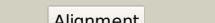
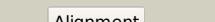
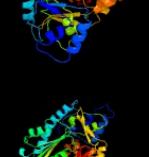


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1660_(pks10)_1874167_1875228
Date	Fri Aug 2 13:30:25 BST 2019
Unique Job ID	60d37fbc683936e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4jatB</a>			100.0	74	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> alpha-pyrone synthesis polyketide synthase-like pks11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis pks11 reveals 2 intermediates in the synthesis of methyl-branched alkylpyrones
2	<a href="#">c3v7iA</a>			100.0	26	<b>PDB header:</b> transferase, lyase <b>Chain:</b> A; <b>PDB Molecule:</b> putative polyketide synthase; <b>PDBTitle:</b> germicidin synthase (gcs) from streptomyces coelicolor, a type iii2 polyketide synthase
3	<a href="#">c1u0mA</a>			100.0	28	<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
4	<a href="#">c1cmIA</a>			100.0	25	<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
5	<a href="#">c4b0nB</a>			100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase iii; <b>PDBTitle:</b> crystal structure of pks-i from the brown algae ectocarpus siliculosus
6	<a href="#">c5wc4A</a>			100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> bis3 biphenyl synthase; <b>PDBTitle:</b> crystal structure of biphenyl synthase from malus domestica complexed2 with benzoyl-coa
7	<a href="#">c3aleB</a>			100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> os07g0271500 protein; <b>PDBTitle:</b> a type iii polyketide synthase that produces diarylheptanoid
8	<a href="#">c3a5qA</a>			100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> benzalacetone synthase; <b>PDBTitle:</b> benzalacetone synthase from rheum palmatum
9	<a href="#">c2h84A</a>			100.0	27	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> steely1; <b>PDBTitle:</b> crystal structure of the c-terminal type iii polyketide synthase (pks2 iii) domain of 'steely1' (a type i/iii pks hybrid from dictyostelium)
10	<a href="#">c1ee0A</a>			100.0	25	<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
11	<a href="#">c1xetD</a>			100.0	25	<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

12	<a href="#">c5ucoB</a>	Alignment		100.0	24	<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
13	<a href="#">c3e1hA</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a type iii polyketide synthase pksiiinc from2 neurospora crassa
14	<a href="#">c3oitB</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> os07g0271500 protein; <b>PDBTitle:</b> crystal structure of curcuminoid synthase cus from oryza sativa
15	<a href="#">c5yptA</a>	Alignment		100.0	27	<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 (chs1)
16	<a href="#">c2p0ub</a>	Alignment		100.0	26	<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)
17	<a href="#">d1teda</a>	Alignment		100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
18	<a href="#">c3tsyA</a>	Alignment		100.0	26	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol <b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein
19	<a href="#">c3wy0A</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein csyb; <b>PDBTitle:</b> the i375w mutant of csyb complexed with coa-sh
20	<a href="#">c3ov3A</a>	Alignment		100.0	27	<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
21	<a href="#">c3euoB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type iii pentaketide synthase; <b>PDBTitle:</b> crystal structure of a fungal type iii polyketide synthase,2 oras
22	<a href="#">c5wx3C</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldiketide-coa synthase; <b>PDBTitle:</b> alkyldiketide-coa synthase from evodia rutaecarpa
23	<a href="#">c3wd8D</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> type iii polyketide synthase quinolone synthase; <b>PDBTitle:</b> typeiii polyketide synthases
24	<a href="#">c2d3mA</a>	Alignment	not modelled	100.0	22	<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
25	<a href="#">c6dxFB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> chalcone synthase; <b>PDBTitle:</b> crystal structure of chalcone synthase from selaginella moellendorffii2 - hydrogen peroxide treated
26	<a href="#">c5yo9A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-(acp)] synthase iii c terminal <b>PDBTitle:</b> crystal structure of kas iii from acinetobacter baumannii
27	<a href="#">c6a9nA</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 3; <b>PDBTitle:</b> crystal structure of kas iii from propionibacterium acnes
28	<a href="#">c4x0oG</a>	Alignment	not modelled	100.0	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

29	<a href="#">c4efiA</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; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl-carrier protein) synthase from2 burkholderia xenovorans lb400
30	<a href="#">c3fk5A</a>	Alignment	not modelled	100.0	21	<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
31	<a href="#">c1mzjB</a>	Alignment	not modelled	100.0	24	<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
32	<a href="#">c4dfeB</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 3; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from burkholderia xenovorans
33	<a href="#">c3h76A</a>	Alignment	not modelled	100.0	25	<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
34	<a href="#">c5dwzC</a>	Alignment	not modelled	100.0	20	<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 pqsbc, a condensing2 enzyme in the biosynthesis of the pseudomonas aeruginosa quinolone3 signal
35	<a href="#">c4v2pB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> keto synthase; <b>PDBTitle:</b> keto synthase mxnb
36	<a href="#">c3il3A</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 3; <b>PDBTitle:</b> structure of haemophilus influenzae fabh
37	<a href="#">c3ledA</a>	Alignment	not modelled	100.0	17	<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
38	<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
39	<a href="#">c3vs9F</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> type iii polyketide synthase; <b>PDBTitle:</b> crystal structure of type iii pks arsc mutant
40	<a href="#">c4ewpD</a>	Alignment	not modelled	100.0	23	<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
41	<a href="#">c2qnxA</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 3; <b>PDBTitle:</b> crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxycarbonyl)dithio]-undecanoic acid
42	<a href="#">c4rybA</a>	Alignment	not modelled	100.0	24	<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) from neisseria meningitidis
43	<a href="#">c5mg5P</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> a multi-component acyltransferase phabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
44	<a href="#">c5gk2A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> keto synthase stld; <b>PDBTitle:</b> the structure of the h302a mutant of stld
45	<a href="#">c2x3eA</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 3; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase iii,2 fabh from pseudomonas aeruginosa pao1
46	<a href="#">c2ebdB</a>	Alignment	not modelled	100.0	24	<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
47	<a href="#">c3il5D</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> structure of e. faecalis fabh in complex with 2-({4-bromo-3-2 [(diethylamino)sulfonyl]benzoyl}amino)benzoic acid
48	<a href="#">c2gyoB</a>	Alignment	not modelled	100.0	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
49	<a href="#">c1ub7A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] synthase; <b>PDBTitle:</b> the crystal analysis of beta-keroyacyl-[acyl carrier protein] synthase2 iii (fabh)from thermus thermophilus.
50	<a href="#">c1zowB</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 iii; <b>PDBTitle:</b> crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii
51	<a href="#">cEfba</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] synthase

51	<a href="#">c3045m</a>	Alignment	not modelled	100.0	17	3; <b>PDBTitle:</b> s. pneumoniae fabh with small molecule inhibitor 4
52	<a href="#">c3s3IB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cerj; <b>PDBTitle:</b> crystal structure of cerj from streptomyces tendae
53	<a href="#">c2f9aA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl coenzyme a synthase 1; <b>PDBTitle:</b> hmg-coa synthase from brassica juncea in complex with f-244
54	<a href="#">c4xsbB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> daunorubicin-doxorubicin polyketide synthase; <b>PDBTitle:</b> determining the molecular basis for starter unit selection during 2 daunorubicin biosynthesis
55	<a href="#">c2p8uB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
56	<a href="#">c1x9eB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hmg-coa synthase; <b>PDBTitle:</b> crystal structure of hmg-coa synthase from enterococcus2 faecalis
57	<a href="#">c2v4wB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase, <b>PDBTitle:</b> crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2)
58	<a href="#">c1txtB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coa synthase; <b>PDBTitle:</b> staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
59	<a href="#">c5kp8A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> curd; <b>PDBTitle:</b> crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-acp
60	<a href="#">c6esql</a>	Alignment	not modelled	100.0	18	<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 thermolithrophicus soaked with acetyl-coa
61	<a href="#">c5hwra</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> mvas in complex with coenzyme a
62	<a href="#">c3lehA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> the crystal structure of smu.943c from streptococcus mutans ua159
63	<a href="#">d1u0ma1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
64	<a href="#">d1bi5a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
65	<a href="#">d1ee0a1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
66	<a href="#">d1u0ua1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
67	<a href="#">c5dwzA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl carrier protein) synthase iii; <b>PDBTitle:</b> structural and functional characterization of pqsbc, a condensing2 enzyme in the biosynthesis of the pseudomonas aeruginosa quinolone3 signal
68	<a href="#">d1u0va1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
69	<a href="#">d1mzja1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
70	<a href="#">d1ub7a1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
71	<a href="#">d1hnja1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
72	<a href="#">d1xpma1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
73	<a href="#">d1u6ea1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
74	<a href="#">d1u0ua2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
75	<a href="#">d1ee0a2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
76	<a href="#">d1u0ma2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like

