

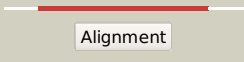

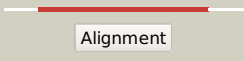

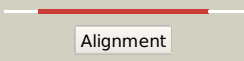

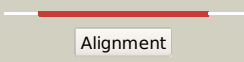

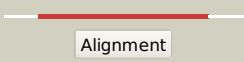

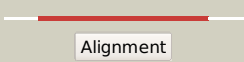

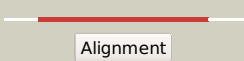

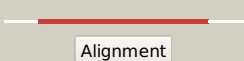

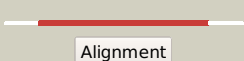

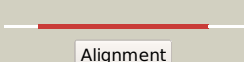








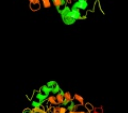



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3540c_(ltp2)_3979678_3980838
Date	Fri Aug 9 18:20:22 BST 2019
Unique Job ID	0ca0cf648924c55b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ok1A_</a>	 Alignment		100.0	71	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid-transfer protein; <b>PDBTitle:</b> ltp2-chsh2(duf35) aldolase
2	<a href="#">c3zbgA_</a>	 Alignment		100.0	22	<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	25	<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="#">c6hspB_</a>	 Alignment		100.0	25	<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
5	<a href="#">c4u4eA_</a>	 Alignment		100.0	38	<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
6	<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.
7	<a href="#">c5mg5R_</a>	 Alignment		100.0	23	<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 (mapg)
8	<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
9	<a href="#">c5lp7A_</a>	 Alignment		100.0	18	<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.
10	<a href="#">c5bz4K_</a>	 Alignment		100.0	17	<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
11	<a href="#">c1ulqD_</a>	 Alignment		100.0	18	<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

12	<a href="#">c4o9cC_</a>	Alignment		100.0	20	<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
13	<a href="#">c5zrvH_</a>	Alignment		100.0	16	<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
14	<a href="#">c4n45B_</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 reduced form of thiolase from clostridium2 acetobutylicum
15	<a href="#">c4wysB_</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 thiolase from escherichia coli
16	<a href="#">c3ss6B_</a>	Alignment		100.0	17	<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
17	<a href="#">c2vu2D_</a>	Alignment		100.0	16	<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="#">c2d3tC_</a>	Alignment		100.0	20	<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
19	<a href="#">c4nzsA_</a>	Alignment		100.0	18	<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
20	<a href="#">c4yzoD_</a>	Alignment		100.0	23	<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
21	<a href="#">c4c2jA_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">c6aaqA_</a>	Alignment	not modelled	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
23	<a href="#">c6bjbB_</a>	Alignment	not modelled	100.0	16	<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
24	<a href="#">c4dd5A_</a>	Alignment	not modelled	100.0	17	<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
25	<a href="#">c2c7yB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2; <b>PDBTitle:</b> plant enzyme
26	<a href="#">c2wuaA_</a>	Alignment	not modelled	100.0	13	<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
27	<a href="#">c6bjjaA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <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
28	<a href="#">c6bn2A_</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> crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1
						<b>PDB header:</b> transferase

29	<a href="#">c4ubwB_</a>	Alignment	not modelled	100.0	19	<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
30	<a href="#">c2ibyD_</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">c1afwB_</a>	Alignment	not modelled	100.0	13	<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
32	<a href="#">c1wl5A_</a>	Alignment	not modelled	100.0	18	<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
33	<a href="#">c2iikA_</a>	Alignment	not modelled	100.0	15	<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 (acaal)
34	<a href="#">c3goaA_</a>	Alignment	not modelled	100.0	19	<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="#">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
36	<a href="#">c4e1lC_</a>	Alignment	not modelled	100.0	20	<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
37	<a href="#">c4egvC_</a>	Alignment	not modelled	100.0	22	<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
38	<a href="#">d1m3ka1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
39	<a href="#">d1ulqa1</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="#">d1wdkc1</a>	Alignment	not modelled	100.0	20	<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	11	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
42	<a href="#">c5e5nB_</a>	Alignment	not modelled	100.0	12	<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)
43	<a href="#">c2gfvA_</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> structure of e. coli fabf (kasi) c163q mutant
44	<a href="#">c4opeD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> npps/pks; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
45	<a href="#">c2qo3A_</a>	Alignment	not modelled	100.0	19	<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
46	<a href="#">c4kc5D_</a>	Alignment	not modelled	100.0	16	<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
47	<a href="#">c5erbB_</a>	Alignment	not modelled	100.0	13	<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
48	<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
49	<a href="#">c4ti2A_</a>	Alignment	not modelled	100.0	15	<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 streptomycetes2 platensis
50	<a href="#">c4tktA_</a>	Alignment	not modelled	100.0	16	<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 mgsf ks6
51	<a href="#">c4wkyB_</a>	Alignment	not modelled	100.0	20	<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
52	<a href="#">c4mz0B_</a>	Alignment	not modelled	100.0	17	<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
53	<a href="#">c4b3yB_</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> cryo-em structure of the mycobacterial fatty acid synthase
54	<a href="#">c6fikA_</a>	Alignment	not modelled	100.0	17	<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 <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
55	<a href="#">c4oqjA_</a>	Alignment	not modelled	100.0	15
56	<a href="#">c4ls5A_</a>	Alignment	not modelled	100.0	19
57	<a href="#">c2vz8A_</a>	Alignment	not modelled	100.0	17
58	<a href="#">c6c9uA_</a>	Alignment	not modelled	100.0	17
59	<a href="#">c2iwyB_</a>	Alignment	not modelled	100.0	23
60	<a href="#">c5elpA_</a>	Alignment	not modelled	100.0	13
61	<a href="#">c2hg4A_</a>	Alignment	not modelled	100.0	20
62	<a href="#">c2vz8B_</a>	Alignment	not modelled	100.0	16
63	<a href="#">c4z37A_</a>	Alignment	not modelled	100.0	13
64	<a href="#">c5e5nD_</a>	Alignment	not modelled	100.0	16
65	<a href="#">c1tqyC_</a>	Alignment	not modelled	100.0	20
66	<a href="#">c4na3A_</a>	Alignment	not modelled	100.0	17
67	<a href="#">c4ddoA_</a>	Alignment	not modelled	100.0	20
68	<a href="#">c1oxhD_</a>	Alignment	not modelled	100.0	15
69	<a href="#">c2gqdB_</a>	Alignment	not modelled	100.0	16
70	<a href="#">c4qyrA_</a>	Alignment	not modelled	100.0	16
71	<a href="#">c3hhdC_</a>	Alignment	not modelled	100.0	17
72	<a href="#">c1j3nB_</a>	Alignment	not modelled	100.0	21
73	<a href="#">c1e5mA_</a>	Alignment	not modelled	100.0	17
74	<a href="#">c4b7vA_</a>	Alignment	not modelled	100.0	18
75	<a href="#">c4ewgA_</a>	Alignment	not modelled	100.0	17
76	<a href="#">c5bp1A_</a>	Alignment	not modelled	100.0	20
77	<a href="#">c4jgaA_</a>	Alignment	not modelled	100.0	19

