1tv8a_	Alignment		99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
19	c3rfaB_	Alignment		99.7	14	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	c3rfaA_	Alignment		99.7	13	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
21	c6fz6B_	Alignment	not modelled	99.7	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
22	c5v1tA_	Alignment	not modelled	99.7	12	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
23	c5vslB_	Alignment	not modelled	99.6	10	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)
24	c6efnA_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: A; PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
25	c3c8fA_	Alignment	not modelled	99.5	7	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
26	c2yx0A_	Alignment	not modelled	99.5	16	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
27	c6b4cH_	Alignment	not modelled	99.4	7	PDB header: antiviral protein Chain: H; PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
28	c4k39A_	Alignment	not modelled	99.4	8	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic sulfatase-maturing enzyme;

28	c4k39A	Alignment	not modelled	99.4	8	PDBTitle: native ansmecepe with bound adomet and cp18cys peptide PDB header: isomerase
29	c2a5hC	Alignment	not modelled	99.3	13	Chain: C; PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
30	c4fheA	Alignment	not modelled	99.3	17	PDB header: lyase Chain: A; PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
31	d1ka9f	Alignment	not modelled	99.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
32	c4m7tA	Alignment	not modelled	99.1	13	PDB header: metal binding protein Chain: A; PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doa
33	c5wggA	Alignment	not modelled	99.1	8	PDB header: peptide binding protein Chain: A; PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
34	d1thfd	Alignment	not modelled	99.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
35	c5th5C	Alignment	not modelled	98.9	8	PDB header: lyase Chain: C; PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
36	c5zmyF	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: F; PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
37	c2ftpA	Alignment	not modelled	98.8	19	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
38	c2cw6B	Alignment	not modelled	98.7	15	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
39	d1h5ya	Alignment	not modelled	98.6	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
40	c3ivuB	Alignment	not modelled	98.6	11	PDB header: transferase Chain: B; PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
41	c1nvmG	Alignment	not modelled	98.6	12	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
42	c3bleA	Alignment	not modelled	98.5	13	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
43	c3eegB	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
44	c3rmjB	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
45	c6c8vA	Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: A; PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
46	c1ydoC	Alignment	not modelled	98.4	13	PDB header: lyase Chain: C; PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
47	c4jn6C	Alignment	not modelled	98.4	14	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
48	c3ewbX	Alignment	not modelled	98.4	12	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
49	d1nvma2	Alignment	not modelled	98.3	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
50	c6e1jB	Alignment	not modelled	98.3	14	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
51	c1ydnA	Alignment	not modelled	98.3	14	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.
52	c2z2uA	Alignment	not modelled	98.1	12	PDB header: metal binding protein Chain: A; PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
						PDB header: isomerase

53	c4axkB_	Alignment	not modelled	98.1	21	Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
54	c4gj1A_	Alignment	not modelled	98.0	18	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
55	d1h1ya_	Alignment	not modelled	98.0	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
56	c4ov9A_	Alignment	not modelled	97.9	12	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
57	c4x2rA_	Alignment	not modelled	97.9	18	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
58	d2flia1	Alignment	not modelled	97.9	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
59	c6oviA_	Alignment	not modelled	97.9	16	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
60	c4nu7C_	Alignment	not modelled	97.8	16	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.
61	c6nhbB_	Alignment	not modelled	97.8	9	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
62	d1rpxa_	Alignment	not modelled	97.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
63	c1sr9A_	Alignment	not modelled	97.8	11	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
64	c1rr2A_	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
65	c2zyfA_	Alignment	not modelled	97.8	15	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
66	d1wbha1	Alignment	not modelled	97.7	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	c4lrtc_	Alignment	not modelled	97.7	13	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
68	d1jvna1	Alignment	not modelled	97.7	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
69	d1tqja_	Alignment	not modelled	97.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
70	d1tqxa_	Alignment	not modelled	97.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
71	c3ct7E_	Alignment	not modelled	97.7	14	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
72	c3canA_	Alignment	not modelled	97.7	13	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
73	c5vooB_	Alignment	not modelled	97.6	15	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8
74	c4e38A_	Alignment	not modelled	97.6	15	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)
75	c5umfB_	Alignment	not modelled	97.6	14	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
76	c2nx9B_	Alignment	not modelled	97.6	17	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha;

