# Phyre$^2$

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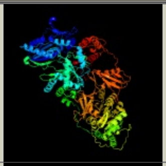
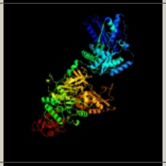
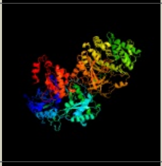
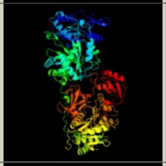
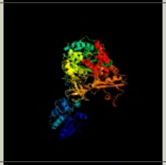
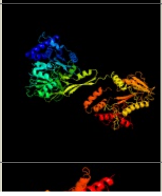
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2379c_(mbtF)_2657710_2662095 |
| Date | Mon Aug 5 13:25:53 BST 2019 |
| Unique Job ID | 50daf3b4802d489f |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2vsqA_ | Alignment |  | 100.0 | 27 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3;<br>**PDBTitle:** structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module |
| 2 | c6n8eA_ | Alignment |  | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**holo-obif1;<br>**PDBTitle:** crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa |
| 3 | c5ja2A_ | Alignment |  | 100.0 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**enterobactin synthase component f;<br>**PDBTitle:** entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412 |
| 4 | c4zxiA_ | Alignment |  | 100.0 | 22 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**tyrocidine synthetase 3;<br>**PDBTitle:** crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine |
| 5 | c4zxjA_ | Alignment |  | 100.0 | 26 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**enterobactin synthase component f;<br>**PDBTitle:** crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation |
| 6 | c5u89A_ | Alignment |  | 100.0 | 27 | **PDB header:**hydrolase/inhibitor<br>**Chain:** A: **PDB Molecule:**amino acid adenylation domain protein;<br>**PDBTitle:** crystal structure of a cross-module fragment from the dimodular nrps2 dhbf |
| 7 | c6p1jA_ | Alignment |  | 100.0 | 32 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**txo2;<br>**PDBTitle:** the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module |
| 8 | c6ozvA_ | Alignment |  | 100.0 | 31 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**txo1;<br>**PDBTitle:** the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp |
| 9 | c5es8A_ | Alignment |  | 100.0 | 28 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**linear gramicidin synthetase subunit a;<br>**PDBTitle:** crystal structure of the initiation module of lgra in the thiolation2 state |
| 10 | c6eqoB_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acetyl-coenzyme a synthetase;<br>**PDBTitle:** tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester |
| 11 | c5wmmA_ | Alignment |  | 100.0 | 26 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**nrps;<br>**PDBTitle:** crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios |
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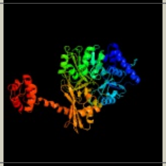
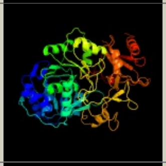
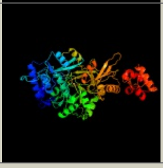
| 12 | c5mssA_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioester reductase domain-containing protein;<br>**PDBTitle:** structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp |
| 13 | c5ifiA_ | Alignment |  | 100.0 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**acetyl-coenzyme a synthetase;<br>**PDBTitle:** crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99 |
| 14 | c4dg9A_ | Alignment |  | 100.0 | 27 | **PDB header:**ligase/inhibitor<br>**Chain:** A: **PDB Molecule:**pa1221;<br>**PDBTitle:** structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor |
| 15 | d1pg4a_ | Alignment |  | 100.0 | 19 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 16 | c3rg2H_ | Alignment |  | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** H: **PDB Molecule:**enterobactin synthase component e (ente), 2,3-dihydro-2,3-<br>**PDBTitle:** structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis |
| 17 | c4wd1A_ | Alignment |  | 100.0 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**acetoacetate-coa ligase;<br>**PDBTitle:** acetoacetyl-coa synthetase from streptomyces lividans |
| 18 | c5gxdA_ | Alignment |  | 100.0 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase;<br>**PDBTitle:** structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12 |
| 19 | d1ry2a_ | Alignment |  | 100.0 | 22 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 20 | c4r0mA_ | Alignment |  | 100.0 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**mcyg protein;<br>**PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate |
| 21 | c5msdA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**carboxylic acid reductase;<br>**PDBTitle:** structure of the a domain of carboxylic acid reductase (car) from2 nocardia iowensis in complex with amp and benzoic acid |
| 22 | c3tsyA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**ligase, transferase<br>**Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol<br>**PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein |
| 23 | c5mstA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioester reductase domain-containing protein;<br>**PDBTitle:** structure of the a domain of carboxylic acid reductase (car) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid |
| 24 | c3e7wA_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1;<br>**PDBTitle:** crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains |
| 25 | c5x8gA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase;<br>**PDBTitle:** binary complex structure of a double mutant i454ra456k of o-2 succinylbenzoate coa synthetase (mene) from bacillus subtilis bound3 with its product analogue osb-ncoa at 1.90 angstrom |
| 26 | c3vnqA_ | Alignment | not modelled | 100.0 | 32 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**nrps adenylation protein cytc1;<br>**PDBTitle:** co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces |
| 27 | d1mdba_ | Alignment | not modelled | 100.0 | 24 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| | | | | | | **Fold:**Acetyl-CoA synthetase-like |

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| 28 | d3cw9a1 | Alignment | not modelled | 100.0 | 23 | **Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 29 | c4gr5B_ | Alignment | not modelled | 100.0 | 33 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase;<br>**PDBTitle:** crystal structure of slgn1deltaasub in complex with ampcpp |
| 30 | c4dg8A_ | Alignment | not modelled | 100.0 | 28 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pa1221;<br>**PDBTitle:** structure of pa1221, an nrps protein containing adenylation and pcp2 domains |
| 31 | c4wv3A_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase/ligase inhibitor<br>**Chain:** A: **PDB Molecule:**anthranilate-coa ligase;<br>**PDBTitle:** crystal structure of the anthranilate coa ligase auaeii in complex2 with anthranoyl-amp |
| 32 | c5ey8D_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**acyl-coa synthase;<br>**PDBTitle:** structure of fadd32 from mycobacterium smegmatis complexed to ampc20 |
| 33 | c5ie2A_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**oxalate--coa ligase;<br>**PDBTitle:** crystal structure of a plant enzyme |
| 34 | c5aplA_ | Alignment | not modelled | 100.0 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenylation domain;<br>**PDBTitle:** structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure |
| 35 | d1amua_ | Alignment | not modelled | 100.0 | 27 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 36 | c4eatB_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase;<br>**PDBTitle:** crystal structure of a benzoate coenzyme a ligase |
| 37 | c3etcB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**amp-binding protein;<br>**PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298 |
| 38 | c3iteB_ | Alignment | not modelled | 100.0 | 27 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**sidn siderophore synthetase;<br>**PDBTitle:** the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase |
| 39 | c3kxwA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b;<br>**PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila |
| 40 | c3gqwB_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**fatty acid amp ligase;<br>**PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound |
| 41 | c3ni2A_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**4-coumarate:coa ligase;<br>**PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase |
| 42 | c1amuB_ | Alignment | not modelled | 100.0 | 27 | **PDB header:**peptide synthetase<br>**Chain:** B: **PDB Molecule:**gramicidin synthetase 1;<br>**PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine |
| 43 | c5wm7A_ | Alignment | not modelled | 100.0 | 27 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**salicylate-amp ligase;<br>**PDBTitle:** crystal structure of cahj in complex with amp |
| 44 | c4d56A_ | Alignment | not modelled | 100.0 | 34 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**apnaa1;<br>**PDBTitle:** understanding bi-specificity of a-domains |
| 45 | c3r44A_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**fatty acyl coa synthetase fadd13 (fatty-acyl-coa<br>**PDBTitle:** mycobacterium tuberculosis fatty acyl coa synthetase |
| 46 | c6h1bA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**fatty acid coa ligase;<br>**PDBTitle:** structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans |
| 47 | c4oxiA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**enterobactin synthetase component f-related protein;<br>**PDBTitle:** crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycyl-adenosine-5'-phosphate |
| 48 | c5u2aA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase;<br>**PDBTitle:** crystal structure of brucella canis acyl-coa synthetase |
| 49 | c4r0mB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**mcyg protein;<br>**PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate |
| 50 | c3eynB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a;<br>**PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa |
| 51 | c5keiA_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**2,3-dihydroxybenzoate-amp ligase;<br>**PDBTitle:** mycobacterium smegmatis mbta apo structure |
| 52 | c2v7bB_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase;<br>**PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400 |
| 53 | c4ir7A_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**long chain fatty acid coa ligase fadd10;<br>**PDBTitle:** crystal structure of mtb fadd10 in complex with dodecanoyl-amp |

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| 54 | c5jjqB_ | Alignment | not modelled | 100.0 | 27 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**amp-dependent synthetase and ligase;<br>**PDBTitle:** crystal structure of idnl1 |
| 55 | c2d1tA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase;<br>**PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue |
| 56 | c6ijbA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**amp-binding domain protein;<br>**PDBTitle:** structure of 3-methylmercaptopropionate coa ligase mutant k523a in2 complex with amp and mmpa |
