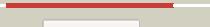
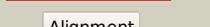
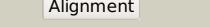
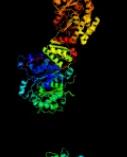
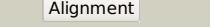
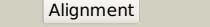
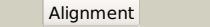
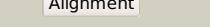
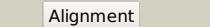
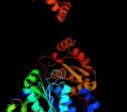


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1664_(pks9)_1888033_1891086
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	9d0b2d3b0ec0071b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vz8A_</a>			100.0	29	<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>			100.0	29	<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>			100.0	30	<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>			100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> erya ii erythromycin polyketide synthase modules 3 and 4; <b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthonolide b synthase
5	<a href="#">c6c9uA_</a>			100.0	42	<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 deoxyerthonolide b synthase in complex with antibody fragment (fab)
6	<a href="#">c2hg4A_</a>			100.0	42	<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="#">c3hhdc_</a>			100.0	30	<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.
8	<a href="#">c5bp1A_</a>			100.0	38	<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
9	<a href="#">c4mz0B_</a>			100.0	43	<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
10	<a href="#">c4oqjA_</a>			100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmq ks1
11	<a href="#">c4kc5D_</a>			100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rhe protein; <b>PDBTitle:</b> crystal structure of the c-terminal part of rhe from burkholderia2 rhizoxinica

12	<a href="#">c4wkyB</a>	Alignment		100.0	50	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
13	<a href="#">c5erbB</a>	Alignment		100.0	35	<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
14	<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 c0zgq5 (trans-at pk5)2 from brevibacillus brevis
15	<a href="#">c4na3A</a>	Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pk5j; <b>PDBTitle:</b> crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
16	<a href="#">c5e5nB</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase pk5l; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
17	<a href="#">c4gyrA</a>	Alignment		100.0	45	<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
18	<a href="#">c4tl2A</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> crystal structure of ketosynthase domain from mgsf from streptomyces2 platensis
19	<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
20	<a href="#">c4opeD</a>	Alignment		100.0	44	<b>PDB header:</b> ligase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nrps/pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmn ks7
21	<a href="#">c5elpA</a>	Alignment	not modelled	100.0	34	<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
22	<a href="#">c5e5nD</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> polyketide synthase pk5l; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
23	<a href="#">c3hmjB</a>	Alignment	not modelled	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
24	<a href="#">c4b3yB</a>	Alignment	not modelled	100.0	21	<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
25	<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
26	<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
27	<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
28	<a href="#">c2vkzC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <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
						<b>PDB header:</b> transferase

29	<a href="#">c2uv8C</a>		Alignment	not modelled	100.0	19	<b>Chain: C: 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  <b>PDB header:</b> transferase
30	<a href="#">c2uv9B</a>		Alignment	not modelled	100.0	17	<b>Chain: 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
31	<a href="#">c4opfA</a>		Alignment	not modelled	100.0	41	<b>Chain: A: PDB Molecule:</b> nmps/pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmh ks8  <b>PDB header:</b> transferase
32	<a href="#">c4cw4A</a>		Alignment	not modelled	100.0	17	<b>Chain: A: PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa
33	<a href="#">c2iwyB</a>		Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> human mitochondrial beta-ketoacyl acp synthase
34	<a href="#">c1tqyC</a>		Alignment	not modelled	100.0	27	<b>Chain: C: PDB Molecule:</b> actinorhodin polyketide putative beta-ketoacyl synthase 1; <b>PDBTitle:</b> the actinorhodin ketosynthase/chain length factor
35	<a href="#">c2gqdB</a>		Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain: 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
36	<a href="#">c4ls5A</a>		Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain: A: 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="#">c4b7vA</a>		Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of wild type pseudomonas aeruginosa fabf (kasii)
38	<a href="#">c4qavB</a>		Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> the structure of beta-ketoacyl -(acyl carrier protein) synthase ii fabf (fabf) from neisseria meningitidis
39	<a href="#">c1e5mA</a>		Alignment	not modelled	100.0	27	<b>PDB header:</b> condensing enzyme <b>Chain: A: PDB Molecule:</b> beta ketoacyl acyl carrier protein synthase ii; <b>PDBTitle:</b> beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp.
40	<a href="#">c4igaA</a>		Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain: A: 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
41	<a href="#">c3o04A</a>		Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> beta-keto-acyl carrier protein synthase ii; <b>PDBTitle:</b> crystal structure of the beta-keto-acyl carrier protein synthase ii (lmo2201) from listeria monocytogenes
42	<a href="#">c1j3nB</a>		Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) synthase ii; from thermus thermophilus hb8
43	<a href="#">c4ddoA</a>		Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain: A: 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="#">c2gfvA</a>		Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of e. coli fabf (kasii) c163q mutant
45	<a href="#">c1oxhD</a>		Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain: D: 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="#">c3e60A</a>		Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain: A: 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
47	<a href="#">c2ix4B</a>		Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain: 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="#">c2gp6B</a>		Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain: 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 (mtkabs)
49	<a href="#">c2wggA</a>		Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm
50	<a href="#">c4ewgA</a>		Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815
51	<a href="#">c3lrfA</a>		Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> beta-ketoacyl synthase;

51	<a href="#">c2lita</a>	Alignment	not modelled	100.0	22	<b>PDBTitle:</b> crystal structure of beta-ketoacyl synthase from brucella2 melitensis <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
52	<a href="#">c2buiC</a>	Alignment	not modelled	100.0	24	<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
53	<a href="#">c1tqyD</a>	Alignment	not modelled	100.0	28	<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
54	<a href="#">c3tzA</a>	Alignment	not modelled	100.0	28	<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="#">c6iytA</a>	Alignment	not modelled	100.0	41	<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
56	<a href="#">c6iyoA</a>	Alignment	not modelled	100.0	48	<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
57	<a href="#">c6qspA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> ketosynthase (apec)2 in complex with its chain length factor (apec)2 from xenorhabdus douceiae
58	<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
59	<a href="#">c4qbuA</a>	Alignment	not modelled	100.0	30	<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
60	<a href="#">c5ydmA</a>	Alignment	not modelled	100.0	35	<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
61	<a href="#">c2jfkD</a>	Alignment	not modelled	100.0	26	<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
62	<a href="#">c4ammA</a>	Alignment	not modelled	100.0	31	<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
63	<a href="#">c4rl1A</a>	Alignment	not modelled	100.0	38	<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
64	<a href="#">c3tqeA</a>	Alignment	not modelled	100.0	27	<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
65	<a href="#">c3rgiA</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disd protein; <b>PDBTitle:</b> trans-acting transferase from disorazole synthase
66	<a href="#">c3ptwA</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 clostridium perfringens atcc 13124
67	<a href="#">c3eenA</a>	Alignment	not modelled	100.0	33	<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
68	<a href="#">c3im8A</a>	Alignment	not modelled	100.0	35	<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
69	<a href="#">c3qatB</a>	Alignment	not modelled	100.0	33	<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
70	<a href="#">c2g2oA</a>	Alignment	not modelled	100.0	32	<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
71	<a href="#">c2cuyA</a>	Alignment	not modelled	100.0	38	<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
72	<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
73	<a href="#">c4rr5A</a>	Alignment	not modelled	100.0	32	<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
74	<a href="#">c3im9A</a>	Alignment	not modelled	100.0	32	<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
75	<a href="#">c5vnuA</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein

75	<a href="#">c3yvva</a>	Alignment	not modelled	100.0	33	transacylase; <b>PDBTitle:</b> crystal structure of fabd from acinetobacter baumannii
76	<a href="#">c3ezoA</a>	Alignment	not modelled	100.0	31	<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
77	<a href="#">c2cdh9</a>	Alignment	not modelled	100.0	28	<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.
78	<a href="#">c2h1yA</a>	Alignment	not modelled	100.0	26	<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
79	<a href="#">c3g87A</a>	Alignment	not modelled	100.0	33	<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
80	<a href="#">c5dz7A</a>	Alignment	not modelled	100.0	28	<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
81	<a href="#">c5dz6A</a>	Alignment	not modelled	100.0	33	<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
82	<a href="#">c2c2nA</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> structure of human mitochondrial malonyltransferase
83	<a href="#">c5czcA</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> the structure of vink
84	<a href="#">d1tqya2</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
85	<a href="#">d1e5ma1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
86	<a href="#">d1j3na1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
87	<a href="#">d2ix4a1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
88	<a href="#">d2gfva1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
89	<a href="#">d1ox0a1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
90	<a href="#">d1tqyb2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
91	<a href="#">d2vbaa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
92	<a href="#">d1mlaa1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
93	<a href="#">d1nm2a1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
94	<a href="#">c4egvC</a>	Alignment	not modelled	100.0	19	<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
95	<a href="#">d2gfva2</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
96	<a href="#">d1e5ma2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
97	<a href="#">d1j3na2</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
98	<a href="#">d1tqyb1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
99	<a href="#">d1tqya1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
100	<a href="#">d2ix4a2</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related

101	<a href="#">d1ox0a2</a>		not modelled	100.0	25	<b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
102	<a href="#">c2d3mA</a>		not modelled	100.0	12	<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
103	<a href="#">c6et9D</a>		not modelled	100.0	19	<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 thermolithothrophicus at 2.75 a
104	<a href="#">d2vbaa2</a>		not modelled	100.0	33	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
105	<a href="#">c6hspB</a>		not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> scp2-thiolase (type-1); <b>PDBTitle:</b> crystal structure of the zebrafish peroxisomal scp2-thiolase (type-1)2 in complex with coa and octanoyl-coa
106	<a href="#">c4u4eA</a>		not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiolase; <b>PDBTitle:</b> crystal structure of putative thiolase from sphaerobacter thermophilus2 dsm 20745
107	<a href="#">c5ab6E</a>		not modelled	100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> scp2-thiolase like protein; <b>PDBTitle:</b> crystal structure of trypanosoma brucei scp2-thiolase like2 protein (tbslp) in complex with acetoacetyl-coa.
108	<a href="#">c4ro5A</a>		not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sat domain from cazm; <b>PDBTitle:</b> crystal structure of the sat domain from the non-reducing fungal2 polyketide synthase cazm
109	<a href="#">c2vkzH</a>		not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type I2 multienzyme complex
110	<a href="#">c4n45B</a>		not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of reduced form of thiolase from clostridium2 acetobutylicum
111	<a href="#">c4e1IC</a>		not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetoacetyl-coa thiolase 2; <b>PDBTitle:</b> crystal structure of acetoacetyl-coa thiolase (thla2) from clostridium2 difficile
112	<a href="#">c2uval</a>		not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
113	<a href="#">c3zbgA</a>		not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase-like protein; <b>PDBTitle:</b> crystal structure of wild-type scp2 thiolase from leishmania2 mexicana at 1.85 a
114	<a href="#">c4dd5A</a>		not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> biosynthetic thiolase (thla1) from clostridium difficile
115	<a href="#">c3ledA</a>		not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-acyl carrier protein synthase iii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase iii2 from rhodopseudomonas palustris cga009
116	<a href="#">c5mg5R</a>		not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> R: <b>PDB Molecule:</b> 2,4-diacetylphloroglucinol biosynthesis protein phlc; <b>PDBTitle:</b> a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (magp)
117	<a href="#">c4o9cC</a>		not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of beta-ketothiolase (phaa) from ralstonia eutropha2 h16
118	<a href="#">c5bz4K</a>		not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> beta-ketothiolase; <b>PDBTitle:</b> crystal structure of a t1-like thiolase (coa-complex) from mycobacterium smegmatis
119	<a href="#">c2wuaA</a>		not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl coa thiolase; <b>PDBTitle:</b> structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
120	<a href="#">c6bjbB</a>		not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a; <b>PDBTitle:</b> crystal structure of acat2-c91s thiolase from ascaris suum in complex2 with propionyl-coa and nitrate