

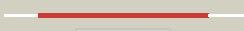








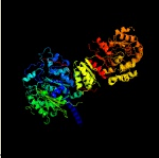

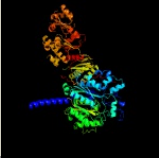

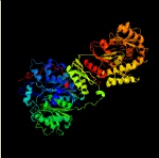

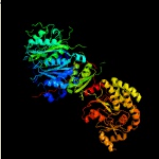

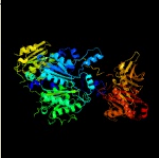




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2933_(ppsC)_3255695_3262261
Date	Thu Aug 8 16:20:09 BST 2019
Unique Job ID	cd746b15f7b52a84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vz8A_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
2	c2vz8B_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
3	c6fikA_	 Alignment		100.0	30	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	c2qo3A_	 Alignment		100.0	41	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 deoxyerythronolide b synthase
5	c6c9uA_	 Alignment		100.0	40	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 deoxyerythronolide b synthase in complex with antibody fragment (fab)
6	c2hg4A_	 Alignment		100.0	40	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	42	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	30	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	44	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	29	PDB header: transferase Chain: D: PDB Molecule: rhie protein; PDBTitle: crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica
11	c4oqiA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1

12	c5erbB_	Alignment		100.0	37	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
13	c5e5nB_	Alignment		100.0	37	PDB header: hydrolase Chain: B; PDB Molecule: polyketide synthase pks1; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
14	c4na3A_	Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
15	c4qyrA_	Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: at-less polyketide synthase; PDBTitle: streptomyces platensis isomigrastatin ketosynthase domain mgse ks3
16	c4z37A_	Alignment		100.0	34	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	c4wkyB_	Alignment		100.0	38	PDB header: transferase Chain: B; PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
18	c3hmiB_	Alignment		100.0	16	PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
19	c4tktA_	Alignment		100.0	40	PDB header: transferase Chain: A; PDB Molecule: at-less polyketide synthase; PDBTitle: streptomyces platensis isomigrastatin ketosynthase domain mgsf ks6
20	c4opeD_	Alignment		100.0	34	PDB header: ligase, transferase Chain: D; PDB Molecule: nrps/pks; PDBTitle: streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
21	c4tl2A_	Alignment	not modelled	100.0	37	PDB header: transferase Chain: A; PDB Molecule: at-less polyketide synthase; PDBTitle: crystal structure of ketosynthase domain from mgfsf from streptomyces2 platensis
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	20	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	37	PDB header: hydrolase Chain: D; PDB Molecule: polyketide synthase pks1; 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	17	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	17	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	17	PDB header: transferase Chain: D; PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
28	c6fn6A_	Alignment	not modelled	100.0	25	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)
						PDB header: transferase

29	c2uv8C	Alignment	not modelled	100.0	17	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	c2vkzC	Alignment	not modelled	100.0	16	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
31	c2uv9B	Alignment	not modelled	100.0	16	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
32	c4cw4A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A; PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa
33	c3slkB	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: B; PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase
34	c4opfA	Alignment	not modelled	100.0	39	PDB header: ligase, transferase Chain: A; PDB Molecule: nrps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks8
35	c2iwyB	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: human mitochondrial beta-ketoacyl acp synthase
36	c4ls5A	Alignment	not modelled	100.0	26	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
37	c1tqyC	Alignment	not modelled	100.0	27	PDB header: transferase Chain: C; PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 1; PDBTitle: the actinorhodin ketosynthase/chain length factor
38	c4jgaA	Alignment	not modelled	100.0	25	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
39	c4b7vA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of wild type pseudomonas aeruginosa fabf (kasii)
40	c2gqdB	Alignment	not modelled	100.0	25	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
41	c4qavB	Alignment	not modelled	100.0	29	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	c3o04A	Alignment	not modelled	100.0	24	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
43	c2ix4B	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex
44	c1e5mA	Alignment	not modelled	100.0	25	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.
45	c1j3nB	Alignment	not modelled	100.0	29	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
46	c4ddoA	Alignment	not modelled	100.0	29	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
47	c1oxhD	Alignment	not modelled	100.0	26	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	c2gp6B	Alignment	not modelled	100.0	26	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)
49	c2gfvA	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of e. coli fabf (kasii) c163q mutant
50	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
51	c2wggA	Alignment	not modelled	100.0	26	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
52	c4ewgA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815
53	c3tzzA	Alignment	not modelled	100.0	30	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
54	c2buiC	Alignment	not modelled	100.0	27	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
55	c1tqyD	Alignment	not modelled	100.0	24	PDB header: transferase Chain: D: PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 2; PDBTitle: the actinorhodin ketosynthase/chain length factor
56	c3lrfA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of beta-ketoacyl synthase from brucella2 melitensis
57	c6iytA	Alignment	not modelled	100.0	32	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
58	c6iyrA	Alignment	not modelled	100.0	34	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
59	c6iyoA	Alignment	not modelled	100.0	30	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
60	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
61	c5ydmA	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: pks; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
62	c4qbuA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
63	c2jfkD	Alignment	not modelled	100.0	22	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
64	c4ammA	Alignment	not modelled	100.0	21	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
65	c4r1A	Alignment	not modelled	100.0	32	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
66	c3mjsA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: amphb; PDBTitle: structure of a-type ketoreductases from modular polyketide synthase
67	c3tqeA	Alignment	not modelled	100.0	22	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
68	c3rgiA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
69	c3ptwA	Alignment	not modelled	100.0	21	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
70	c3qp9C	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase
71	c2fr1A	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2)
72	c3eenA	Alignment	not modelled	100.0	26	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
73	c5ypvA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
74	c4impB	Alignment	not modelled	100.0	34	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase extender modules 3-4; PDBTitle: the missing linker: a dimerization motif located within polyketide2 synthase modules
75	c3im8A	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae

76	c2cuyA	Alignment	not modelled	100.0	25	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
77	c4rr5A	Alignment	not modelled	100.0	27	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
78	c2h1yA	Alignment	not modelled	100.0	18	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
79	c2g2oA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
80	c3im9A	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
81	c3qatB	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from bartonella henselae
82	c2qj3B	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
83	c3ezoA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein s-malonyltransferase from burkholderia pseudomallei 1710b
84	c2cdh9	Alignment	not modelled	100.0	20	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
85	c3g87A	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 burkholderia pseudomallei using dried seaweed as nucleant or3 protease
86	c5dz6A	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
87	c5dz7A	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
88	c4l4xA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: an a2-type ketoreductase from a modular polyketide synthase
89	c4di7A	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: structure of a2-type ketoreductase of modular polyketide synthases
90	c2z5lA	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: tylactone synthase starter module and modules 1 & 2; PDBTitle: the first ketoreductase of the tylosin pks
91	c5d2eA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: mlne; PDBTitle: crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line
92	c2c2nA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
93	d1tqya2	Alignment	not modelled	100.0	28	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
94	c5czcA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
95	c4pivB	Alignment	not modelled	100.0	25	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069
96	d1tqyb2	Alignment	not modelled	100.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
97	c4hxyA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: plm1; PDBTitle: plmkr1-ketoreductase from the first module of phoslactomycin2 biosynthesis in streptomyces sp. hk803
98	d2ix4a1	Alignment	not modelled	100.0	25	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
99	d1e5ma1	Alignment	not modelled	100.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
						Fold: Thiolase-like

100	d1j3na1	Alignment	not modelled	100.0	28	Superfamily: Thiolase-like Family: Thiolase-related
101	d2gfva1	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
102	d1ox0a1	Alignment	not modelled	100.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
103	c4jlsA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line
104	c4egvC	Alignment	not modelled	100.0	16	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
105	d2vbaa1	Alignment	not modelled	100.0	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
106	c5ktkA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: polyketide synthase pksj; PDBTitle: ketoreductase from module 3 of the bacillaene synthase from bacillus2 subtilis 168
107	d1mlaa1	Alignment	not modelled	100.0	28	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
108	d1nm2a1	Alignment	not modelled	100.0	28	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
109	d1j3na2	Alignment	not modelled	100.0	28	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
110	d1e5ma2	Alignment	not modelled	100.0	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
111	c2d3mA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
112	d2ix4a2	Alignment	not modelled	100.0	33	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
113	d2gfva2	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
114	c3s8mA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A; PDB Molecule: enoyl-acyl reductase; PDBTitle: the crystal structure of fabv
115	c4ggoA	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A; PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
116	d1ox0a2	Alignment	not modelled	100.0	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
117	d1tqyb1	Alignment	not modelled	100.0	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
118	c6et9D	Alignment	not modelled	100.0	17	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
119	d1tqya1	Alignment	not modelled	100.0	25	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
120	d2vbaa2	Alignment	not modelled	100.0	33	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related