| 57 | c6ac3B_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**luminescent protein<br>**Chain:** B: **PDB Molecule:**red-bioluminescence eliciting luciferase;<br>**PDBTitle:** structure of a natural red emitting luciferase from phrixothrix hirtus2 (p3121 crystal form) |
| 58 | c5e7qB_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**acyl-coa synthetase;<br>**PDBTitle:** acyl-coa synthetase ptma2 from streptomyces platensis |
| 59 | c3l8cA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1;<br>**PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes |
| 60 | c5buqA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase;<br>**PDBTitle:** unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms |
| 61 | c3dhvA_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase;<br>**PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate |
| 62 | c4fuqD_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**malonyl coa synthetase;<br>**PDBTitle:** crystal structure of apo matb from rhodopseudomonas palustris |
| 63 | c2jgpA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**tyrocidine synthetase 3;<br>**PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc |
| 64 | c6akdA_ | Alignment | not modelled | 100.0 | 29 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase;<br>**PDBTitle:** crystal structure of idnl7 |
| 65 | c3iplB_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase;<br>**PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50 |
| 66 | d1v25a_ | Alignment | not modelled | 100.0 | 27 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 67 | c3nyrA_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**malonyl-coa ligase;<br>**PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound |
| 68 | c3g7sA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1);<br>**PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus |
| 69 | d1lcia_ | Alignment | not modelled | 100.0 | 18 | **Fold:**Acetyl-CoA synthetase-like<br>**Superfamily:**Acetyl-CoA synthetase-like<br>**Family:**Acetyl-CoA synthetase-like |
| 70 | c5c5hA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase;<br>**PDBTitle:** r195k e. coli mene with bound osb-ams |
| 71 | c5t81A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**epob;<br>**PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum |
| 72 | c4tx3B_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**peptide synthetase, module 7;<br>**PDBTitle:** complex of the x-domain and oxyb from teicoplanin biosynthesis |
| 73 | c5jjpB_ | Alignment | not modelled | 100.0 | 27 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**nonribosomal peptide synthase;<br>**PDBTitle:** crystal structure of cmis6 |
| 74 | c6cgoB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**condensation domain protein;<br>**PDBTitle:** molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase |
| 75 | c4jn3B_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**cda peptide synthetase i;<br>**PDBTitle:** crystal structures of the first condensation domain of the cda2 synthetase |
| 76 | c6ad3A_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**lovastatin nonaketide synthase moka;<br>**PDBTitle:** structural characterization of the condensation domain from monacolin2 k polyketide synthase moka |
| 77 | c5t3eA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**bacillamide synthetase heterocyclization domain;<br>**PDBTitle:** crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain. |
| 78 | c4znmB_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**c-domain type ii peptide synthetase;<br>**PDBTitle:** crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form) |
| 79 | c5n81B_ | Alignment | not modelled | 100.0 | 30 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**tyrocidine synthase 1; |

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| 79 | [illegible] | Alignment | not modelled | 100.0 | 30 | **PDBTitle:** crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog |
| 80 | c3o82B_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**peptide arylation enzyme;<br>**PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine |
| 81 | c4w8oA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**luciferase-like enzymeamp-coa-ligase;<br>**PDBTitle:** structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm |
| 82 | c4lgcA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**bile acid-coenzyme a ligase;<br>**PDBTitle:** crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution |
| 83 | c6m7lB_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**putative non-ribosomal peptide synthetase;<br>**PDBTitle:** complex of oxya with the x-domain from gpa biosynthesis |
| 84 | c2xhgA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**tyrocidine synthetase a;<br>**PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis |
| 85 | c3o82A_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**peptide arylation enzyme;<br>**PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine |
| 86 | c3wv4B_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase;<br>**PDBTitle:** crystal structure of vinn |
| 87 | c6aefB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**polyketide synthase associated protein papa2;<br>**PDBTitle:** papa2 acyl transferase |
| 88 | c5m6pB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**tyrocidine synthase 2;<br>**PDBTitle:** crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e) |
