
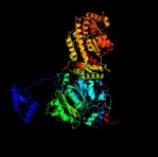

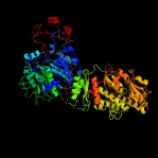















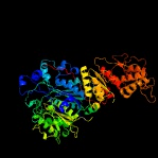




Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3800c_(pks13)_4256123_4261324 |
| Date | Fri Aug 9 18:20:51 BST 2019 |
| Unique Job ID | 2cac12c43b2f0d39 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c6fikA_ |  Alignment |  | 100.0 | 28 | PDB header: biosynthetic protein Chain: A; PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks |
| 2 | c2vz8A_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: A; PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase |
| 3 | c2vz8B_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase |
| 4 | c2qo3A_ |  Alignment |  | 100.0 | 38 | PDB header: transferase Chain: A; PDB Molecule: eryaii erythromycin polyketide synthase modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase |
| 5 | c6c9uA_ |  Alignment |  | 100.0 | 38 | PDB header: transferase/immune system Chain: A; PDB Molecule: 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase in complex with antibody fragment (fab) |
| 6 | c2hg4A_ |  Alignment |  | 100.0 | 39 | PDB header: transferase Chain: A; PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs. |
| 7 | c4mz0B_ |  Alignment |  | 100.0 | 36 | PDB header: transferase Chain: B; PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase |
| 8 | c3hhdC_ |  Alignment |  | 100.0 | 31 | PDB header: transferase, hydrolase Chain: C; PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design. |
| 9 | c5bp1A_ |  Alignment |  | 100.0 | 39 | PDB header: transferase Chain: A; PDB Molecule: mycocerosic acid synthase; PDBTitle: condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks |
| 10 | c4oqiA_ |  Alignment |  | 100.0 | 36 | PDB header: hydrolase Chain: A; PDB Molecule: pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1 |
| 11 | c4kc5D_ |  Alignment |  | 100.0 | 31 | PDB header: transferase Chain: D; PDB Molecule: rhie protein; PDBTitle: crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c4b3yB_ | Alignment | | 100.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase |
| 13 | c3hmjB_ | Alignment | | 100.0 | 17 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i |
| 14 | c4na3A_ | Alignment | | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic |
| 15 | c4z37A_ | Alignment | | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: putative mixed polyketide synthase/non-ribosomal peptide PDBTitle: structure of the ketosynthase of module 2 of c0zqg5 (trans-at pks)2 from brevibacillus brevis |
| 16 | c4wkyB_ | Alignment | | 100.0 | 40 | PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2 |
| 17 | c5erbB_ | Alignment | | 100.0 | 39 | PDB header: transferase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42 |
| 18 | c5e5nB_ | Alignment | | 100.0 | 36 | PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase pksl; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1) |
| 19 | c4tl2A_ | Alignment | | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: crystal structure of ketosynthase domain from mgsf from streptomycetes2 platensis |
| 20 | c4qyrA_ | Alignment | | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomycetes platensis isomigrastatin ketosynthase domain mgse ks3 |
| 21 | c4tktA_ | Alignment | not modelled | 100.0 | 39 | PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomycetes platensis isomigrastatin ketosynthase domain mgsf ks6 |
| 22 | c4opeD_ | Alignment | not modelled | 100.0 | 38 | PDB header: ligase, transferase Chain: D: PDB Molecule: nrps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7 |
| 23 | c5elpA_ | Alignment | not modelled | 100.0 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: nrps/pks protein; PDBTitle: ketosynthase from module 1 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42 |
| 24 | c5e5nD_ | Alignment | not modelled | 100.0 | 36 | PDB header: hydrolase Chain: D: PDB Molecule: polyketide synthase pksl; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1) |
| 25 | c2pffA_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 26 | c2pffG_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: G: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 27 | c2pffD_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 28 | c2vkzC_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex PDB header: transferase |

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|----|-------------------------|-----------|--------------|-------|-----|---|
| 29 | c2uv8C_ | Alignment | not modelled | 100.0 | 20 | Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution |
| 30 | c2uv9B_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase alpha subunits; PDBTitle: 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 | c4cw4A_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of the noncanonical ketosynthase faby2 from p. aeruginosa |
| 32 | c4qpFA_ | Alignment | not modelled | 100.0 | 41 | PDB header: ligase, transferase Chain: A: PDB Molecule: nmps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks8 |
| 33 | c2iwyB_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: human mitochondrial beta-ketoacyl acp synthase |
| 34 | c1tqyC_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: C: PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 1; PDBTitle: the actinorhodin ketosynthase/chain length factor |
| 35 | c4ls5A_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: crystal structure of beta-ketoacyl-acp synthase ii (fabf) from2 bacillus subtilis |
| 36 | c4b7vA_ | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of wild type pseudomonas aeruginosa fabf (kasii) |
| 37 | c4jgaA_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: x-ray crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase 22 from rickettsia rickettsii |
| 38 | c2gqdB_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: the crystal structure of b-ketoacyl-acp synthase ii (fabf) from2 staphylococcus aureus |
| 39 | c3tzzA_ | Alignment | not modelled | 100.0 | 100 | PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a |
| 40 | c4qavB_ | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: the structure of beta-ketoacyl -(acyl carrier protein) synthase ii2 (fabf) from neisseria meningitidis |
| 41 | c3o04A_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: beta-keto-acyl carrier protein synthase ii; PDBTitle: crystal structure of the beta-keto-acyl carrier protein synthase ii2 (lmo2201) from listeria monocytogenes |
| 42 | c4ddoA_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase ii from2 burkholderia vietnamiensis |
| 43 | c1e5mA_ | Alignment | not modelled | 100.0 | 29 | PDB header: condensing enzyme Chain: A: PDB Molecule: beta ketoacyl acyl carrier protein synthase ii; PDBTitle: beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp. |
| 44 | c1j3nB_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) synthase ii; PDBTitle: crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8 |
| 45 | c2ix4B_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex |
| 46 | c1oxhD_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: D: PDB Molecule: beta ketoacyl-acyl carrier protein synthase; PDBTitle: the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form |
| 47 | c3e60A_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase ii; PDBTitle: crystal structure of 3-oxoacyl-(acyl carrier protein) synthase ii from2 bartonella henselae |
| 48 | c2gfvA_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of e. coli fabf (kasii) c163q mutant |
| 49 | c2gp6B_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: x-ray crystal structure of mycobacterium tuberculosis beta-ketoacyl2 acyl carrier protein synthase ii (mtkasb) |
| 50 | c2wggA_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 1; PDBTitle: crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm |
| | | | | | | PDB header: transferase |