						PDBTitle: crystal structure of the carboxyltransferase domain of the 2-oxaloacetate decarboxylase Na ⁺ pump from <i>Vibrio cholerae</i>
77	d1mxsa_	Alignment	not modelled	97.5	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
78	c3tsmB_	Alignment	not modelled	97.4	15	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from <i>Brucella melitensis</i>
79	c3k13A_	Alignment	not modelled	97.3	15	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain of 5-2-methyltetrahydrofolate-homocysteine methyltransferase from <i>Bacteroides thetaiotaomicron</i>
80	d1vc4a_	Alignment	not modelled	97.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
81	c4wd0A_	Alignment	not modelled	97.3	21	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)] PDBTitle: crystal structure of HisP from <i>Arthrobacter aurescens</i>
82	c3e02A_	Alignment	not modelled	97.3	11	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein DUF849; PDBTitle: crystal structure of a DUF849 family protein (BXE_C0271) from <i>Brucella xenovorans</i> LB400 at 1.90 Å resolution
83	c6bmaA_	Alignment	not modelled	97.3	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168
84	c4njka_	Alignment	not modelled	97.2	10	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of Quee from <i>Burkholderia multivorans</i> in complex 2 with adomet, 7-carboxy-7-deazaguanine, and Mg ²⁺
85	c3labA_	Alignment	not modelled	97.2	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative KDPG (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative KDPG (2-keto-3-deoxy-6-phosphogluconate) aldolase from <i>Oleispira antarctica</i>
86	c2y85D_	Alignment	not modelled	97.2	19	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase A; PDBTitle: crystal structure of <i>Mycobacterium tuberculosis</i> phosphoribosyl isomerase with bound RCDP
87	c2v82A_	Alignment	not modelled	97.2	19	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: KDPGAL complexed to KDPGAL
88	c3a9IA_	Alignment	not modelled	97.0	16	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from <i>Thermus thermophilus</i> 2 complexed with lys
89	c3bg3B_	Alignment	not modelled	97.0	11	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin 2-carboxylase domain at the N-terminus)
90	c3inpA_	Alignment	not modelled	97.0	14	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 Å resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from <i>Francisella tularensis</i> .
91	c5aheA_	Alignment	not modelled	97.0	17	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of <i>Salmonella enterica</i> HisA
92	c3qjaA_	Alignment	not modelled	97.0	19	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the <i>Mycobacterium tuberculosis</i> indole-3-glycerol 2-phosphate synthase (trpC) in apo form
93	d1a53a_	Alignment	not modelled	97.0	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
94	c3chvA_	Alignment	not modelled	97.0	13	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (DUF849) with a TIM PDBTitle: crystal structure of a prokaryotic domain of unknown function (DUF849) 2 member (SPOA0042) from <i>Silicibacter pomeroyi</i> DSS-3 at 1.45 Å resolution
95	c1jvnB_	Alignment	not modelled	96.9	14	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein HisHf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel through a (beta/alpha) ₈ barrel joins two active sites
96	c3e49A_	Alignment	not modelled	96.9	15	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 (BXE_C0966) from <i>Burkholderia xenovorans</i> LB4003 at 1.75 Å resolution
97	d1xcfa_	Alignment	not modelled	96.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
98	d1vhca_	Alignment	not modelled	96.8	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c3no5C_	Alignment	not modelled	96.8	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a Pfam DUF849 domain containing protein 2 (REUT_A1631) from <i>Ralstonia eutropha</i> JMP134 at 1.90 Å resolution

100	c5n2pA_	Alignment	not modelled	96.8	9	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
101	c5ks8D_	Alignment	not modelled	96.7	10	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from <i>Methylobacillus flagellatus</i>
102	c2c3zA_	Alignment	not modelled	96.7	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 <i>Sulfolobus solfataricus</i>
103	c4bk9B_	Alignment	not modelled	96.6	17	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 from <i>Zymomonas mobilis</i> atcc 29191
104	c3qc3B_	Alignment	not modelled	96.6	19	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 <i>Homo sapiens</i> at 2.20 Å resolution
105	c3dxiB_	Alignment	not modelled	96.6	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative 2-aldolase (bvu_2661) from <i>Bacteroides vulgatus</i>
106	d1ajza_	Alignment	not modelled	96.5	23	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
107	c4cczA_	Alignment	not modelled	96.4	13	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine methyltransferase, the homocysteine and folate binding domains
108	c1tx2A_	Alignment	not modelled	96.4	22	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from <i>Bacillus anthracis</i>
109	d1tx2a_	Alignment	not modelled	96.4	22	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
110	c3f4wA_	Alignment	not modelled	96.2	18	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65 Å crystal structure of 3-hexulose-6-phosphate 2-synthase from <i>Salmonella typhimurium</i>
111	c3hpxB_	Alignment	not modelled	96.2	11	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of <i>Mycobacterium tuberculosis</i> leuA active site 2 domain 1-425 (truncation mutant delta:426-644)
112	c3lotC_	Alignment	not modelled	96.2	15	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 Å resolution
113	d1rd5a_	Alignment	not modelled	96.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
114	d1piia2	Alignment	not modelled	96.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
115	c3b0vD_	Alignment	not modelled	96.0	17	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from <i>Thermus thermophilus</i> in complex with 2 trna
116	c3exsB_	Alignment	not modelled	96.0	14	PDB header: lyase Chain: B: PDB Molecule: rrmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from <i>Streptococcus mutans</i> in 2-complex with d-r5p
117	d1w0ma_	Alignment	not modelled	96.0	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
118	c6ei9A_	Alignment	not modelled	95.9	14	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of <i>E. coli</i> trna-dihydrouridine synthase b (dusb)
119	c2y7eA_	Alignment	not modelled	95.9	10	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme 2 (kce) from <i>Candidatus Cloacamonas acidaminovorans</i> (tetragonal form)
120	d1vzwa1	Alignment	not modelled	95.8	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes