

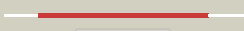












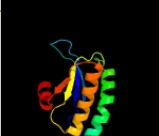








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3421c_(-)_3839239_3839874
Date	Fri Aug 9 18:20:09 BST 2019
Unique Job ID	baf30f97be4d6ead

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5br9C_	 Alignment		100.0	27	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa
2	c6n9aB_	 Alignment		100.0	26	PDB header: biosynthetic protein Chain: B; PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of thermotoga maritima threonylcarbamoyladenine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
3	c1okjB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B; PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
4	c3r6mD_	 Alignment		100.0	32	PDB header: hydrolase Chain: D; PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
5	c2a6aB_	 Alignment		100.0	33	PDB header: hydrolase Chain: B; PDB Molecule: hypothetical protein tm0874; PDBTitle: crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
6	d2a6aa1	 Alignment		100.0	35	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
7	d1okja1	 Alignment		100.0	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
8	c4k25A_	 Alignment		99.8	23	PDB header: biosynthetic protein Chain: A; PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: crystal structure of yeast qri7 homodimer
9	c3zeuE_	 Alignment		99.8	23	PDB header: hydrolase Chain: E; PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: structure of a salmonella typhimurium ygdj-yeaz heterodimer bound to2 atpgammas
10	c2ivoC_	 Alignment		99.8	23	PDB header: hydrolase Chain: C; PDB Molecule: up1; PDBTitle: structure of up1 protein
11	c3enoB_	 Alignment		99.8	20	PDB header: hydrolase/unknown function Chain: B; PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1

12	c3en9B_	Alignment		99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
13	c6gwjK_	Alignment		99.8	21	PDB header: rna binding protein Chain: K: PDB Molecule: probable trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: protein complex
14	c6fpeG_	Alignment		99.8	23	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
15	c3vewA_	Alignment		99.3	19	PDB header: transferase Chain: A: PDB Molecule: o-carbamoyltransferase tobz; PDBTitle: crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
16	d1okja2	Alignment		98.0	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
17	d1hjra_	Alignment		95.6	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
18	d1huxa_	Alignment		95.2	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
19	d1saza1	Alignment		94.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
20	d1ulqa1	Alignment		94.7	8	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
21	d1m3ka1	Alignment	not modelled	94.6	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
22	c4ehtA_	Alignment	not modelled	94.5	15	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
23	c2iikA_	Alignment	not modelled	94.4	26	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
24	c2wuaA_	Alignment	not modelled	94.2	21	PDB header: transferase Chain: A: PDB Molecule: acetoacetyl coa thiolase; PDBTitle: structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
25	c3goaA_	Alignment	not modelled	93.8	19	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: crystal structure of the salmonella typhimurium fada 3-ketoacyl-coa2 thiolase
26	c1ulqD_	Alignment	not modelled	93.8	7	PDB header: transferase Chain: D: PDB Molecule: putative acetyl-coa acetyltransferase; PDBTitle: crystal structure of tt0182 from thermus thermophilus hb8
27	c4n45B_	Alignment	not modelled	93.7	14	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of reduced form of thiolase from clostridium2 acetobutylicum
28	c2qm1D_	Alignment	not modelled	93.4	13	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
						PDB header: transferase

29	c4dd5A_	Alignment	not modelled	93.4	16	Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase (thla1) from clostridium difficile
30	c5bz4K_	Alignment	not modelled	93.4	14	PDB header: transferase Chain: K: PDB Molecule: beta-ketothiolase; PDBTitle: crystal structure of a t1-like thiolase (coa-complex) from2 mycobacterium smegmatis
31	c6bjbB_	Alignment	not modelled	92.9	17	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase a; PDBTitle: crystal structure of acat2-c91s thiolase from ascaris suum in complex2 with propionyl-coa and nitrate
32	c2c7yB_	Alignment	not modelled	92.8	16	PDB header: transferase Chain: B: PDB Molecule: 3-ketoacyl-coa thiolase 2; PDBTitle: plant enzyme
33	d1afwa1	Alignment	not modelled	92.0	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
34	d1wdkc1	Alignment	not modelled	92.0	11	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
35	c4wysB_	Alignment	not modelled	91.9	17	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of thiolase from escherichia coli
36	c6bjaa_	Alignment	not modelled	91.8	14	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase a; PDBTitle: crystal structure of acat5 thiolase from ascaris suum in complex with2 coenzyme a
37	d1zc6a1	Alignment	not modelled	91.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
38	d1vhxa_	Alignment	not modelled	91.5	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
39	c2vu2D_	Alignment	not modelled	91.2	16	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.
40	c3gg4B_	Alignment	not modelled	91.1	14	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
41	c4nzsA_	Alignment	not modelled	90.9	26	PDB header: transferase Chain: A: PDB Molecule: beta-ketothiolase bktb; PDBTitle: crystal structure of beta-ketothiolase bktb b from ralstonia eutropha2 h16
42	c5ya2A_	Alignment	not modelled	90.7	17	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of Isrk-hpr complex with adp
43	c4e1C_	Alignment	not modelled	90.7	22	PDB header: transferase Chain: C: PDB Molecule: acetoacetyl-coa thiolase 2; PDBTitle: crystal structure of acetoacetyl-coa thiolase (thla2) from clostridium2 difficile
44	c3ss6B_	Alignment	not modelled	90.6	15	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
45	c1sazA_	Alignment	not modelled	90.6	12	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
46	d1nu0a_	Alignment	not modelled	89.8	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
47	c3ezwD_	Alignment	not modelled	89.8	14	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
48	c6ok1A_	Alignment	not modelled	89.7	25	PDB header: transport protein Chain: A: PDB Molecule: lipid-transfer protein; PDBTitle: ltp2-chsh2(duf35) aldolase
49	c3vovC_	Alignment	not modelled	89.6	17	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
50	c2aa4B_	Alignment	not modelled	89.3	16	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
51	c4o9cC_	Alignment	not modelled	88.7	18	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of beta-ketothiolase (phaa) from ralstonia eutropha2 h16
52	c2dnpB_	Alignment	not modelled	88.4	17	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
53	d3eeqa1	Alignment	not modelled	88.2	8	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
54	c1zc6A_	Alignment	not modelled	87.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics

						target3 cvr23.
55	c2e2pA_	Alignment	not modelled	87.7	11	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
56	d2p3ra1	Alignment	not modelled	87.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
57	c5lp7A_	Alignment	not modelled	87.3	18	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of 3-ketoacyl-coa thiolase (mmga) from bacillus2 subtilis.
58	c2d4wA_	Alignment	not modelled	86.8	24	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
59	c4db3A_	Alignment	not modelled	86.8	12	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
60	c4c2jA_	Alignment	not modelled	86.7	13	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, mitochondrial; PDBTitle: crystal structure of human mitochondrial 3-ketoacyl-coa2 thiolase in complex with coa
61	c5xyjA_	Alignment	not modelled	86.7	18	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: purification,crystallization and structural analysis of cytoplasmic2 acetoacetyl-coa thiolase from saccharomyces cerevisiae
62	c2ibyD_	Alignment	not modelled	86.7	10	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
63	c2h3gX_	Alignment	not modelled	86.6	14	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
64	c4e1jA_	Alignment	not modelled	86.5	19	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
65	c1glbG_	Alignment	not modelled	86.5	14	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
66	c3flcX_	Alignment	not modelled	86.2	16	PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
67	c2cgbB_	Alignment	not modelled	86.0	9	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
68	c4u4eA_	Alignment	not modelled	85.8	19	PDB header: transferase Chain: A: PDB Molecule: thiolase; PDBTitle: crystal structure of putative thiolase from sphaerobacter thermophilus2 dsm 20745
69	c3ifrB_	Alignment	not modelled	85.5	22	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
70	c6bn2A_	Alignment	not modelled	85.5	19	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1
71	d1a9xb2	Alignment	not modelled	85.3	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
72	c3hz6A_	Alignment	not modelled	85.3	13	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
73	c1ee0A_	Alignment	not modelled	85.2	10	PDB header: transferase Chain: A: PDB Molecule: 2-pyrone synthase; PDBTitle: 2-pyrone synthase complexed with acetoacetyl-coa
74	c2d3tC_	Alignment	not modelled	84.9	11	PDB header: lyase, oxidoreductase/transferase Chain: C: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
75	c1keeH_	Alignment	not modelled	84.7	14	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
76	c2zf5O_	Alignment	not modelled	84.3	17	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
77	c3g25B_	Alignment	not modelled	84.1	11	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
78	c3wxiB_	Alignment	not modelled	84.1	19	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
79	c3vthB_	Alignment	not modelled	83.9	13	PDB header: transferase Chain: B: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form

80	c5zrvH_	Alignment	not modelled	83.5	12	PDB header: liase, oxidoreductase/transferase Chain: H: PDB Molecule: trifunctional enzyme subunit beta, mitochondrial; PDBTitle: structure of human mitochondrial trifunctional protein, octamer
81	c6et9D_	Alignment	not modelled	83.2	22	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase thiolase; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
82	c2d3mA_	Alignment	not modelled	83.1	12	PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
83	d1iv0a_	Alignment	not modelled	83.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
84	d3bzka5	Alignment	not modelled	82.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
85	c1afwB_	Alignment	not modelled	82.4	14	PDB header: thiolase Chain: B: PDB Molecule: 3-ketoacetyl-coa thiolase; PDBTitle: the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae
86	c3vthA_	Alignment	not modelled	82.2	12	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
87	c4ep5A_	Alignment	not modelled	81.0	19	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
88	c5nckA_	Alignment	not modelled	80.7	11	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
89	c4ubwB_	Alignment	not modelled	79.9	14	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase fada5; PDBTitle: apo structure of the 3-ketoacyl-coa thiolase fada5 from m.2 tuberculosis
90	c3i8bA_	Alignment	not modelled	79.8	18	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
91	c6dxfB_	Alignment	not modelled	79.8	13	PDB header: transferase Chain: B: PDB Molecule: chalcone synthase; PDBTitle: crystal structure of chalcone synthase from selaginella moellendorffii2 - hydrogen peroxide treated
92	c2ap1A_	Alignment	not modelled	79.4	16	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
93	c3djca_	Alignment	not modelled	79.1	10	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
94	c5hv7A_	Alignment	not modelled	78.4	11	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with coa and potassium ions
95	c3vpzA_	Alignment	not modelled	77.6	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
96	d1u6ea2	Alignment	not modelled	77.4	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
97	d1bi5a1	Alignment	not modelled	77.4	10	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
98	d1z6ra2	Alignment	not modelled	77.4	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
99	c6aaqA_	Alignment	not modelled	77.4	19	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions
100	c2qnxA_	Alignment	not modelled	76.4	31	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxy carbonyl)dithio]-undecanoic acid
101	d1mzja1	Alignment	not modelled	76.2	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
102	c5mg5R_	Alignment	not modelled	76.2	20	PDB header: transferase Chain: R: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein phlc; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (magp)
103	d1ee0a2	Alignment	not modelled	75.5	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
104	c1u0mA_	Alignment	not modelled	75.2	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of 1,3,6,8-tetrahydroxynaphthalene

104	c1u0n1A	Alignment	not modelled	73.2	17	synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
105	d1ub7a2	Alignment	not modelled	75.1	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
106	d2a9va1	Alignment	not modelled	74.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
107	c3v7iA	Alignment	not modelled	73.6	23	PDB header: transferase, lyase Chain: A: PDB Molecule: putative polyketide synthase; PDBTitle: germicidin synthase (gcs) from streptomyces coelicolor, a type iii2 polyketide synthase
108	c5wx3C	Alignment	not modelled	73.4	12	PDB header: transferase Chain: C: PDB Molecule: alkyldiketide-coa synthase; PDBTitle: alkyldiketide-coa synthase from evodia rutaecarpa
109	c4b46A	Alignment	not modelled	73.1	27	PDB header: structural protein Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: cetz1 from haloferax volcanii - gdp bound monomer
110	d2a6aa2	Alignment	not modelled	72.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
111	c2w40C	Alignment	not modelled	72.7	12	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
112	c6esqI	Alignment	not modelled	72.6	18	PDB header: transferase Chain: I: PDB Molecule: hydroxymethylglutaryl-coa synthase; PDBTitle: structure of the acetoacetyl-coa thiolase/hmg-coa synthase complex2 from methanothermococcus thermolithotrophicus soaked with acetyl-coa
113	d1mzja2	Alignment	not modelled	72.4	33	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
114	c3ii5D	Alignment	not modelled	72.1	13	PDB header: transferase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: structure of e. faecalis fabh in complex with 2-({4-bromo-3-2 [(diethylamino)sulfonyl]benzoyl}amino)benzoic acid
115	d1u0ua2	Alignment	not modelled	71.9	13	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
116	c4ijaA	Alignment	not modelled	71.5	10	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
117	c2gyoB	Alignment	not modelled	71.0	15	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: methanethiol-cys 112 inhibition complex of e. coli ketoacyl synthase2 iii (fabh) and coenzyme a
118	c3aleB	Alignment	not modelled	70.3	20	PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: a type iii polyketide synthase that produces diarylheptanoid
119	c1z6rC	Alignment	not modelled	69.8	13	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
120	c4bc2A	Alignment	not modelled	69.7	19	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate