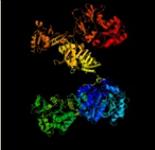
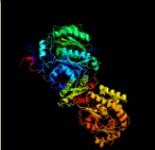
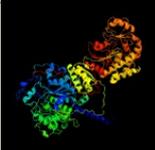
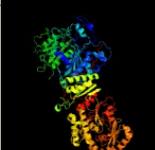
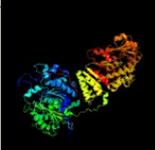
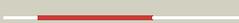
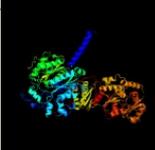
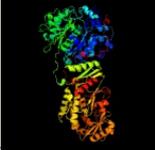
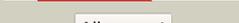
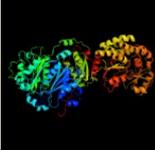
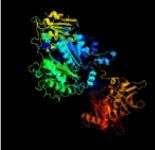
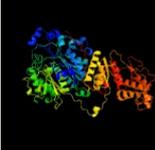


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1662_(pks8)_1881711_1886519
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	92a6a136063edba1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vz8A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
2	c2vz8B_	 Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
3	c6fikA_	 Alignment		100.0	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
4	c6c9uA_	 Alignment		100.0	50	PDB header: transferase/immune system Chain: A: PDB Molecule: 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase in complex with antibody fragment (fab)
5	c2qo3A_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: eryaii erythromycin polyketide synthase modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase
6	c2hg4A_	 Alignment		100.0	52	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
7	c4mz0B_	 Alignment		100.0	46	PDB header: transferase Chain: B: PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
8	c3hhdC_	 Alignment		100.0	29	PDB header: transferase, hydrolase Chain: C: PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
9	c5bp1A_	 Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: mycocerosic acid synthase; PDBTitle: condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks
10	c4kc5D_	 Alignment		100.0	27	PDB header: transferase Chain: D: PDB Molecule: rhie protein; PDBTitle: crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica
11	c4oqjA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1

12	c5erbB	Alignment		100.0	41	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
13	c4wkyB	Alignment		100.0	42	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
14	c4na3A	Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pkjsj; PDBTitle: crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
15	c4qyrA	Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomcyes platensis isomigrastatin ketosynthase domain mgse ks3
16	c4z37A	Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: putative mixed polyketide synthase/non-ribosomal peptide PDBTitle: structure of the ketosynthase of module 2 of c0zqg5 (trans-at pks)2 from brevibacillus brevis
17	c4tl2A	Alignment		100.0	41	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: crystal structure of ketosynthase domain from mgsf from streptomcyes2 platensis
18	c4tktA	Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomcyes platensis isomigrastatin ketosynthase domain mgsf ks6
19	c5e5nB	Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase pkjsj; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
20	c3hmjB	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
21	c4opeD	Alignment	not modelled	100.0	35	PDB header: ligase, transferase Chain: D: PDB Molecule: nrps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
22	c5elpA	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: nrps/pks protein; PDBTitle: ketosynthase from module 1 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
23	c4b3yB	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
24	c5e5nD	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: D: PDB Molecule: polyketide synthase pkjsj; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
25	c2pffA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
26	c2pffG	Alignment	not modelled	100.0	20	PDB header: transferase Chain: G: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
27	c2pffD	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
28	c2vkzC	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
						PDB header: transferase

29	c2uv8C_	Alignment	not modelled	100.0	20	Chain: C; PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
30	c2uv9B_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase alpha subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
31	c4cw4A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa
32	c4qpFA_	Alignment	not modelled	100.0	37	PDB header: ligase, transferase Chain: A; PDB Molecule: ntps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks8
33	c2iwyB_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: human mitochondrial beta-ketoacyl acp synthase
34	c6fn6A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: fatty acid synthase 1, isoform a; PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
35	c4ls5A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: crystal structure of beta-ketoacyl-acp synthase ii (fabf) from2 bacillus subtilis
36	c1tqyC_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: C; PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 1; PDBTitle: the actinorhodin ketosynthase/chain length factor
37	c4b7vA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of wild type pseudomonas aeruginosa fabf (kasii)
38	c2gqdB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: the crystal structure of b-ketoacyl-acp synthase ii (fabf) from2 staphylococcus aureus
39	c4jgaA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: x-ray crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase 22 from rickettsia rickettsii
40	c3o04A_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A; PDB Molecule: beta-keto-acyl carrier protein synthase ii; PDBTitle: crystal structure of the beta-keto-acyl carrier protein synthase ii2 (lmo2201) from listeria monocytogenes
41	c4qavB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: the structure of beta-ketoacyl -(acyl carrier protein) synthase ii2 (fabf) from neisseria meningitidis
42	c1e5mA_	Alignment	not modelled	100.0	26	PDB header: condensing enzyme Chain: A; PDB Molecule: beta ketoacyl acyl carrier protein synthase ii; PDBTitle: beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp.
43	c3tzzA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A; PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
44	c1j3nB_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-(acyl-carrier protein) synthase ii; PDBTitle: crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8
45	c4ddoA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase ii from2 burkholderia vietnamiensis
46	c2ix4B_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex
47	c1oxhD_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D; PDB Molecule: beta ketoacyl-acyl carrier protein synthase; PDBTitle: the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form
48	c2gfvA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of e. coli fabf (kasii) c163q mutant
49	c3e60A_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase ii; PDBTitle: crystal structure of 3-oxoacyl-(acyl carrier protein) synthase ii from2 bartonella henselae
50	c6iytA_	Alignment	not modelled	100.0	37	PDB header: transferase Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
51	c2gp6B_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2;

						PDBTitle: x-ray crystal structure of mycobacterium tuberculosis beta-ketoacyl2 acyl carrier protein synthase ii (mtkasb)
52	c6iy0A_	Alignment	not modelled	100.0	49	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
53	c2wggA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 1; PDBTitle: crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm
54	c6iyrA_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
55	c4ewgA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815
56	c5ydmA_	Alignment	not modelled	100.0	36	PDB header: transferase Chain: A: PDB Molecule: pkcs; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
57	c1tqyD_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: D: PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 2; PDBTitle: the actinorhodin ketosynthase/chain length factor
58	c2buiC_	Alignment	not modelled	100.0	22	PDB header: synthase Chain: C: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase i; PDBTitle: e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k
59	c3lrfA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of beta-ketoacyl synthase from brucella2 melitensis
60	c4qbuA_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
61	c2jfkD_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
62	c6qspA_	Alignment	not modelled	100.0	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: ketosynthase (apeo) in complex with its chain length factor (apec)2 from xenorhabdus doucetiae
63	c4amma_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
64	c4r1A_	Alignment	not modelled	100.0	34	PDB header: transferase Chain: A: PDB Molecule: type i polyketide synthase aves 1; PDBTitle: structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
65	c3slkB_	Alignment	not modelled	100.0	53	PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase
66	c3tqeA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
67	c3ptwA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
68	c3eenA_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
69	c3rgiA_	Alignment	not modelled	100.0	34	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
70	c5ypvA_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
71	c2cuyA_	Alignment	not modelled	100.0	39	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-[acyl carrier protein] transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
72	c3qatB_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
73	c3im8A_	Alignment	not modelled	100.0	33	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
74	c2g2oA_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
75	c3im9A_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase;

						PDBTitle: crystal structure of mcat from staphylococcus aureus PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
76	c4rr5A	Alignment	not modelled	100.0	33	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
77	c2qj3B	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
78	c3ezoA	Alignment	not modelled	100.0	30	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
79	c2cdh9	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: malonyl coenzyme a-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
80	c2h1yA	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
81	c3g87A	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
82	c5dz7A	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
83	c5dz6A	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
84	c5czcA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
85	c2c2nA	Alignment	not modelled	100.0	27	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
86	d1mlaa1	Alignment	not modelled	100.0	35	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
87	d1tqya2	Alignment	not modelled	100.0	26	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
88	d1nm2a1	Alignment	not modelled	100.0	38	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
89	d1e5ma1	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
90	d2ix4a1	Alignment	not modelled	100.0	22	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
91	d1tqyb2	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
92	d1j3na1	Alignment	not modelled	100.0	29	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
93	d2gfva1	Alignment	not modelled	100.0	25	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
94	d1ox0a1	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
95	d2vbaa1	Alignment	not modelled	100.0	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
96	c3krtC	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
97	c4egvC	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis
98	c3el6A	Alignment	not modelled	100.0	39	PDB header: lyase Chain: A: PDB Molecule: erythromycin dehydratase; PDBTitle: crystal structure of the erythromycin dehydratase
99	c6obvB	Alignment	not modelled	100.0	45	PDB header: lyase Chain: B: PDB Molecule: fluvirucin b1 dh domain from module 1; PDBTitle: structural insights into dehydratase substrate selection for the2 borrelidin and fluvirucin polyketide synthases
100	c4ln9A	Alignment	not modelled	100.0	45	PDB header: lyase Chain: A: PDB Molecule: rifamycin polyketide synthase; PDBTitle: crystal structure of the dehydratase domain from the terminal module2 of the rifamycin polyketide synthase

101	d1j3na2	Alignment	not modelled	100.0	30	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
102	d1e5ma2	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
103	c2d3mA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
104	d2gfva2	Alignment	not modelled	100.0	28	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
105	c6obtA	Alignment	not modelled	100.0	45	PDB header: lyase Chain: A: PDB Molecule: borrelidin polyketide synthase, type i; PDBTitle: structural insights into dehydratase substrate selection for the2 borrelidin and fluvirucin polyketide synthases
106	c3kg9A	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A: PDB Molecule: curk; PDBTitle: dehydratase domain from curk module of curacin polyketide synthase
107	d2ix4a2	Alignment	not modelled	100.0	31	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
108	c5o16B	Alignment	not modelled	100.0	41	PDB header: lyase Chain: B: PDB Molecule: ambc; PDBTitle: crystal structure of bifunctional dehydratase-cyclase domain in2 ambruticin biosynthesis
109	c3kg6C	Alignment	not modelled	100.0	22	PDB header: lyase Chain: C: PDB Molecule: curf; PDBTitle: dehydratase domain from curf module of curacin polyketide synthase
110	d1tqyb1	Alignment	not modelled	100.0	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
111	d1ox0a2	Alignment	not modelled	100.0	28	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
112	c3kg8A	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: curj; PDBTitle: dehydratase domain from curj module of curacin polyketide synthase
113	c3kg7C	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: curh; PDBTitle: dehydratase domain from curh module of curacin polyketide synthase
114	d1tqya1	Alignment	not modelled	100.0	30	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
115	c5j6oA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of a trans-at pks dehydratase domain of c0zgg7 from2 brevibacillus brevis
116	c5il6A	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: polyketide synthase/nonribosomal peptide synthetase hybrid PDBTitle: crystal structure of the dehydratase domain of rzxb from pseudomonas2 fluorescens
117	c5bp2A	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: mycocerosic acid synthase-like polyketide synthase; PDBTitle: dehydratase domain (dh) of a mycocerosic acid synthase-like (mas-like)2 pks, crystal form 1
118	c4gi2B	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: crotonyl-coa carboxylase/reductase; PDBTitle: crotonyl-coa carboxylase/reductase
119	c4ro5A	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: sat domain from cazm; PDBTitle: crystal structure of the sat domain from the non-reducing fungal2 polyketide synthase cazm
120	c6mbgA	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: gphf; PDBTitle: gphf dehydratase p1711l variant for improved crystallization