					<b>Family:</b> Chalcone synthase-like
77	<a href="#">d1bi5a2</a>	Alignment	not modelled	100.0	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
78	<a href="#">c4e1IC</a>	Alignment	not modelled	100.0	<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
79	<a href="#">c4dd5A</a>	Alignment	not modelled	100.0	<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
80	<a href="#">c6ok1A</a>	Alignment	not modelled	100.0	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid-transfer protein; <b>PDBTitle:</b> ltp2-chsh2(duf35) aldolase
81	<a href="#">c2vu2D</a>	Alignment	not modelled	100.0	<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.
82	<a href="#">c2iikA</a>	Alignment	not modelled	100.0	<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)
83	<a href="#">c6aqpA</a>	Alignment	not modelled	100.0	<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
84	<a href="#">c4c2jA</a>	Alignment	not modelled	100.0	<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
85	<a href="#">c4n45B</a>	Alignment	not modelled	100.0	<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
86	<a href="#">c4wysB</a>	Alignment	not modelled	100.0	<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
87	<a href="#">c3ss6B</a>	Alignment	not modelled	99.9	<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
88	<a href="#">c4o9cc</a>	Alignment	not modelled	99.9	<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
89	<a href="#">d1hnja2</a>	Alignment	not modelled	99.9	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
90	<a href="#">d1ub7a2</a>	Alignment	not modelled	99.9	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
91	<a href="#">c6bjbB</a>	Alignment	not modelled	99.9	<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
92	<a href="#">c2c7yB</a>	Alignment	not modelled	99.9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2; <b>PDBTitle:</b> plant enzyme
93	<a href="#">c5lp7A</a>	Alignment	not modelled	99.9	<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.
94	<a href="#">d1mzja2</a>	Alignment	not modelled	99.9	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
95	<a href="#">d1u6ea2</a>	Alignment	not modelled	99.9	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
96	<a href="#">c6bn2A</a>	Alignment	not modelled	99.9	<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
97	<a href="#">c2wuaA</a>	Alignment	not modelled	99.9	<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
98	<a href="#">c2ibyD</a>	Alignment	not modelled	99.9	<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
99	<a href="#">c3goaA</a>	Alignment	not modelled	99.9	<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
100	<a href="#">c4nzsA</a>	Alignment	not modelled	99.9	<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
101	<a href="#">c6bjaa</a>	Alignment	not modelled	99.9	<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
102	<a href="#">c1wl5A</a>	Alignment	not modelled	99.9	<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

103	<a href="#">c4ubwB</a>	Alignment	not modelled	99.9	16	<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
104	<a href="#">c4opfA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nrrps/pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmrh ks8
105	<a href="#">c1ulqD</a>	Alignment	not modelled	99.9	24	<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
106	<a href="#">c5bz4K</a>	Alignment	not modelled	99.9	22	<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
107	<a href="#">c5xyjA</a>	Alignment	not modelled	99.9	18	<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
108	<a href="#">c5e5nD</a>	Alignment	not modelled	99.9	16	<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)
109	<a href="#">c2hg4A</a>	Alignment	not modelled	99.9	17	<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.
110	<a href="#">c3hhcC</a>	Alignment	not modelled	99.9	16	<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.
111	<a href="#">c4u4eA</a>	Alignment	not modelled	99.9	16	<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
112	<a href="#">c4opeD</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nrrps/pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmrh ks7
113	<a href="#">c4wkyB</a>	Alignment	not modelled	99.9	17	<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
114	<a href="#">c1afwB</a>	Alignment	not modelled	99.9	14	<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
115	<a href="#">c5bp1A</a>	Alignment	not modelled	99.9	17	<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
116	<a href="#">c4egvC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis
117	<a href="#">c4oqjA</a>	Alignment	not modelled	99.9	16	<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
118	<a href="#">c5ab6E</a>	Alignment	not modelled	99.9	20	<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.
119	<a href="#">c4qavB</a>	Alignment	not modelled	99.9	18	<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
120	<a href="#">c2vz8A</a>	Alignment	not modelled	99.9	16	<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