78	<a href="#">c2gp6B_</a>	Alignment	not modelled	100.0	14	<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)
79	<a href="#">c3e60A_</a>	Alignment	not modelled	100.0	18	<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
80	<a href="#">c4qavB_</a>	Alignment	not modelled	100.0	19	<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
81	<a href="#">c4cw4A_</a>	Alignment	not modelled	100.0	13	<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
82	<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
83	<a href="#">c2wggA_</a>	Alignment	not modelled	100.0	16	<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
84	<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
85	<a href="#">c3o04A_</a>	Alignment	not modelled	100.0	17	<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
86	<a href="#">c4qpFA_</a>	Alignment	not modelled	100.0	18	<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
87	<a href="#">c3gwaA_</a>	Alignment	not modelled	100.0	18	<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
88	<a href="#">c6qspA_</a>	Alignment	not modelled	100.0	15	<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
89	<a href="#">c3fk5A_</a>	Alignment	not modelled	100.0	16	<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
90	<a href="#">c1mzjB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <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
91	<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
92	<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
93	<a href="#">c1ee0A_</a>	Alignment	not modelled	99.9	15	<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
94	<a href="#">c4ewpD_</a>	Alignment	not modelled	99.9	17	<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
95	<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
96	<a href="#">c2buiC_</a>	Alignment	not modelled	99.9	19	<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
97	<a href="#">c2p0uB_</a>	Alignment	not modelled	99.9	17	<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)
98	<a href="#">c3hmjB_</a>	Alignment	not modelled	99.9	20	<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
99	<a href="#">c5dwzC_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> structural and functional characterization of pqsbcb, a condensing2 enzyme in the biosynthesis of the pseudomonas aeruginosa quinolone3 signal
100	<a href="#">c4dfeB_</a>	Alignment	not modelled	99.9	17	<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 burkholderia xenovorans <b>PDB header:</b> transferase



101	<a href="#">c4jatB_</a>	Alignment	not modelled	99.9	19	<b>Chain:</b> B: <b>PDB Molecule:</b> alpha-pyrone synthesis polyketide synthase-like pks11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis pks11 reveals2 intermediates in the synthesis of methyl-branched alkylpyrones
102	<a href="#">c2qnxA_</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> 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
103	<a href="#">c1u0mA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide synthase; <b>PDBTitle:</b> crystal structure of 1,3,6,8-tetrahydroxynaphthalene synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
104	<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
105	<a href="#">c3lrfA_</a>	Alignment	not modelled	99.9	17	<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
106	<a href="#">c3il3A_</a>	Alignment	not modelled	99.9	14	<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
107	<a href="#">c3h76A_</a>	Alignment	not modelled	99.9	19	<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
108	<a href="#">c2gyoB_</a>	Alignment	not modelled	99.9	16	<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
109	<a href="#">c6a9nA_</a>	Alignment	not modelled	99.9	17	<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="#">c2d3mA_</a>	Alignment	not modelled	99.9	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
111	<a href="#">c1cmIA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (chalcone synthase); <b>PDBTitle:</b> chalcone synthase from alfalfa complexed with malonyl-coa
112	<a href="#">c4efiA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) synthase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl-carrier protein) synthase from2 burkholderia xenovorans lb400
113	<a href="#">c3a5qA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> benzalacetone synthase; <b>PDBTitle:</b> benzalacetone synthase from rheum palmatum
114	<a href="#">c6esqI_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> structure of the acetoacetyl-coa thiolase/hmg-coa synthase complex2 from methanothermococcus thermolithotrophicus soaked with acetyl-coa
115	<a href="#">c1xetD_</a>	Alignment	not modelled	99.9	15	<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
116	<a href="#">c5ucoB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4,6-trihydroxybenzophenone synthase; <b>PDBTitle:</b> benzophenone synthase from hypericum androsaemum
117	<a href="#">c5yptA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stilbenecarboxylate synthase 1; <b>PDBTitle:</b> crystal structure of marchantia paleacea chalone synthase like 12 (chsl1)
118	<a href="#">c3ov3A_</a>	Alignment	not modelled	99.9	21	<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
119	<a href="#">d1ulqa2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
120	<a href="#">c4rybA_</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 beta-ketoacyl-acp synthase iii (fabh) from2 neisseria meningitidis