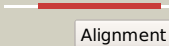
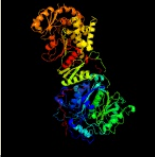
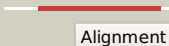

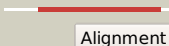
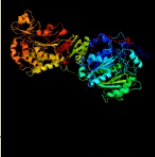

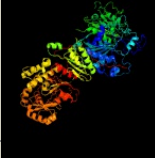

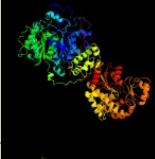


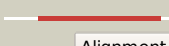


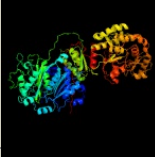



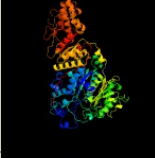










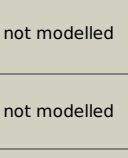


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2935_(ppsE)_3267747_3272213
Date	Thu Aug 8 16:20:09 BST 2019
Unique Job ID	fa8ed31c135bc45b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vz8A_</a>	 Alignment		100.0	28	<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="#">c6fikA_</a>	 Alignment		100.0	28	<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
3	<a href="#">c2vz8B_</a>	 Alignment		100.0	28	<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
4	<a href="#">c2qo3A_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> eryaii erythromycin polyketide synthase modules 3 and 4; <b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase
5	<a href="#">c6c9uA_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; <b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase in complex with antibody fragment (fab)
6	<a href="#">c2hg4A_</a>	 Alignment		100.0	35	<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>	 Alignment		100.0	27	<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>	 Alignment		100.0	35	<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>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> curlr; <b>PDBTitle:</b> structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
10	<a href="#">c4oqiA_</a>	 Alignment		100.0	47	<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
11	<a href="#">c4kc5D_</a>	 Alignment		100.0	36	<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

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> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
13	<a href="#">c5erbB_</a>	Alignment		100.0	39	<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="#">c4qyrA_</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> streptomcyes platensis isomigrastatin ketosynthase domain mgse ks3
15	<a href="#">c5e5nB_</a>	Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase pksI; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
16	<a href="#">c5elpA_</a>	Alignment		100.0	40	<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
17	<a href="#">c4z37A_</a>	Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mixed polyketide synthase/non-ribosomal peptide <b>PDBTitle:</b> structure of the ketosynthase of module 2 of c0zqg5 (trans-at pks)2 from brevibacillus brevis
18	<a href="#">c4tl2A_</a>	Alignment		100.0	38	<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 streptomcyes2 platensis
19	<a href="#">c4na3A_</a>	Alignment		100.0	36	<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
20	<a href="#">c4tktA_</a>	Alignment		100.0	42	<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 mgsf ks6
21	<a href="#">c4opeD_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> ligase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nrps/pks; <b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
22	<a href="#">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
23	<a href="#">c5e5nD_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> polyketide synthase pksI; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
24	<a href="#">c4b3yB_</a>	Alignment	not modelled	100.0	18	<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="#">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
27	<a href="#">c2pffA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
28	<a href="#">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 stalled acyl carrier protein at 3.1 angstrom resolution
						<b>PDB header:</b> transferase

29	<a href="#">c2vkzC_</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> C; <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
30	<a href="#">c2uv9B_</a>	Alignment	not modelled	100.0	17	<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
31	<a href="#">c2iwyB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> human mitochondrial beta-ketoacyl acp synthase
32	<a href="#">c4opfA_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nrps/pks; <b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmh ks8
33	<a href="#">c1tqyC_</a>	Alignment	not modelled	100.0	25	<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
34	<a href="#">c4cw4A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa
35	<a href="#">c4ls5A_</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 2; <b>PDBTitle:</b> crystal structure of beta-ketoacyl-acp synthase ii (fabf) from2 bacillus subtilis
36	<a href="#">c2gqdB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> the crystal structure of b-ketoacyl-acp synthase ii (fabf) from2 staphylococcus aureus
37	<a href="#">c4b7vA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of wild type pseudomonas aeruginosa fabf (kasii)
38	<a href="#">c4jqaA_</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 2; <b>PDBTitle:</b> x-ray crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase 22 from rickettsia rickettsii
39	<a href="#">c3o04A_</a>	Alignment	not modelled	100.0	24	<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
40	<a href="#">c4qavB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> the structure of beta-ketoacyl -(acyl carrier protein) synthase ii2 (fabf) from neisseria meningitidis
41	<a href="#">c1e5mA_</a>	Alignment	not modelled	100.0	23	<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.
42	<a href="#">c4ddoA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase ii from2 burkholderia vietnamiensis
43	<a href="#">c2gp6B_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> x-ray crystal structure of mycobacterium tuberculosis beta-ketoacyl2 acyl carrier protein synthase ii (mtkasb)
44	<a href="#">c3e60A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein ] synthase ii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase ii from2 bartonella henselae
45	<a href="#">c1oxhD_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> beta ketoacyl-acyl carrier protein synthase; <b>PDBTitle:</b> the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form
46	<a href="#">c2ix4B_</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> arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex
47	<a href="#">c2gfvA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2; <b>PDBTitle:</b> structure of e. coli fabf (kasii) c163q mutant
48	<a href="#">c1j3nB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) synthase ii; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8
49	<a href="#">c2wggA_</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 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:</b> A; <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815
51	<a href="#">c2huifC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> synthase <b>Chain:</b> C; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase i;

51	<a href="#">c2v0c_</a>	Alignment	not modelled	100.0	41	<b>PDBTitle:</b> e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k <b>PDB header:</b> transferase
52	<a href="#">c1tqyD_</a>	Alignment	not modelled	100.0	25	<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="#">c3lrfA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of beta-ketoacyl synthase from brucella2 melitensis
54	<a href="#">c3tzzA_</a>	Alignment	not modelled	100.0	24	<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
55	<a href="#">c6qspA_</a>	Alignment	not modelled	100.0	22	<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
56	<a href="#">c6iytA_</a>	Alignment	not modelled	100.0	27	<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
57	<a href="#">c6iyrA_</a>	Alignment	not modelled	100.0	30	<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
58	<a href="#">c5ydmA_</a>	Alignment	not modelled	100.0	39	<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
59	<a href="#">c6iyoA_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
60	<a href="#">c5u89A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
61	<a href="#">c4qbuA_</a>	Alignment	not modelled	100.0	31	<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
62	<a href="#">c2jgpA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 bycc
63	<a href="#">c2jfkD_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> structure of the mat domain of human fas with malonyl-coa
64	<a href="#">c6n8eA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
65	<a href="#">c4ammA_</a>	Alignment	not modelled	100.0	27	<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
66	<a href="#">c5t81A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
67	<a href="#">c6cgoB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
68	<a href="#">c2vsqA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
69	<a href="#">c2xhgA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase a; <b>PDBTitle:</b> crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
70	<a href="#">c4zxiA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
71	<a href="#">c4r1A_</a>	Alignment	not modelled	100.0	31	<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
72	<a href="#">c5m6pB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 2; <b>PDBTitle:</b> crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
73	<a href="#">c6p1jA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo2; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
74	<a href="#">c4zxiA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
75	<a href="#">c3tqeA_</a>	Alignment	not modelled	100.0	23	<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
						<b>PDB header:</b> ligase

76	<a href="#">c5ja2A_</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
77	<a href="#">c3ptwA_</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> crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
78	<a href="#">c3eenA_</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 transacylase2 (fabd); <b>PDBTitle:</b> crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
79	<a href="#">c3rgiA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disd protein; <b>PDBTitle:</b> trans-acting transferase from disorazole synthase
80	<a href="#">c3im8A_</a>	Alignment	not modelled	100.0	29	<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
81	<a href="#">c4znmB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> c-domain type ii peptide synthetase; <b>PDBTitle:</b> crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
82	<a href="#">c5ypvA_</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> crystal structure of fabd from acinetobacter baumannii
83	<a href="#">c6aefB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
84	<a href="#">c3qatB_</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> crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
85	<a href="#">c2g2oA_</a>	Alignment	not modelled	100.0	29	<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
86	<a href="#">c2cuyA_</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 malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
87	<a href="#">c3ezoA_</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> crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
88	<a href="#">c4tx3B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide synthetase, module 7; <b>PDBTitle:</b> complex of the x-domain and oxyb from teicoplanin biosynthesis
89	<a href="#">c3im9A_</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> crystal structure of mcat from staphylococcus aureus
90	<a href="#">c6ozvA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
91	<a href="#">c6m7lB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
92	<a href="#">c4rr5A_</a>	Alignment	not modelled	100.0	26	<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
93	<a href="#">c2qj3B_</a>	Alignment	not modelled	100.0	21	<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
94	<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.
95	<a href="#">c4jn3B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cda peptide synthetase i; <b>PDBTitle:</b> crystal structures of the first condensation domain of the cda2 synthetase
96	<a href="#">c5t3eA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
97	<a href="#">c2h1yA_</a>	Alignment	not modelled	100.0	27	<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
98	<a href="#">c3g87A_</a>	Alignment	not modelled	100.0	29	<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



99	<a href="#">c5dz7A_</a>	Alignment	not modelled	100.0	25	<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
100	<a href="#">c5dz6A_</a>	Alignment	not modelled	100.0	28	<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
101	<a href="#">c6ad3A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> lovastatin nonaketide synthase moka; <b>PDBTitle:</b> structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
102	<a href="#">c1l5aA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> amide synthase; <b>PDBTitle:</b> crystal structure of vibh, an nrps condensation enzyme
103	<a href="#">c2c2nA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> structure of human mitochondrial malonyltransferase
104	<a href="#">c5czcA_</a>	Alignment	not modelled	100.0	17	<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
105	<a href="#">d1tqya2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
106	<a href="#">c5dijA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
107	<a href="#">d2ix4a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
108	<a href="#">d1e5ma1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
109	<a href="#">d1tqyb2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
110	<a href="#">d1j3na1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
111	<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
112	<a href="#">d2gfva1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
113	<a href="#">d2vbaa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
114	<a href="#">d1mlaa1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
115	<a href="#">d1nm2a1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
116	<a href="#">c4hvmC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallysomycin biosynthesis protein tlmii
117	<a href="#">c4egvc_</a>	Alignment	not modelled	100.0	15	<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
118	<a href="#">c3fotA_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 15-o-acetyltransferase; <b>PDBTitle:</b> structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
119	<a href="#">d1e5ma2</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
120	<a href="#">d2gfva2</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related