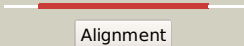

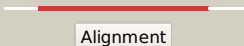

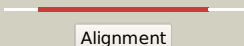







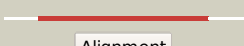











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1627c_(-)_1828872_1830080
Date	Fri Aug 2 13:30:22 BST 2019
Unique Job ID	0006547775dc62f9

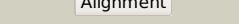
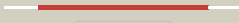
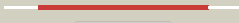



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hspB_</a>	 Alignment		100.0	30	<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
2	<a href="#">c3zbgA_</a>	 Alignment		100.0	27	<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
3	<a href="#">c6et9D_</a>	 Alignment		100.0	30	<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
4	<a href="#">c5ab6E_</a>	 Alignment		100.0	23	<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.
5	<a href="#">c6ok1A_</a>	 Alignment		100.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid-transfer protein; <b>PDBTitle:</b> ltp2-chsh2(duf35) aldolase
6	<a href="#">c5mg5R_</a>	 Alignment		100.0	25	<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 (magg)
7	<a href="#">c4u4eA_</a>	 Alignment		100.0	25	<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
8	<a href="#">c2d3tC_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
9	<a href="#">c1ulqD_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of tt0182 from thermus thermophilus hb8
10	<a href="#">c5zrvH_</a>	 Alignment		100.0	15	<b>PDB header:</b> liase, oxidoreductase/transferase <b>Chain:</b> H: <b>PDB Molecule:</b> trifunctional enzyme subunit beta, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, octamer
11	<a href="#">c5bz4K_</a>	 Alignment		100.0	18	<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) from2 mycobacterium smegmatis

12	<a href="#">c5xyjA_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> purification,crystallization and structural analysis of cytoplasmic2 acetoacetyl-coa thiolase from saccharomyces cerevisiae
13	<a href="#">c4o9cC_</a>	Alignment		100.0	23	<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
14	<a href="#">c4wysB_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of thiolase from escherichia coli
15	<a href="#">c3ss6B_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
16	<a href="#">c4yzoD_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acyl-coa acyltransferase; <b>PDBTitle:</b> crystal structure analysis of thiolase-like protein, st0096 from2 sulfolobus tokodaii
17	<a href="#">c2vu2D_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.
18	<a href="#">c4nzsA_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketothiolase bktb; <b>PDBTitle:</b> crystal structure of beta-ketothiolase bktb b from ralstonia eutropha2 h16
19	<a href="#">c4n45B_</a>	Alignment		100.0	18	<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
20	<a href="#">c6aaqA_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions
21	<a href="#">c2wuaA_</a>	Alignment	not modelled	100.0	20	<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
22	<a href="#">c5lp7A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-coa thiolase (mmga) from bacillus2 subtilis.
23	<a href="#">c2c7yB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2; <b>PDBTitle:</b> plant enzyme
24	<a href="#">c6bn2A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1
25	<a href="#">c4c2jA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial 3-ketoacyl-coa2 thiolase in complex with coa
26	<a href="#">c1wl5A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coenzyme a acetyltransferase 2; <b>PDBTitle:</b> human cytosolic acetoacetyl-coa thiolase
27	<a href="#">c4ubwB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase fada5; <b>PDBTitle:</b> apo structure of the 3-ketoacyl-coa thiolase fada5 from m.2 tuberculosis
28	<a href="#">c1afwB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> thiolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacetyl-coa thiolase; <b>PDBTitle:</b> the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae
29	<a href="#">c6hkhB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a;

29	<a href="#">c6bjbA</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of acat2-c91s thiolase from ascaris suum in complex with propionyl-coa and nitrate <b>PDB header:</b> transferase
30	<a href="#">c6bjaA</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a; <b>PDBTitle:</b> crystal structure of acat5 thiolase from ascaris suum in complex with2 coenzyme a
31	<a href="#">c2ibyD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
32	<a href="#">c4dd5A</a>	Alignment	not modelled	100.0	18	<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
33	<a href="#">c2iikA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, peroxisomal; <b>PDBTitle:</b> crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
34	<a href="#">c3goaA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase; <b>PDBTitle:</b> crystal structure of the salmonella typhimurium fada 3-ketoacyl-coa2 thiolase
35	<a href="#">c4egvC</a>	Alignment	not modelled	100.0	21	<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
36	<a href="#">c3svkB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
37	<a href="#">c4e1lC</a>	Alignment	not modelled	100.0	19	<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
38	<a href="#">d1wdkc1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
39	<a href="#">d1m3ka1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
40	<a href="#">d1ulqa1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
41	<a href="#">d1afwa1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
42	<a href="#">c2vz8B</a>	Alignment	not modelled	100.0	20	<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
43	<a href="#">c2vz8A</a>	Alignment	not modelled	100.0	20	<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
44	<a href="#">c5e5nB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase pks1; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
45	<a href="#">c4opeD</a>	Alignment	not modelled	100.0	23	<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
46	<a href="#">c6fikA</a>	Alignment	not modelled	100.0	18	<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
47	<a href="#">c4b3yB</a>	Alignment	not modelled	100.0	23	<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
48	<a href="#">c2qo3A</a>	Alignment	not modelled	100.0	22	<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 deoxyerthronolide b synthase
49	<a href="#">c4kc5D</a>	Alignment	not modelled	100.0	18	<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
50	<a href="#">c5erbB</a>	Alignment	not modelled	100.0	18	<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
51	<a href="#">c4tktA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase; <b>PDBTitle:</b> streptomcyes platensis isomigrastatin ketosynthase domain mgfsf ks6
52	<a href="#">c4tl2A</a>	Alignment	not modelled	100.0	23	<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 mgfsf from streptomcyes2 platensis
53	<a href="#">c4mz0B</a>	Alignment	not modelled	100.0	21	<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
54	<a href="#">c4wkyB</a>	Alignment	not modelled	100.0	22	<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 <b>PDB header:</b> transferase

55	<a href="#">c4z37A_</a>	Alignment	not modelled	100.0	18	<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 c0zgg5 (trans-at pks)2 from brevibacillus brevis
56	<a href="#">c4na3A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> polyketide synthase pksj; <b>PDBTitle:</b> crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
57	<a href="#">c4oqjA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> pks; <b>PDBTitle:</b> streptomycetes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1
58	<a href="#">c6c9uA_</a>	Alignment	not modelled	100.0	22	<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 deoxyerthronolide b synthase in complex with antibody fragment (fab)
59	<a href="#">c5elpA_</a>	Alignment	not modelled	100.0	20	<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
60	<a href="#">c2hg4A_</a>	Alignment	not modelled	100.0	24	<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.
61	<a href="#">c4qyrA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> at-less polyketide synthase; <b>PDBTitle:</b> streptomycetes platensis isomigrastatin ketosynthase domain mgse ks3
62	<a href="#">c5e5nD_</a>	Alignment	not modelled	100.0	21	<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)
63	<a href="#">c4ls5A_</a>	Alignment	not modelled	100.0	22	<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
64	<a href="#">c3hhdC_</a>	Alignment	not modelled	100.0	19	<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.
65	<a href="#">c2iwyB_</a>	Alignment	not modelled	100.0	25	<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
66	<a href="#">c2gfvA_</a>	Alignment	not modelled	100.0	23	<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
67	<a href="#">c2gqdB_</a>	Alignment	not modelled	100.0	22	<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
68	<a href="#">c4cw4A_</a>	Alignment	not modelled	100.0	20	<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
69	<a href="#">c2ix4B_</a>	Alignment	not modelled	100.0	20	<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
70	<a href="#">c1oxhD_</a>	Alignment	not modelled	100.0	24	<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
71	<a href="#">c1tqyC_</a>	Alignment	not modelled	100.0	18	<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
72	<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
73	<a href="#">c3o04A_</a>	Alignment	not modelled	100.0	19	<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
74	<a href="#">c1j3nB_</a>	Alignment	not modelled	100.0	23	<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
75	<a href="#">c4ewgA_</a>	Alignment	not modelled	100.0	20	<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
76	<a href="#">c4b7vA_</a>	Alignment	not modelled	100.0	21	<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)
77	<a href="#">c5bp1A_</a>	Alignment	not modelled	100.0	20	<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
78	<a href="#">c1e5mA_</a>	Alignment	not modelled	100.0	19	<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.

79	<a href="#">c2uv9B_</a>	 Alignment	not modelled	100.0	25	<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
80	<a href="#">c2gp6B_</a>	 Alignment	not modelled	100.0	20	<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)
81	<a href="#">c4ddoA_</a>	 Alignment	not modelled	100.0	23	<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
82	<a href="#">c2vkzC_</a>	 Alignment	not modelled	100.0	20	<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
83	<a href="#">c4qavB_</a>	 Alignment	not modelled	100.0	23	<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
84	<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
85	<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
86	<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
87	<a href="#">c3e60A_</a>	 Alignment	not modelled	100.0	22	<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
88	<a href="#">c4jgaA_</a>	 Alignment	not modelled	100.0	20	<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
89	<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
90	<a href="#">c4opfA_</a>	 Alignment	not modelled	100.0	17	<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
91	<a href="#">c2wggA_</a>	 Alignment	not modelled	100.0	20	<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
92	<a href="#">c1tqyD_</a>	 Alignment	not modelled	100.0	22	<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
93	<a href="#">c2buiC_</a>	 Alignment	not modelled	100.0	18	<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
94	<a href="#">c3lrfA_</a>	 Alignment	not modelled	100.0	19	<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
95	<a href="#">c6qspA_</a>	 Alignment	not modelled	100.0	19	<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
96	<a href="#">d1ulqa2</a>	 Alignment	not modelled	100.0	22	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
97	<a href="#">d1wdkc2</a>	 Alignment	not modelled	100.0	19	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
98	<a href="#">d1m3ka2</a>	 Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
99	<a href="#">d1afwa2</a>	 Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
100	<a href="#">c2ebdB_</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5
101	<a href="#">c1zowB_</a>	 Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase iii; <b>PDBTitle:</b> crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii
102	<a href="#">c3ledA_</a>	 Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-acyl carrier protein synthase iii;



102	<a href="#">c3e9A_</a>	Alignment	not modelled	99.9	19	<b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase iii2 from rhodospseudomonas palustris cga009 <b>PDB header:</b> transferase
103	<a href="#">c1mzjB_</a>	Alignment	not modelled	99.9	18	<b>Chain:</b> B; <b>PDB Molecule:</b> beta-ketoacylsynthase iii; <b>PDBTitle:</b> crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
104	<a href="#">c4ewpD_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> crystal structure of fabh from micrococcus luteus
105	<a href="#">c2p0uB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> stilbenecarboxylate synthase 2; <b>PDBTitle:</b> crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
106	<a href="#">c1ee0A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-pyrone synthase; <b>PDBTitle:</b> 2-pyrone synthase complexed with acetoacetyl-coa
107	<a href="#">c2d3mA_</a>	Alignment	not modelled	99.9	18	<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
108	<a href="#">c3ov3A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> curcumin synthase; <b>PDBTitle:</b> g211f mutant of curcumin synthase 1 from curcuma longa
109	<a href="#">c6a9nA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> crystal structure of kas iii from propionibacterium acnes
110	<a href="#">c3a5qA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> benzalacetone synthase; <b>PDBTitle:</b> benzalacetone synthase from rheum palmatum
111	<a href="#">c1xetD_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> dihydropinosylvin synthase; <b>PDBTitle:</b> crystal structure of stilbene synthase from pinus sylvestris,2 complexed with methylmalonyl coa
112	<a href="#">c5gk2A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ketosynthase stld; <b>PDBTitle:</b> the structure of the h302a mutant of stld
113	<a href="#">c2qnxA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxy carbonyl)dithio]-undecanoic acid
114	<a href="#">c2gyoB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> methanethiol-cys 112 inhibition complex of e. coli ketoacyl synthase2 iii (fabh) and coenzyme a
115	<a href="#">c3h76A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> pqs biosynthetic enzyme; <b>PDBTitle:</b> crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway
116	<a href="#">c4x0oG_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 2; <b>PDBTitle:</b> beta-ketoacyl-(acyl carrier protein) synthase iii-2 (fabh2) from2 vibrio cholerae soaked with acetyl-coa
117	<a href="#">c3fk5A_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-synthase iii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase iii, fabh (xoo4209) from xanthomonas oryzae pv.3 oryzae kacc10331
118	<a href="#">c5bqsA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> s. pneumoniae fabh with small molecule inhibitor 4
119	<a href="#">c3gwaA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) synthase iii; <b>PDBTitle:</b> 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii
120	<a href="#">c3il3A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> structure of haemophilus influenzae fabh