







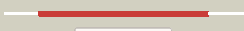
























# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3523\_(ltp3)\_3959708\_3960892  
 Date Fri Aug 9 18:20:20 BST 2019  
 Unique Job ID f1ba65f0892f0fc6

Detailed template information

| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                   |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3zbgA_</a> | <br>Alignment   |    | 100.0      | 25     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase-like protein;<br><b>PDBTitle:</b> crystal structure of wild-type scp2 thiolase from leishmania2 mexicana at 1.85 a                                                     |
| 2  | <a href="#">c6et9D_</a> | <br>Alignment   |    | 100.0      | 26     | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase thiolase;<br><b>PDBTitle:</b> structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a         |
| 3  | <a href="#">c6hspB_</a> | <br>Alignment   |    | 100.0      | 28     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> scp2-thiolase (type-1);<br><b>PDBTitle:</b> crystal structure of the zebrafish peroxisomal scp2-thiolase (type-1)2 in complex with coa and octanoyl-coa                                        |
| 4  | <a href="#">c5ab6E_</a> | <br>Alignment   |    | 100.0      | 22     | <b>PDB header:</b> transport protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> scp2-thiolase like protein;<br><b>PDBTitle:</b> crystal structure of trypanosoma brucei scp2-thiolase like2 protein (tbslp) in complex with acetoacetyl-coa.                             |
| 5  | <a href="#">c6ok1A_</a> | <br>Alignment |  | 100.0      | 27     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lipid-transfer protein;<br><b>PDBTitle:</b> ltp2-chsh2(duf35) aldolase                                                                                                                   |
| 6  | <a href="#">c5mg5R_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> R: <b>PDB Molecule:</b> 2,4-diacetylphloroglucinol biosynthesis protein phlc;<br><b>PDBTitle:</b> a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapp) |
| 7  | <a href="#">c4u4eA_</a> | <br>Alignment |  | 100.0      | 28     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thiolase;<br><b>PDBTitle:</b> crystal structure of putative thiolase from sphaerobacter thermophilus2 dsm 20745                                                                                |
| 8  | <a href="#">c4yzoD_</a> | <br>Alignment |  | 100.0      | 34     | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative acyl-coa acyltransferase;<br><b>PDBTitle:</b> crystal structure analysis of thiolase-like protein, st0096 from2 sulfolobus tokodaii                                                   |
| 9  | <a href="#">c5zrvH_</a> | <br>Alignment |  | 100.0      | 17     | <b>PDB header:</b> liase, oxidoreductase/transferase<br><b>Chain:</b> H: <b>PDB Molecule:</b> trifunctional enzyme subunit beta, mitochondrial;<br><b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, octamer                                    |
| 10 | <a href="#">c5xyjA_</a> | <br>Alignment |  | 100.0      | 18     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> purification,crystallization and structural analysis of cytoplasmic2 acetoacetyl-coa thiolase from saccharomyces cerevisiae                  |
| 11 | <a href="#">c2d3tC_</a> | <br>Alignment |  | 100.0      | 17     | <b>PDB header:</b> lyase, oxidoreductase/transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase;<br><b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v                                               |

|    |                         |           |                                                                                     |       |    |                                                                                                                                                                                                                                         |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c5bz4K_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> K: <b>PDB Molecule:</b> beta-ketothiolase;<br><b>PDBTitle:</b> crystal structure of a t1-like thiolase (coa-complex) from2 mycobacterium smegmatis                                      |
| 13 | <a href="#">c1ulqD_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of tt0182 from thermus thermophilus hb8                                            |
| 14 | <a href="#">c4o9cC_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of beta-ketothiolase (phaa) from ralstonia eutropha2 h16                                    |
| 15 | <a href="#">c3ss6B_</a> | Alignment |    | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase                                     |
| 16 | <a href="#">c4wysB_</a> | Alignment |    | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of thiolase from escherichia coli                                                           |
| 17 | <a href="#">c2wuaA_</a> | Alignment |    | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl coa thiolase;<br><b>PDBTitle:</b> structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower                                               |
| 18 | <a href="#">c4n45B_</a> | Alignment |  | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of reduced form of thiolase from clostridium2 acetobutylicum                                |
| 19 | <a href="#">c4nzsA_</a> | Alignment |  | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketothiolase bktb;<br><b>PDBTitle:</b> crystal structure of beta-ketothiolase bktb b from ralstonia eutropha2 h16                                          |
| 20 | <a href="#">c2c7yB_</a> | Alignment |  | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2;<br><b>PDBTitle:</b> plant enzyme                                                                                                     |
| 21 | <a href="#">c5lp7A_</a> | Alignment | not modelled                                                                        | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of 3-ketoacyl-coa thiolase (mmga) from bacillus2 subtilis.                                  |
| 22 | <a href="#">c2vu2D_</a> | Alignment | not modelled                                                                        | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.                             |
| 23 | <a href="#">c6aaqA_</a> | Alignment | not modelled                                                                        | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions           |
| 24 | <a href="#">c6bn2A_</a> | Alignment | not modelled                                                                        | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1                       |
| 25 | <a href="#">c6bjbB_</a> | Alignment | not modelled                                                                        | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a;<br><b>PDBTitle:</b> crystal structure of acat2-c91s thiolase from ascaris suum in complex2 with propionyl-coa and nitrate       |
| 26 | <a href="#">c4c2jA_</a> | Alignment | not modelled                                                                        | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human mitochondrial 3-ketoacyl-coa2 thiolase in complex with coa               |
| 27 | <a href="#">c4ubwB_</a> | Alignment | not modelled                                                                        | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase fada5;<br><b>PDBTitle:</b> apo structure of the 3-ketoacyl-coa thiolase fada5 from m.2 tuberculosis                                |
| 28 | <a href="#">c2ibyD_</a> | Alignment | not modelled                                                                        | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><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                                                                                                                                                                                                |
| 29 | <a href="#">c6bjaA</a>  | Alignment | not modelled | 100.0 | 16<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a;<br><b>PDBTitle:</b> crystal structure of acat5 thiolase from ascaris suum in complex with2 coenzyme a                                   |
| 30 | <a href="#">c4egvC</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis              |
| 31 | <a href="#">c1wl5A</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coenzyme a acetyltransferase 2;<br><b>PDBTitle:</b> human cytosolic acetoacetyl-coa thiolase                                                                     |
| 32 | <a href="#">c1afwB</a>  | Alignment | not modelled | 100.0 | 14<br><b>PDB header:</b> thiolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacetyl-coa thiolase;<br><b>PDBTitle:</b> the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae                         |
| 33 | <a href="#">c2iikA</a>  | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, peroxisomal;<br><b>PDBTitle:</b> crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)                                 |
| 34 | <a href="#">c4dd5A</a>  | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> biosynthetic thiolase (thla1) from clostridium difficile                                                              |
| 35 | <a href="#">c3goaA</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase;<br><b>PDBTitle:</b> crystal structure of the salmonella typhimurium fada 3-ketoacyl-coa2 thiolase                                              |
| 36 | <a href="#">c4e1lC</a>  | Alignment | not modelled | 100.0 | 20<br><b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> acetoacetyl-coa thiolase 2;<br><b>PDBTitle:</b> crystal structure of acetoacetyl-coa thiolase (thla2) from clostridium2 difficile                                       |
| 37 | <a href="#">c3svkB</a>  | Alignment | not modelled | 100.0 | 23<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase;<br><b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium                                           |
| 38 | <a href="#">c2vz8B</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase;<br><b>PDBTitle:</b> crystal structure of mammalian fatty acid synthase                                                                             |
| 39 | <a href="#">c2vz8A</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase;<br><b>PDBTitle:</b> crystal structure of mammalian fatty acid synthase                                                                             |
| 40 | <a href="#">c6fikA</a>  | Alignment | not modelled | 100.0 | 15<br><b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase;<br><b>PDBTitle:</b> acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks                                          |
| 41 | <a href="#">d1wdk1</a>  | Alignment | not modelled | 100.0 | 15<br><b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                              |
| 42 | <a href="#">d1m3ka1</a> | Alignment | not modelled | 100.0 | 15<br><b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                              |
| 43 | <a href="#">c4b3yB</a>  | Alignment | not modelled | 100.0 | 14<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase;<br><b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase                                                                     |
| 44 | <a href="#">c4kc5D</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> rhie protein;<br><b>PDBTitle:</b> crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica                                                       |
| 45 | <a href="#">c4opeD</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> ligase, transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nrps/pks;<br><b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7                                                               |
| 46 | <a href="#">c5e5nB</a>  | Alignment | not modelled | 100.0 | 16<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase pks1;<br><b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)            |
| 47 | <a href="#">d1afwa1</a> | Alignment | not modelled | 100.0 | 12<br><b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                              |
| 48 | <a href="#">d1ulqa1</a> | Alignment | not modelled | 100.0 | 17<br><b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                              |
| 49 | <a href="#">c4tl2A</a>  | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase;<br><b>PDBTitle:</b> crystal structure of ketosynthase domain from mgsf from streptomyces2 platensis                                        |
| 50 | <a href="#">c4oqjA</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pks;<br><b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1                                                                              |
| 51 | <a href="#">c2qo3A</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> eryaii erythromycin polyketide synthase modules 3 and 4;<br><b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase |
| 52 | <a href="#">c4wkyB</a>  | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-ketoacyl synthase;<br><b>PDBTitle:</b> streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2                                                         |
| 53 | <a href="#">c5erbB</a>  | Alignment | not modelled | 100.0 | 21<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase;<br><b>PDBTitle:</b> ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42                                   |
| 54 | <a href="#">c4tktA</a>  | Alignment | not modelled | 100.0 | 20<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase;<br><b>PDBTitle:</b> streptomyces platensis isomigrastatin ketosynthase                                                                     |

|    |                         |           |              |       |                                                                                                                                                                                                                                                                                                             |
|----|-------------------------|-----------|--------------|-------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |       | domain mgsf ks6                                                                                                                                                                                                                                                                                             |
| 55 | <a href="#">c5elpA_</a> | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nrps/pks protein;<br><b>PDBTitle:</b> ketosynthase from module 1 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42                                                                                              |
| 56 | <a href="#">c4na3A_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pksj;<br><b>PDBTitle:</b> crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic                                                       |
| 57 | <a href="#">c4qyrA_</a> | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> at-less polyketide synthase;<br><b>PDBTitle:</b> streptomyces platensis isomigrastatin ketosynthase domain mgse ks3                                                                                                           |
| 58 | <a href="#">c4z37A_</a> | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative mixed polyketide synthase/non-ribosomal peptide<br><b>PDBTitle:</b> structure of the ketosynthase of module 2 of c0zqg5 (trans-at pks)2 from brevibacillus brevis                                                    |
| 59 | <a href="#">c4mz0B_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> curl;<br><b>PDBTitle:</b> structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase                                                                                        |
| 60 | <a href="#">c5e5nD_</a> | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> polyketide synthase pksl;<br><b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)                                                                  |
| 61 | <a href="#">c6c9uA_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase/immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide-b synthase erya2, modules 3 and 4;<br><b>PDBTitle:</b> crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase in complex with antibody fragment (fab) |
| 62 | <a href="#">c3hhdC_</a> | Alignment | not modelled | 100.0 | 21<br><b>PDB header:</b> transferase, hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase;<br><b>PDBTitle:</b> structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.                                                                          |
| 63 | <a href="#">c2hg4A_</a> | Alignment | not modelled | 100.0 | 21<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide b synthase;<br><b>PDBTitle:</b> structure of the ketosynthase-acyltransferase didomain of module 52 from debs.                                                                                           |
| 64 | <a href="#">c5bp1A_</a> | Alignment | not modelled | 100.0 | 24<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mycocerosic acid synthase;<br><b>PDBTitle:</b> condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks                                                                                              |
| 65 | <a href="#">c3hmjB_</a> | Alignment | not modelled | 100.0 | 16<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase subunit alpha;<br><b>PDBTitle:</b> saccharomyces cerevisiae fas type i                                                                                                                                    |
| 66 | <a href="#">c4cw4A_</a> | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase;<br><b>PDBTitle:</b> crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa                                                                                                       |
| 67 | <a href="#">c2pffG_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> G: <b>PDB Molecule:</b> fatty acid synthase subunit alpha;<br><b>PDBTitle:</b> structural insights of yeast fatty acid synthase                                                                                                                       |
| 68 | <a href="#">c2pffA_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase subunit alpha;<br><b>PDBTitle:</b> structural insights of yeast fatty acid synthase                                                                                                                       |
| 69 | <a href="#">c2pffD_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> fatty acid synthase subunit alpha;<br><b>PDBTitle:</b> structural insights of yeast fatty acid synthase                                                                                                                       |
| 70 | <a href="#">c4ls5A_</a> | Alignment | not modelled | 100.0 | 20<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> crystal structure of beta-ketoacyl-acp synthase ii (fabf) from2 bacillus subtilis                                                                            |
| 71 | <a href="#">c2ix4B_</a> | Alignment | not modelled | 100.0 | 22<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase;<br><b>PDBTitle:</b> arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex                                                                           |
| 72 | <a href="#">c2gfvA_</a> | Alignment | not modelled | 100.0 | 23<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> structure of e. coli fabf (kasii) c163q mutant                                                                                                               |
| 73 | <a href="#">c1tqyC_</a> | Alignment | not modelled | 100.0 | 21<br><b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> actinorhodin polyketide putative beta-ketoacyl synthase 1;<br><b>PDBTitle:</b> the actinorhodin ketosynthase/chain length factor                                                                                              |
| 74 | <a href="#">c1oxhD_</a> | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> beta ketoacyl-acyl carrier protein synthase;<br><b>PDBTitle:</b> the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form                                     |
| 75 | <a href="#">c1e5mA_</a> | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> condensing enzyme<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta ketoacyl acyl carrier protein synthase ii;<br><b>PDBTitle:</b> beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp.                                                                      |
| 76 | <a href="#">c4qpfa_</a> | Alignment | not modelled | 100.0 | 19<br><b>PDB header:</b> ligase, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nrps/pks;<br><b>PDBTitle:</b> streptomyces albus ja3453 oxazolomycin ketosynthase domain ozmh ks8                                                                                                                     |
| 77 | <a href="#">c4b7vA_</a> | Alignment | not modelled | 100.0 | 20<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> structure of wild type pseudomonas aeruginosa fabf (kasii)                                                                                                   |
| 78 | <a href="#">c2iwyB_</a> | Alignment | not modelled | 100.0 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase;<br><b>PDBTitle:</b> human mitochondrial beta-ketoacyl acp synthase                                                                                                                 |

|     |                         |           |              |       |    |                                                                                                                                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------|-----------|--------------|-------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79  | <a href="#">c4ewgA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase;<br><b>PDBTitle:</b> crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815                                                                                                                                                                                                                      |
| 80  | <a href="#">c2uv8C</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha (fas2);<br><b>PDBTitle:</b> crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution                                                                                                                                                                        |
| 81  | <a href="#">c2gqdB</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> the crystal structure of b-ketoacyl-acp synthase ii (fabf) from2 staphylococcus aureus                                                                                                                                                                                           |
| 82  | <a href="#">c4jgaA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> x-ray crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase 22 from rickettsia rickettsii                                                                                                                                                                               |
| 83  | <a href="#">c2vkzC</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha;<br><b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex                                                                                                                                                                                                |
| 84  | <a href="#">c4ddoA</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase ii from2 burkholderia vietnamiensis                                                                                                                                                                               |
| 85  | <a href="#">c2gp6B</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> x-ray crystal structure of mycobacterium tuberculosis beta-ketoacyl2 acyl carrier protein synthase ii (mtkasb)                                                                                                                                                                   |
| 86  | <a href="#">c1j3nB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) synthase ii;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8                                                                                                                                                                                |
| 87  | <a href="#">c2uv9B</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase alpha subunits;<br><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 |
| 88  | <a href="#">c4qavB</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 2;<br><b>PDBTitle:</b> the structure of beta-ketoacyl -(acyl carrier protein) synthase ii2 (fabf) from neisseria meningitidis                                                                                                                                                                           |
| 89  | <a href="#">c3e60A</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein ] synthase ii;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-(acyl carrier protein) synthase ii from2 bartonella henselae                                                                                                                                                                                    |
| 90  | <a href="#">c3o04A</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-keto-acyl carrier protein synthase ii;<br><b>PDBTitle:</b> crystal structure of the beta-keto-acyl carrier protein synthase ii2 (lmo2201) from listeria monocytogenes                                                                                                                                                                        |
| 91  | <a href="#">c2wggA</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 1;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm                                                                                                                                                                                               |
| 92  | <a href="#">c2buiC</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> synthase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase i;<br><b>PDBTitle:</b> e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k                                                                                                                                                                                         |
| 93  | <a href="#">c1tqyD</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> actinorhodin polyketide putative beta-ketoacyl synthase 2;<br><b>PDBTitle:</b> the actinorhodin ketosynthase/chain length factor                                                                                                                                                                                                                  |
| 94  | <a href="#">c3lrfA</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase;<br><b>PDBTitle:</b> crystal structure of beta-ketoacyl synthase from brucella2 melitensis                                                                                                                                                                                                                                 |
| 95  | <a href="#">c6qspA</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase;<br><b>PDBTitle:</b> ketosynthase (apeo) in complex with its chain length factor (apec)2 from xenorhabdus doucetiae                                                                                                                                                                                               |
| 96  | <a href="#">d1ulqa2</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                                                                                                                                                                                                        |
| 97  | <a href="#">d1wdkc2</a> | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                                                                                                                                                                                                        |
| 98  | <a href="#">d1m3ka2</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                                                                                                                                                                                                        |
| 99  | <a href="#">c2ebdB</a>  | Alignment | not modelled | 99.9  | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5                                                                                                                                                                                    |
| 100 | <a href="#">d1afwa2</a> | Alignment | not modelled | 99.9  | 18 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Thiolase-related                                                                                                                                                                                                                                                                                                                        |
| 101 | <a href="#">c4ewpD</a>  | Alignment | not modelled | 99.9  | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> crystal structure of fabh from micrococcus luteus<br><b>PDB header:</b> transferase                                                                                                                                                                                              |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                   |
|-----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 102 | <a href="#">c1mzjB_</a> | Alignment | not modelled | 99.9 | 22 | <b>Chain:</b> B: <b>PDB Molecule:</b> beta-ketoacylsynthase iii;<br><b>PDBTitle:</b> crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway                                                                                                                           |
| 103 | <a href="#">c6a9nA_</a> | Alignment | not modelled | 99.9 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> crystal structure of kas iii from propionibacterium acnes                                                                                                                |
| 104 | <a href="#">c1zowB_</a> | Alignment | not modelled | 99.9 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase iii;<br><b>PDBTitle:</b> crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii                                                                                       |
| 105 | <a href="#">c2d3mA_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pentaketide chromone synthase;<br><b>PDBTitle:</b> pentaketide chromone synthase complexed with coenzyme a                                                                                                                                |
| 106 | <a href="#">c4x0oG_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> G: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 2;<br><b>PDBTitle:</b> beta-ketoacyl-(acyl carrier protein) synthase iii-2 (fabh2) from2 vibrio cholerae soaked with acetyl-coa                                                       |
| 107 | <a href="#">c2p0uB_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> stilbenecarboxylate synthase 2;<br><b>PDBTitle:</b> crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)                                                                                                    |
| 108 | <a href="#">c2qnxA_</a> | Alignment | not modelled | 99.9 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><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 |
| 109 | <a href="#">c3il3A_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> structure of haemophilus influenzae fabh                                                                                                                                 |
| 110 | <a href="#">c4dfeB_</a> | Alignment | not modelled | 99.9 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from burkholderia xenovorans                                                                         |
| 111 | <a href="#">c3gwaA_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) synthase iii;<br><b>PDBTitle:</b> 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii                                                                                       |
| 112 | <a href="#">c5bqsA_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> s. pneumoniae fabh with small molecule inhibitor 4                                                                                                 |
| 113 | <a href="#">c5ucoB_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2,4,6-trihydroxybenzophenone synthase;<br><b>PDBTitle:</b> benzophenone synthase from hypericum androsaemum                                                                                                                               |
| 114 | <a href="#">c3ov3A_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> curcumin synthase;<br><b>PDBTitle:</b> g211f mutant of curcumin synthase 1 from curcuma longa                                                                                                                                             |
| 115 | <a href="#">c5gk2A_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ketosynthase stld;<br><b>PDBTitle:</b> the structure of the h302a mutant of stld                                                                                                                                                          |
| 116 | <a href="#">c1ee0A_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-pyrone synthase;<br><b>PDBTitle:</b> 2-pyrone synthase complexed with acetoacetyl-coa                                                                                                                                                   |
| 117 | <a href="#">c2gyoB_</a> | Alignment | not modelled | 99.9 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> methanethiol-cys 112 inhibition complex of e. coli ketoacyl synthase2 iii (fabh) and coenzyme a                                                                          |
| 118 | <a href="#">c5dwzC_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3;<br><b>PDBTitle:</b> structural and functional characterization of pqsb, a condensing2 enzyme in the biosynthesis of the pseudomonas aeruginosa quinolone3 signal                             |
| 119 | <a href="#">c5yo9A_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-(acp)] synthase iii c terminal<br><b>PDBTitle:</b> crystal structure of kas iii from acinetobacter baumannii                                                                                                      |
| 120 | <a href="#">c3h76A_</a> | Alignment | not modelled | 99.9 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pqs biosynthetic enzyme;<br><b>PDBTitle:</b> crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway                                                                                     |