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|----|------------------------|-----------|--------------|-------|----|--|
| 51 | c6iytA | Alignment | not modelled | 100.0 | 27 | Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase |
| 52 | c4ewgA | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of a beta-ketoacyl synthase from burkholderia2 phymatum stm815 |
| 53 | c2buiC | Alignment | not modelled | 100.0 | 29 | PDB header: synthase Chain: C: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase i; PDBTitle: e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k |
| 54 | c3lrfA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of beta-ketoacyl synthase from brucella2 melitensis |
| 55 | c1tqyD | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: D: PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 2; PDBTitle: the actinorhodin ketosynthase/chain length factor |
| 56 | c6iyrA | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase |
| 57 | c6iyoA | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase |
| 58 | c6qspA | Alignment | not modelled | 100.0 | 25 | PDB header: biosynthetic protein Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: ketosynthase (apeo) in complex with its chain length factor (apec)2 from xenorhabdus doucetiae |
| 59 | c5ydmA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: pks; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl |
| 60 | c4qbuA | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa |
| 61 | c2jfkD | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa |
| 62 | c4ammA | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity |
| 63 | c4rl1A | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: type i polyketide synthase aves 1; PDBTitle: structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase |
| 64 | c3tqeA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii |
| 65 | c3ptwA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124 |
| 66 | c5ypvA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii |
| 67 | c3eenA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331 |
| 68 | c3rgiA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase |
| 69 | c3im8A | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae |
| 70 | c2cuyA | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-[acyl carrier protein] transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8 |
| 71 | c3qatB | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae |
| 72 | c3im9A | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus |
| 73 | c2g2oA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate |
| 74 | c2h1yA | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: malonyl coenzyme a-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori |
| | | | | | | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 75 | c4rr5A | Alignment | not modelled | 100.0 | 25 | transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase |
| 76 | c2cdh9 | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 77 | c4zxiA | Alignment | not modelled | 100.0 | 22 | PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine |
| 78 | c2qj3B | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd |
| 79 | c3ezoA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b |
| 80 | c3g87A | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease |
| 81 | c5dz6A | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks |
| 82 | c5dz7A | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase |
| 83 | c2c2nA | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase |
| 84 | c5czcA | Alignment | not modelled | 100.0 | 15 | PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink |
| 85 | c2vsqA | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module |
| 86 | d1tqya2 | Alignment | not modelled | 100.0 | 30 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 87 | d1tqyb2 | Alignment | not modelled | 100.0 | 30 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 88 | c5ja2A | Alignment | not modelled | 100.0 | 23 | PDB header: ligase Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412 |
| 89 | d1e5ma1 | Alignment | not modelled | 100.0 | 29 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 90 | d2ix4a1 | Alignment | not modelled | 100.0 | 26 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 91 | d1j3na1 | Alignment | not modelled | 100.0 | 27 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 92 | d2gfva1 | Alignment | not modelled | 100.0 | 27 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 93 | d1mlaa1 | Alignment | not modelled | 100.0 | 27 | Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like |
| 94 | d1nm2a1 | Alignment | not modelled | 100.0 | 24 | Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like |
| 95 | d1ox0a1 | Alignment | not modelled | 100.0 | 28 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 96 | c4egvC | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis |
| 97 | d2vbaa1 | Alignment | not modelled | 100.0 | 25 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 98 | c6n8eA | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa |
| 99 | c2roqA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: enterobactin synthetase component f; PDBTitle: solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f |
| 100 | d1j3na2 | Alignment | not modelled | 100.0 | 38 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 101 | d1e5ma2 | Alignment | not modelled | 100.0 | 29 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 102 | d2gfva2 | Alignment | not modelled | 100.0 | 32 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 103 | d2ix4a2 | Alignment | not modelled | 100.0 | 29 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 104 | d1ox0a2 | Alignment | not modelled | 100.0 | 28 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 105 | c2d3mA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a |
| 106 | d1tqyb1 | Alignment | not modelled | 100.0 | 22 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 107 | c6et9D_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase thiolase; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a |
| 108 | d1tqya1 | Alignment | not modelled | 100.0 | 26 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 109 | d2vbaa2 | Alignment | not modelled | 100.0 | 35 | Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related |
| 110 | c4ro5A_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: sat domain from cazm; PDBTitle: crystal structure of the sat domain from the non-reducing fungal2 polyketide synthase cazm |
| 111 | c6hspB_ | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: B: PDB Molecule: scp2-thiolase (type-1); PDBTitle: crystal structure of the zebrafish peroxisomal scp2-thiolase (type-1)2 in complex with coa and octanoyl-coa |
| 112 | d1jmkc_ | Alignment | not modelled | 100.0 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 113 | c4u4eA_ | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: thiolase; PDBTitle: crystal structure of putative thiolase from sphaerobacter thermophilus2 dsm 20745 |
| 114 | c2cbgA_ | Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster |
| 115 | c5ab6E_ | Alignment | not modelled | 100.0 | 15 | PDB header: transport protein Chain: E: PDB Molecule: scp2-thiolase like protein; PDBTitle: crystal structure of trypanosoma brucei scp2-thiolase like2 protein (tblsp) in complex with acetoacetyl-coa. |
| 116 | d2h7xa1 | Alignment | not modelled | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 117 | d1mo2a_ | Alignment | not modelled | 100.0 | 23 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 118 | c1mo2A_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5 |
| 119 | c2h7xA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label |
| 120 | c2p0uB_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: B: PDB Molecule: stilbenecarboxylate synthase 2; PDBTitle: crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2) |