| 89 | c5burB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase;<br>**PDBTitle:** o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion |
| 90 | c1l5aA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**amide synthase;<br>**PDBTitle:** crystal structure of vibh, an nrps condensation enzyme |
| 91 | c3qyaA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**luciferase;<br>**PDBTitle:** crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase |
| 92 | c5dijA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**tqaa;<br>**PDBTitle:** the crystal structure of ct |
| 93 | c3ivrA_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase;<br>**PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009 |
| 94 | c5oe3C_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**anthranilate--coa ligase;<br>**PDBTitle:** crystal structure of the n-terminal domain of pqsa in complex with2 anthraniloyl-amp (crystal form 1) |
| 95 | c3e53A_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28;<br>**PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis |
| 96 | c3t5cA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**probable chain-fatty-acid-coa ligase fadd13;<br>**PDBTitle:** crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2 |
| 97 | c5jjpC_ | Alignment | not modelled | 100.0 | 28 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**nonribosomal peptide synthase;<br>**PDBTitle:** crystal structure of cmis6 |
| 98 | c4hvmC_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**biosynthetic protein<br>**Chain:** C: **PDB Molecule:**tlmii;<br>**PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii |
| 99 | c6abhG_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**luminescent protein<br>**Chain:** G: **PDB Molecule:**red-bioluminescence eliciting luciferase;<br>**PDBTitle:** structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form) |
| 100 | c4gs5A_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like<br>**PDBTitle:** the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053 |
| 101 | c2y4oA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase;<br>**PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate |
| 102 | c2y27B_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase;<br>**PDBTitle:** crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia |
| 103 | c3qovD_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase;<br>**PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution |

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| 104 | c3fotA_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**15-o-acetyltransferase;<br>**PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides |
| 105 | c1q9jA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5;<br>**PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis |
| 106 | c6chjB_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**diacylglycerol o-acyltransferase;<br>**PDBTitle:** wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8 |
| 107 | d1l5aa1 | Alignment | not modelled | 100.0 | 21 | **Fold:**CoA-dependent acyltransferases<br>**Superfamily:**CoA-dependent acyltransferases<br>**Family:**NRPS condensation domain (amide synthase) |
| 108 | c3hguB_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**ehpf;<br>**PDBTitle:** structure of phenazine antibiotic biosynthesis protein |
| 109 | d1l5aa2 | Alignment | not modelled | 100.0 | 14 | **Fold:**CoA-dependent acyltransferases<br>**Superfamily:**CoA-dependent acyltransferases<br>**Family:**NRPS condensation domain (amide synthase) |
| 110 | c6dd2A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable hydroxycinnamoyl transferase;<br>**PDBTitle:** crystal structure of selaginella moellendorffii hct |
| 111 | d1q9ja1 | Alignment | not modelled | 99.9 | 19 | **Fold:**CoA-dependent acyltransferases<br>**Superfamily:**CoA-dependent acyltransferases<br>**Family:**NRPS condensation domain (amide synthase) |
| 112 | c4g0bA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa shikimate/quinate<br>**PDBTitle:** structure of native hct from coffea canephora |
| 113 | d1q9ja2 | Alignment | not modelled | 99.8 | 10 | **Fold:**CoA-dependent acyltransferases<br>**Superfamily:**CoA-dependent acyltransferases<br>**Family:**NRPS condensation domain (amide synthase) |
| 114 | c2e1uA_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acyl transferase;<br>**PDBTitle:** crystal structure of dendranthema morifolium dmat |
| 115 | c2bghA_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**vinorine synthase;<br>**PDBTitle:** crystal structure of vinorine synthase |
| 116 | c5u3hA_ | Alignment | not modelled | 99.8 | 21 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**hmwp2 nonribosomal peptide synthetase;<br>**PDBTitle:** solution structure of apo pcp1 from yersiniabactin synthetase |
| 117 | c5msvB_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thioester reductase domain-containing protein;<br>**PDBTitle:** structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp |
| 118 | c2roqA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**enterobactin synthetase component f;<br>**PDBTitle:** solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f |
| 119 | c2xr7A_ | Alignment | not modelled | 99.6 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**malonyltransferase;<br>**PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa |
| 120 | c2cq8A_ | Alignment | not modelled | 99.6 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase;<br>**PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna |