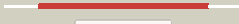








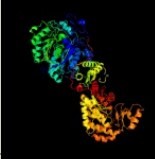





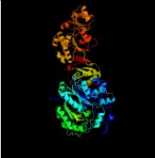

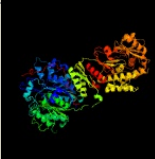







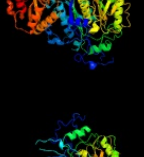

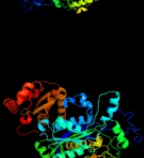


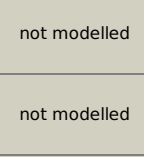


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3825c_(pks2)_4293403_4299783
Date	Fri Aug 9 18:20:53 BST 2019
Unique Job ID	263cb8fab9f2b812

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vz8A_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> crystal structure of mammalian fatty acid synthase
2	<a href="#">c2vz8B_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> crystal structure of mammalian fatty acid synthase
3	<a href="#">c6fikA_</a>	 Alignment		100.0	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
4	<a href="#">c2qo3A_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> eryaii erythromycin polyketide synthase modules 3 and 4; <b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase
5	<a href="#">c6c9uA_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; <b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase in complex with antibody fragment (fab)
6	<a href="#">c2hg4A_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide b synthase; <b>PDBTitle:</b> structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
7	<a href="#">c5bp1A_</a>	 Alignment		100.0	70	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mycocerosic acid synthase; <b>PDBTitle:</b> condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks
8	<a href="#">c4mz0B_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> curl; <b>PDBTitle:</b> structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
9	<a href="#">c3hhdC_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
10	<a href="#">c4kc5D_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rhie protein; <b>PDBTitle:</b> crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica
11	<a href="#">c4oqiA_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pks; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1

12	<a href="#">c5erbB_</a>	Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
13	<a href="#">c4qyrA_</a>	Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase; <b>PDBTitle:</b> streptomyces platensis isomigrastatin ketosynthase domain mgse ks3
14	<a href="#">c4na3A_</a>	Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pkcj; <b>PDBTitle:</b> crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
15	<a href="#">c5e5nB_</a>	Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase pksl; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
16	<a href="#">c4tl2A_</a>	Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase; <b>PDBTitle:</b> crystal structure of ketosynthase domain from mgsf from streptomyces2 platensis
17	<a href="#">c3hmiB_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> saccharomyces cerevisiae fas type i
18	<a href="#">c4z37A_</a>	Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mixed polyketide synthase/non-ribosomal peptide <b>PDBTitle:</b> structure of the ketosynthase of module 2 of c0zqg5 (trans-at pks)2 from brevicibacillus brevis
19	<a href="#">c4wkyB_</a>	Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
20	<a href="#">c4tktA_</a>	Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase; <b>PDBTitle:</b> streptomyces platensis isomigrastatin ketosynthase domain mgsf ks6
21	<a href="#">c4opeD_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> ligase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nrps/pks; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
22	<a href="#">c5elpA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nrps/pks protein; <b>PDBTitle:</b> ketosynthase from module 1 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
23	<a href="#">c4b3yB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase
24	<a href="#">c5e5nD_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> polyketide synthase pksl; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
25	<a href="#">c6fn6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase 1, isoform a; <b>PDBTitle:</b> modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
26	<a href="#">c2pffG_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
27	<a href="#">c2pffA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
28	<a href="#">c2pffD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
						<b>PDB header:</b> transferase

29	<a href="#">c2vkzC</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> C; <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
30	<a href="#">c2uv8C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> fatty acid synthase subunit alpha (fas2); <b>PDBTitle:</b> crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
31	<a href="#">c2uv9B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> fatty acid synthase alpha subunits; <b>PDBTitle:</b> 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	<a href="#">c4cw4A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa
33	<a href="#">c3slkB</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase extender module 2; <b>PDBTitle:</b> structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase
34	<a href="#">c4opfA</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nrps/pks; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks8
35	<a href="#">c2iwyB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> human mitochondrial beta-ketoacyl acp synthase
36	<a href="#">c4ls5A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> crystal structure of beta-ketoacyl-acp synthase ii (fabf) from2 bacillus subtilis
37	<a href="#">c1tqyC</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> actinorhodin polyketide putative beta-ketoacyl synthase 1; <b>PDBTitle:</b> the actinorhodin ketosynthase/chain length factor
38	<a href="#">c4b7vA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of wild type pseudomonas aeruginosa fabf (kasii)
39	<a href="#">c4jgaA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> x-ray crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase 22 from rickettsia rickettsii
40	<a href="#">c2gqdB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> the crystal structure of b-ketoacyl-acp synthase ii (fabf) from2 staphylococcus aureus
41	<a href="#">c4qavB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> the structure of beta-ketoacyl -(acyl carrier protein) synthase ii2 (fabf) from neisseria meningitidis
42	<a href="#">c3o04A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-keto-acyl carrier protein synthase ii; <b>PDBTitle:</b> crystal structure of the beta-keto-acyl carrier protein synthase ii2 (lmo2201) from listeria monocytogenes
43	<a href="#">c4ddoA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase ii from2 burkholderia vietnamiensis
44	<a href="#">c1e5mA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> condensing enzyme <b>Chain:</b> A; <b>PDB Molecule:</b> beta ketoacyl acyl carrier protein synthase ii; <b>PDBTitle:</b> beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp.
45	<a href="#">c1oxhD</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> beta ketoacyl-acyl carrier protein synthase; <b>PDBTitle:</b> the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form
46	<a href="#">c1j3nB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) synthase ii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8
47	<a href="#">c2ix4B</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex
48	<a href="#">c3e60A</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein ] synthase ii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase ii from2 bartonella henselae
49	<a href="#">c2gp6B</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> x-ray crystal structure of mycobacterium tuberculosis beta-ketoacyl2 acyl carrier protein synthase ii (mtkasb)
50	<a href="#">c2gfvA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of e. coli fabf (kasii) c163q mutant
51	<a href="#">c2wggA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 1;

						<b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm
52	<a href="#">c3tzzA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
53	<a href="#">c4ewgA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815
54	<a href="#">c6iytA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
55	<a href="#">c6iyrA_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
56	<a href="#">c1tqyD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> actinorhodin polyketide putative beta-ketoacyl synthase 2; <b>PDBTitle:</b> the actinorhodin ketosynthase/chain length factor
57	<a href="#">c2buiC_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase i; <b>PDBTitle:</b> e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k
58	<a href="#">c3lrfA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of beta-ketoacyl synthase from brucella2 melitensis
59	<a href="#">c6iyoA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
60	<a href="#">c6qspA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> ketosynthase (apeo) in complex with its chain length factor (apec)2 from xenorhabdus doucetiae
61	<a href="#">c5ydmA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pks; <b>PDBTitle:</b> the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
62	<a href="#">c4qbuA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> zmaa; <b>PDBTitle:</b> structure of the acyl transferase domain of zmaa
63	<a href="#">c2jfkD_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> structure of the mat domain of human fas with malonyl-coa
64	<a href="#">c4ammA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dyne8; <b>PDBTitle:</b> crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
65	<a href="#">c4r1A_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i polyketide synthase aves 1; <b>PDBTitle:</b> structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
66	<a href="#">c3rgiA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disd protein; <b>PDBTitle:</b> trans-acting transferase from disorazole synthase
67	<a href="#">c3tqeA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl-coa-[acyl-carrier-protein] transacylase; <b>PDBTitle:</b> structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
68	<a href="#">c3ptwA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
69	<a href="#">c3mjsA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphb; <b>PDBTitle:</b> structure of a-type ketoreductases from modular polyketide synthase
70	<a href="#">c5ypvA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of fabd from acinetobacter baumannii
71	<a href="#">c3eenA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acp transacylase; <b>PDBTitle:</b> crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
72	<a href="#">c3im8A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of mcat from streptococcus pneumoniae
73	<a href="#">c2g2oA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> structure of e.coli fabd complexed with sulfate
74	<a href="#">c3qatB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
75	<a href="#">c2cuyA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-[acyl carrier protein] transacylase; <b>PDBTitle:</b> crystal structure of malonyl coa-acyl carrier protein

						transacylase2 from thermus thermophilus hb8
76	<a href="#">c3im9A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of mcat from staphylococcus aureus
77	<a href="#">c3qp9C_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> type i polyketide synthase pikaii; <b>PDBTitle:</b> the structure of a c2-type ketoreductase from a modular polyketide2 synthase
78	<a href="#">c4rr5A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
79	<a href="#">c4impB_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase extender modules 3-4; <b>PDBTitle:</b> the missing linker: a dimerization motif located within polyketide2 synthase modules
80	<a href="#">c2qj3B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> mycobacterium tuberculosis fabd
81	<a href="#">c3ezoA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
82	<a href="#">c3g87A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
83	<a href="#">c2fr1A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> erythromycin synthase, eryai; <b>PDBTitle:</b> the first ketoreductase of the erythromycin synthase2 (crystal form 2)
84	<a href="#">c5dz7A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis protein pkse; <b>PDBTitle:</b> structural basis of acyl transfer in a trans-at polyketide synthase
85	<a href="#">c5dz6A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis malonyl coa-acyl carrier protein <b>PDBTitle:</b> acyl transferase from bacillaene pks
86	<a href="#">c2h1yA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coenzyme a-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
87	<a href="#">c2cdh9_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> 9: <b>PDB Molecule:</b> acetyl transferase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
88	<a href="#">c2c2nA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> structure of human mitochondrial malonyltransferase
89	<a href="#">c4l4xA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphi; <b>PDBTitle:</b> an a2-type ketoreductase from a modular polyketide synthase
90	<a href="#">c5czcA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl-coa-[acyl-carrier-protein] transacylase; <b>PDBTitle:</b> the structure of vink
91	<a href="#">c4di7A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphi; <b>PDBTitle:</b> structure of a2-type ketoreductase of modular polyketide synthases
92	<a href="#">c2z5lA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tylactone synthase starter module and modules 1 & 2; <b>PDBTitle:</b> the first ketoreductase of the tylosin pks
93	<a href="#">c4pivB_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069
94	<a href="#">d1tqya2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
95	<a href="#">c5d2eA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imlne; <b>PDBTitle:</b> crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line
96	<a href="#">c4j1sA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pksj; <b>PDBTitle:</b> crystal structure of a ketoreductase domain from the bacillaene2 assembly line
97	<a href="#">c4hxyA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> plm1; <b>PDBTitle:</b> plmkr1-ketoreductase from the first module of phoslactomycin2 biosynthesis in streptomyces sp. hk803
98	<a href="#">d1tqyb2</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
99	<a href="#">d2ix4a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related

100	<a href="#">d1e5ma1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
101	<a href="#">d2gfva1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
102	<a href="#">d1j3na1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
103	<a href="#">d1ox0a1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
104	<a href="#">d1mlaa1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
105	<a href="#">c5ktaA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pksj; <b>PDBTitle:</b> ketoreductase from module 3 of the bacillaene synthase from bacillus2 subtilis 168
106	<a href="#">c4egvC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis
107	<a href="#">d1nm2a1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
108	<a href="#">d2vbaa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
109	<a href="#">d1j3na2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
110	<a href="#">d1e5ma2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
111	<a href="#">c2d3mA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pentaketide chromone synthase; <b>PDBTitle:</b> pentaketide chromone synthase complexed with coenzyme a
112	<a href="#">d2gfva2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
113	<a href="#">d2ix4a2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
114	<a href="#">c3s8mA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl reductase; <b>PDBTitle:</b> the crystal structure of fabv
115	<a href="#">d1ox0a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
116	<a href="#">c4ggoA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
117	<a href="#">d1tqyb1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
118	<a href="#">c5bp2A</a>	Alignment	not modelled	100.0	57	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mycocerosic acid synthase-like polyketide synthase; <b>PDBTitle:</b> dehydratase domain (dh) of a mycocerosic acid synthase-like (mas-like)2 pks, crystal form 1
119	<a href="#">c6et9D</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase thiolase; <b>PDBTitle:</b> structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
120	<a href="#">d2vbaa2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related