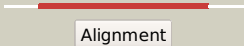

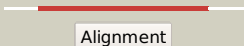
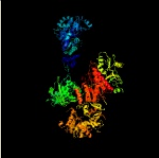
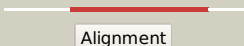

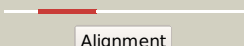
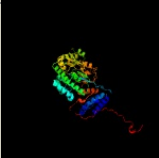
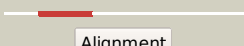


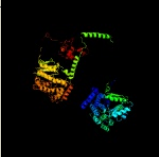
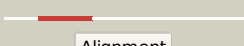


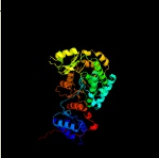



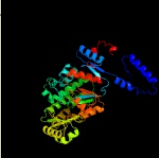

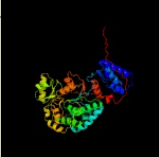

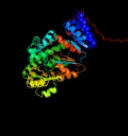

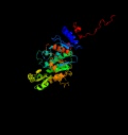



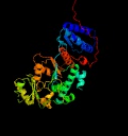



Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2946c_(pks1)_3291513_3296363 |
| Date | Thu Aug 8 16:20:10 BST 2019 |
| Unique Job ID | 3c3bfe4f49755623 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2vz8A_ |  Alignment |  | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase |
| 2 | c2vz8B_ |  Alignment |  | 100.0 | 26 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase |
| 3 | c6fn6A_ |  Alignment |  | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase 1, isoform a; PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas) |
| 4 | c6fikA_ |  Alignment |  | 100.0 | 22 | 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 |
| 5 | c3tzzA_ |  Alignment |  | 100.0 | 27 | 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 |
| 6 | c4b3yB_ |  Alignment |  | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase |
| 7 | c6iytA_ |  Alignment |  | 100.0 | 39 | PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase |
| 8 | 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 deoxyerthronolide b synthase |
| 9 | 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 deoxyerthronolide b synthase in complex with antibody fragment (fab) |
| 10 | c6iyoA_ |  Alignment |  | 100.0 | 51 | 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 |
| 11 | c5bp1A_ |  Alignment |  | 100.0 | 28 | 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 |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | c6iyrA_ | Alignment |  | 100.0 | 36 | 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 |
| 13 | 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. |
| 14 | c3slkB_ | Alignment |  | 100.0 | 49 | PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase |
| 15 | c3hhdC_ | Alignment |  | 100.0 | 24 | 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. |
| 16 | c4qbuA_ | Alignment |  | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa |
| 17 | c5ydmA_ | Alignment |  | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: pk5; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl |
| 18 | c2jfkD_ | Alignment |  | 100.0 | 24 | PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa |
| 19 | c4mz0B_ | Alignment |  | 100.0 | 39 | PDB header: transferase Chain: B: PDB Molecule: curl1; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase |
| 20 | c4ammA_ | Alignment |  | 100.0 | 32 | 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 |
| 21 | c4rl1A_ | Alignment | not modelled | 100.0 | 34 | 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 |
| 22 | c3tqeA_ | Alignment | not modelled | 100.0 | 29 | 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 |
| 23 | c3eenA_ | Alignment | not modelled | 100.0 | 33 | 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 |
| 24 | c3ptwA_ | Alignment | not modelled | 100.0 | 28 | 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 |
| 25 | c3rgiA_ | Alignment | not modelled | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase |
| 26 | c5ypvA_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii |
| 27 | c3im8A_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae |
| 28 | c3im9A_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 28 | c3im9A | Alignment | not modelled | 100.0 | 32 | transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus |
| 29 | c3qatB | Alignment | not modelled | 100.0 | 34 | 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 |
| 30 | c2g2oA | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate |
| 31 | c2cuyA | Alignment | not modelled | 100.0 | 37 | 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 |
| 32 | c2qj3B | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd |
| 33 | c4rr5A | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase |
| 34 | c3ezoA | Alignment | not modelled | 100.0 | 31 | 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 |
| 35 | c2h1yA | Alignment | not modelled | 100.0 | 28 | 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 |
| 36 | c2cdh9 | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 37 | c5dz7A | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase |
| 38 | c3g87A | Alignment | not modelled | 100.0 | 32 | 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 |
| 39 | c5dz6A | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks |
| 40 | c2c2nA | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase |
| 41 | c5czcA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink |
| 42 | c3mjsA | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: amphb; PDBTitle: structure of a-type ketoreductases from modular polyketide synthase |
| 43 | c4impB | Alignment | not modelled | 100.0 | 33 | PDB header: transferase Chain: B: PDB Molecule: polyketide synthase extender modules 3-4; PDBTitle: the missing linker: a dimerization motif located within polyketide2 synthase modules |
| 44 | c3qp9C | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: C: PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase |
| 45 | d1mlaa1 | Alignment | not modelled | 100.0 | 32 | Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like |
| 46 | d1nm2a1 | Alignment | not modelled | 100.0 | 40 | Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like |
| 47 | c2fr1A | Alignment | not modelled | 100.0 | 37 | PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2) |
| 48 | c4l4xA | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: an a2-type ketoreductase from a modular polyketide synthase |
| 49 | c4di7A | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: structure of a2-type ketoreductase of modular polyketide synthases |
| 50 | c2z5IA | Alignment | not modelled | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: tylactone synthase starter module and modules 1 & 2; PDBTitle: the first ketoreductase of the tylosin pks |
| 51 | c4kc5D | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: D: PDB Molecule: rhie protein; PDBTitle: crystal structure of the c-terminal part of rhie from burkholderia2 rhizoxinica |
| | | | | | | PDB header: oxidoreductase |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|---|
| 52 | c5d2eA_ | Alignment | not modelled | 100.0 | 19 | Chain: A: PDB Molecule: mine; PDBTitle: crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line |
| 53 | c4pivB_ | Alignment | not modelled | 100.0 | 25 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069 |
| 54 | c4hxyA_ | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: plm1; PDBTitle: plmkr1-ketoreductase from the first module of phoslactomycin2 biosynthesis in streptomyces sp. hk803 |
| 55 | c4j1sA_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line |
| 56 | c5ktkA_ | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: ketoreductase from module 3 of the bacillaene synthase from bacillus2 subtilis 168 |
| 57 | c2uv8C_ | Alignment | not modelled | 100.0 | 15 | PDB header: transferase 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 |
| 58 | c2uv9B_ | Alignment | not modelled | 100.0 | 16 | 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 |
| 59 | c2vkzC_ | Alignment | not modelled | 100.0 | 16 | 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 |
| 60 | c2pffA_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 61 | c2pffG_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: G: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 62 | c2pffD_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase |
| 63 | c3hmjB_ | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i |
| 64 | c4ro5A_ | Alignment | not modelled | 100.0 | 12 | 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 |
| 65 | c3s8mA_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-accp reductase; PDBTitle: the crystal structure of fabv |
| 66 | c4oqjA_ | Alignment | not modelled | 100.0 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1 |
| 67 | c4ggoA_ | Alignment | not modelled | 100.0 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola |
| 68 | c4ln9A_ | Alignment | not modelled | 100.0 | 47 | PDB header: lyase Chain: A: PDB Molecule: rifamycin polyketide synthase; PDBTitle: crystal structure of the dehydratase domain from the terminal module2 of the rifamycin polyketide synthase |
| 69 | c6obvB_ | Alignment | not modelled | 100.0 | 48 | PDB header: lyase Chain: B: PDB Molecule: fluvirucin b1 dh domain from module 1; PDBTitle: structural insights into dehydratase substrate selection for the2 borrelidin and fluvirucin polyketide synthases |
| 70 | c3el6A_ | Alignment | not modelled | 100.0 | 44 | PDB header: lyase Chain: A: PDB Molecule: erythromycin dehydratase; PDBTitle: crystal structure of the erythromycin dehydratase |
| 71 | c6obtA_ | Alignment | not modelled | 100.0 | 43 | PDB header: lyase Chain: A: PDB Molecule: borrelidin polyketide synthase, type i; PDBTitle: structural insights into dehydratase substrate selection for the2 borrelidin and fluvirucin polyketide synthases |
| 72 | c3kg9A_ | Alignment | not modelled | 100.0 | 24 | PDB header: lyase Chain: A: PDB Molecule: curk; PDBTitle: dehydratase domain from curk module of curacin polyketide synthase |
| 73 | c5o16B_ | Alignment | not modelled | 100.0 | 37 | PDB header: lyase Chain: B: PDB Molecule: ambc; PDBTitle: crystal structure of bifunctional dehydratase-cyclase domain in2 ambruticin biosynthesis |
| 74 | c3kg8A_ | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: A: PDB Molecule: curj; PDBTitle: dehydratase domain from curj module of curacin polyketide synthase |
| 75 | c3kg6C_ | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: C: PDB Molecule: curf; PDBTitle: dehydratase domain from curf module of curacin polyketide synthase |
| 76 | c3kg7C_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: C: PDB Molecule: curh; PDBTitle: dehydratase domain from curh module of curacin polyketide synthase |
| 77 | c6mbgA_ | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: A: PDB Molecule: gphf; PDBTitle: gphf dehydratase p1711l variant for improved |

| | | | | | | |
|-----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | crystallization |
| 78 | c5bp2A | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: A: PDB Molecule: mycocerosic acid synthase-like polyketide synthase; PDBTitle: dehydratase domain (dh) of a mycocerosic acid synthase-like (mas-like) ₂ pks, crystal form 1 |
| 79 | c5il6A | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: polyketide synthase/nonribosomal peptide synthetase hybrid PDBTitle: crystal structure of the dehydratase domain of rzxb from pseudomonas2 fluorescens |
| 80 | c4p7pA | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: A: PDB Molecule: phthiocerol synthesis polyketide synthase type i ppsc; PDBTitle: structure of the dehydratase domain of ppsc from mycobacterium2 tuberculosis in complex with crotonyl-coenzyme a |
| 81 | c5j6oA | Alignment | not modelled | 100.0 | 21 | PDB header: lyase Chain: A: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of a trans-at pks dehydratase domain of c0zgg7 from2 brevibacillus brevis |
| 82 | c5il5A | Alignment | not modelled | 100.0 | 18 | PDB header: lyase Chain: A: PDB Molecule: mlnd; PDBTitle: crystal structure of the dehydratase domain of mlnd from bacillus2 amyloliquefaciens |
| 83 | c5hstB | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: B: PDB Molecule: polyketide synthase type i; PDBTitle: crystal structure of the dehydratase domain of mlnb from bacillus2 amyloliquefaciens |
| 84 | c2vkzH | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i ₂ multienzyme complex |
| 85 | c2uvaI | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400 |
| 86 | c5kkuB | Alignment | not modelled | 100.0 | 14 | PDB header: lyase Chain: B: PDB Molecule: polyketide synthase type i; PDBTitle: crystal structure of an n-terminal dehydratase from diffidin2 assembly line |
| 87 | c5e1vB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase pksI; PDBTitle: crystal structure of a monomeric dehydratase domain from a trans at ₂ polyketide synthase split module |
| 88 | c6b2vA | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: sorb; PDBTitle: pyran synthase domain from module nine of the sorangicin pathway |
| 89 | c3hrqB | Alignment | not modelled | 100.0 | 15 | PDB header: biosynthetic protein Chain: B: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the product template domain from pksA with palmitate bound |
| 90 | c5hqwb | Alignment | not modelled | 100.0 | 24 | PDB header: lyase Chain: B: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of a trans-at pks dehydratase domain of c0zgg6 from2 brevibacillus brevis |
| 91 | c5hu7B | Alignment | not modelled | 100.0 | 18 | PDB header: lyase Chain: B: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of the trans-at pks dehydratase domain of c0zgg42 from brevibacillus brevis |
| 92 | c4u3vA | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: A: PDB Molecule: polyketide synthase pksr; PDBTitle: crystal structure of the trans-acyltransferase polyketide synthase ₂ enoyl-isomerase |
| 93 | c3llsB | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis |
| 94 | d2fr1a1 | Alignment | not modelled | 100.0 | 39 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 95 | c5xi0B | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabv, a new class of enyl-acyl carrier protein ₂ reductase from vibrio fischeri |
| 96 | c3krtC | Alignment | not modelled | 99.9 | 26 | PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2) |
| 97 | c2pffH | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase |
| 98 | c3m1IA | Alignment | not modelled | 99.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a c-terminal truncated mutant of a putative ₂ ketoacyl reductase (fabg4) from mycobacterium tuberculosis h37rv at3 2.5 angstrom resolution |
| 99 | c2pffE | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: E: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase |
| 100 | c2pffB | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase |
| 101 | c4wkvB | Alignment | not modelled | 99.9 | 58 | PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 101 | c4wkyB | Alignment | not modelled | 99.9 | 30 | PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2 PDB header: oxidoreductase |
| 102 | c2et6A | Alignment | not modelled | 99.9 | 23 | Chain: A; PDB Molecule: (3r)-hydroxyacyl-coa dehydrogenase; PDBTitle: (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2 |
| 103 | c4z37A | Alignment | not modelled | 99.9 | 26 | 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 |
| 104 | c5erbB | Alignment | not modelled | 99.8 | 23 | PDB header: transferase Chain: B; PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42 |
| 105 | c4qi2B | Alignment | not modelled | 99.8 | 21 | PDB header: oxidoreductase Chain: B; PDB Molecule: crotonyl-coa carboxylase/reductase; PDBTitle: crotonyl-coa carboxylase/reductase |
| 106 | c1zbgB | Alignment | not modelled | 99.8 | 19 | PDB header: oxidoreductase Chain: B; PDB Molecule: 17-beta-hydroxysteroid dehydrogenase 4; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad |
| 107 | d1zbqa1 | Alignment | not modelled | 99.8 | 19 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 108 | c4na3A | Alignment | not modelled | 99.8 | 20 | 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 |
| 109 | c4a10A | Alignment | not modelled | 99.8 | 27 | PDB header: oxidoreductase Chain: A; PDB Molecule: ooctenoyl-coa reductase/carboxylase; PDBTitle: apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomcyes sp. |
| 110 | c3ioyB | Alignment | not modelled | 99.8 | 24 | PDB header: oxidoreductase Chain: B; PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans |
| 111 | d1gz6a | Alignment | not modelled | 99.8 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 112 | c3omlA | Alignment | not modelled | 99.8 | 23 | PDB header: oxidoreductase, hydrolase Chain: A; PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster |
| 113 | c4wuvB | Alignment | not modelled | 99.8 | 19 | PDB header: oxidoreductase Chain: B; PDB Molecule: 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; PDBTitle: crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad |
| 114 | c6h0jA | Alignment | not modelled | 99.7 | 54 | PDB header: protein binding Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: a1-type acp domain from module 5 of mlsa1 |
| 115 | c4yacA | Alignment | not modelled | 99.7 | 22 | PDB header: oxidoreductase Chain: A; PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6 |
| 116 | c4tktA | Alignment | not modelled | 99.7 | 28 | PDB header: transferase Chain: A; PDB Molecule: at-less polyketide synthase; PDBTitle: streptomcyes platensis isomigrastatin ketosynthase domain mgf6 ks6 |
| 117 | c2ju2A | Alignment | not modelled | 99.7 | 46 | PDB header: transferase Chain: A; PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs) |
| 118 | c4tl2A | Alignment | not modelled | 99.7 | 24 | PDB header: transferase Chain: A; PDB Molecule: at-less polyketide synthase; PDBTitle: crystal structure of ketosynthase domain from mgf6 from streptomcyes2 platensis |
| 119 | d1xsea | Alignment | not modelled | 99.7 | 19 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 120 | c3uogB | Alignment | not modelled | 99.7 | 26 | PDB header: oxidoreductase Chain: B; PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021 |