

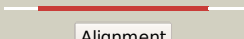

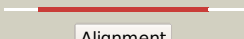




























# Phyre2

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|---------------|--------------------------------|
| Email         | mdejesus@rockefeller.edu       |
| Description   | RVBD0270_(fadD2)_324567_326249 |
| Date          | Tue Jul 23 14:50:33 BST 2019   |
| Unique Job ID | 1769338c7d68b5ca               |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c5es8A_</a> | Alignment    |    | 100.0      | 18     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a;<br><b>PDBTitle:</b> crystal structure of the initiation module of Igra in the thiolation2 state  |
| 2  | <a href="#">c6p1jA_</a> | Alignment    |    | 100.0      | 22     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> txo2;<br><b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module                  |
| 3  | <a href="#">c6eqoB_</a> | Alignment    |    | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase;<br><b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester |
| 4  | <a href="#">c5ja2A_</a> | Alignment    |    | 100.0      | 22     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f;<br><b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412                             |
| 5  | <a href="#">c2vsqA_</a> | Alignment  |  | 100.0      | 21     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3;<br><b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module                                    |
| 6  | <a href="#">d1pg4a_</a> | Alignment  |  | 100.0      | 19     | <b>Fold:</b> Acetyl-CoA synthetase-like<br><b>Superfamily:</b> Acetyl-CoA synthetase-like<br><b>Family:</b> Acetyl-CoA synthetase-like  |
| 7  | <a href="#">c5u89A_</a> | Alignment  |  | 100.0      | 23     | <b>PDB header:</b> hydrolase/inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein;<br><b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf   |
| 8  | <a href="#">c5gxdA_</a> | Alignment  |  | 100.0      | 22     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase;<br><b>PDBTitle:</b> structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl12   |
| 9  | <a href="#">c5ifiA_</a> | Alignment  |  | 100.0      | 23     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase;<br><b>PDBTitle:</b> crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99                 |
| 10 | <a href="#">c5wmmA_</a> | Alignment  |  | 100.0      | 21     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nrps;<br><b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios                     |
| 11 | <a href="#">d1ry2a_</a> | Alignment  |  | 100.0      | 22     | <b>Fold:</b> Acetyl-CoA synthetase-like<br><b>Superfamily:</b> Acetyl-CoA synthetase-like<br><b>Family:</b> Acetyl-CoA synthetase-like  |

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| 12 | <a href="#">c4wd1A_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> acetoacetate-coa ligase;<br><b>PDBTitle:</b> acetoacetyl-coa synthetase from streptomyces lividans   |
| 13 | <a href="#">c4zxiA_</a> | Alignment |    | 100.0 | 22 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> enterobactin synthase component f;<br><b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation   |
| 14 | <a href="#">c4zxiA_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase 3;<br><b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine  |
| 15 | <a href="#">c5msdA_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> carboxylic acid reductase;<br><b>PDBTitle:</b> structure of the a domain of carboxylic acid reductase (car) from2 nocardia iowensis in complex with amp and benzoic acid   |
| 16 | <a href="#">c3e7wA_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1;<br><b>PDBTitle:</b> crystal structure of delta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains                                  |
| 17 | <a href="#">d1mdba_</a> | Alignment |   | 100.0 | 22 | <b>Fold:</b> Acetyl-CoA synthetase-like<br><b>Superfamily:</b> Acetyl-CoA synthetase-like<br><b>Family:</b> Acetyl-CoA synthetase-like  |
| 18 | <a href="#">c4wv3A_</a> | Alignment |  | 100.0 | 23 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> A; <b>PDB Molecule:</b> anthranilate-coa ligase;<br><b>PDBTitle:</b> crystal structure of the anthranilate coa ligase auaeii in complex2 with anthranoyl-amp  |
| 19 | <a href="#">c4eatB_</a> | Alignment |  | 100.0 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> benzoate-coenzyme a ligase;<br><b>PDBTitle:</b> crystal structure of a benzoate coenzyme a ligase  |
| 20 | <a href="#">d3cw9a1</a> | Alignment |  | 100.0 | 26 | <b>Fold:</b> Acetyl-CoA synthetase-like<br><b>Superfamily:</b> Acetyl-CoA synthetase-like<br><b>Family:</b> Acetyl-CoA synthetase-like  |
| 21 | <a href="#">c5ie2A_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> oxalate--coa ligase;<br><b>PDBTitle:</b> crystal structure of a plant enzyme   |
| 22 | <a href="#">c3vngA_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> nrps adenylation protein cytc1;<br><b>PDBTitle:</b> co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces   |
| 23 | <a href="#">c5mssA_</a> | Alignment | not modelled  | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> thioester reductase domain-containing protein;<br><b>PDBTitle:</b> structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp   |
| 24 | <a href="#">c5x8gA_</a> | Alignment | not modelled  | 100.0 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase;<br><b>PDBTitle:</b> 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 |
| 25 | <a href="#">c5wm7A_</a> | Alignment | not modelled  | 100.0 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> salicylate-amp ligase;<br><b>PDBTitle:</b> crystal structure of cahj in complex with amp   |
| 26 | <a href="#">c5mstA_</a> | Alignment | not modelled  | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> thioester reductase domain-containing protein;<br><b>PDBTitle:</b> structure of the a domain of carboxylic acid reductase (car) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid                  |
| 27 | <a href="#">c3ni2A_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> 4-coumarate:coa ligase;<br><b>PDBTitle:</b> crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase<br><b>PDB header:</b> ligase   |

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| 28 | <a href="#">c3etcB_</a> | Alignment | not modelled | 100.0 | 20 | <b>Chain:</b> B; <b>PDB Molecule:</b> amp-binding protein;<br><b>PDBTitle:</b> 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298  |
| 29 | <a href="#">c5u2aA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> amp-dependent synthetase and ligase;<br><b>PDBTitle:</b> crystal structure of brucella canis acyl-coa synthetase   |
| 30 | <a href="#">c4oxiA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enterobactin synthetase component f-related protein;<br><b>PDBTitle:</b> crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycy-adenosine-5'-phosphate  |
| 31 | <a href="#">c6ijbA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> amp-binding domain protein;<br><b>PDBTitle:</b> structure of 3-methylmercaptopyruvate coa ligase mutant k523a in2 complex with amp and mmpa  |
| 32 | <a href="#">c6h1bA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> fatty acid coa ligase;<br><b>PDBTitle:</b> structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans  |
| 33 | <a href="#">d1amua_</a> | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> Acetyl-CoA synthetase-like<br><b>Superfamily:</b> Acetyl-CoA synthetase-like<br><b>Family:</b> Acetyl-CoA synthetase-like  |
| 34 | <a href="#">c3rg2H_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> H; <b>PDB Molecule:</b> enterobactin synthase component e (ente), 2,3-dihydro-2,3-<br><b>PDBTitle:</b> structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis |
| 35 | <a href="#">c3eynB_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> acyl-coenzyme a synthetase acsm2a;<br><b>PDBTitle:</b> crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa   |
| 36 | <a href="#">c5keiA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> 2,3-dihydroxybenzoate-amp ligase;<br><b>PDBTitle:</b> mycobacterium smegmatis mbta apo structure   |
| 37 | <a href="#">c3r44A_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> fatty acyl coa synthetase fadd13 (fatty-acyl-coa<br><b>PDBTitle:</b> mycobacterium tuberculosis fatty acyl coa synthetase  |
| 38 | <a href="#">c5aplA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> adenylation domain;<br><b>PDBTitle:</b> structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure  |
| 39 | <a href="#">c1amuB_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> peptide synthetase<br><b>Chain:</b> B; <b>PDB Molecule:</b> gramicidin synthetase 1;<br><b>PDBTitle:</b> phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine   |
| 40 | <a href="#">c4dg8A_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> pa1221;<br><b>PDBTitle:</b> structure of pa1221, an nrps protein containing adenylation and pcp2 domains   |
| 41 | <a href="#">c2d1tA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> luciferin 4-monooxygenase;<br><b>PDBTitle:</b> crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue                        |
| 42 | <a href="#">c3gqwB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> fatty acid amp ligase;<br><b>PDBTitle:</b> crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound   |
| 43 | <a href="#">c4fuqD_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> D; <b>PDB Molecule:</b> malonyl coa synthetase;<br><b>PDBTitle:</b> crystal structure of apo matb from rhodospseudomonas palustris   |
| 44 | <a href="#">c3tsyA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase, transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol<br><b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein  |
| 45 | <a href="#">c2v7bB_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> benzoate-coenzyme a ligase;<br><b>PDBTitle:</b> crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400  |
| 46 | <a href="#">c5e7qB_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B; <b>PDB Molecule:</b> acyl-coa synthetase;<br><b>PDBTitle:</b> acyl-coa synthetase ptma2 from streptomyces platensis  |
| 47 | <a href="#">c4ir7A_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> long chain fatty acid coa ligase fadd10;<br><b>PDBTitle:</b> crystal structure of mtb fadd10 in complex with dodecanoyl-amp   |
| 48 | <a href="#">c6ac3B_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase;<br><b>PDBTitle:</b> structure of a natural red emitting luciferase from phrixothrix hirtus2 (p3121 crystal form)  |
| 49 | <a href="#">c5ey8D_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> D; <b>PDB Molecule:</b> acyl-coa synthase;<br><b>PDBTitle:</b> structure of fadd32 from mycobacterium smegmatis complexed to ampc20  |
| 50 | <a href="#">c3iteB_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> sidn siderophore synthetase;<br><b>PDBTitle:</b> the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase   |
| 51 | <a href="#">c4d56A_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> apnaa1;<br><b>PDBTitle:</b> understanding bi-specificity of a-domains   |
| 52 | <a href="#">c4dg9A_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase/inhibitor<br><b>Chain:</b> A; <b>PDB Molecule:</b> pa1221;<br><b>PDBTitle:</b> structure of holo-pa1221, an nrps protein containing   |

|    |                         |           |              |       |   |
|----|-------------------------|-----------|--------------|-------|---|
|    |                         |           |              |       | adenylation and2 pcp domains bound to vinylsulfonamide inhibitor<br><b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saframycin mx1 synthetase b;<br><b>PDBTitle:</b> the crystal structure of fatty acid amp ligase from legionella2 pneumophila |
| 53 | <a href="#">c3kxwA_</a> | Alignment | not modelled | 100.0 | 22  |
| 54 | <a href="#">c3dhvA_</a> | Alignment | not modelled | 100.0 | 20  |
| 55 | <a href="#">d1lciA_</a> | Alignment | not modelled | 100.0 | 21  |
| 56 | <a href="#">c4r0mB_</a> | Alignment | not modelled | 100.0 | 21  |
| 57 | <a href="#">c5jjqB_</a> | Alignment | not modelled | 100.0 | 22  |
| 58 | <a href="#">c6akdA_</a> | Alignment | not modelled | 100.0 | 22  |
| 59 | <a href="#">c4r0mA_</a> | Alignment | not modelled | 100.0 | 21  |
| 60 | <a href="#">c3nyrA_</a> | Alignment | not modelled | 100.0 | 23  |
| 61 | <a href="#">c6ozvA_</a> | Alignment | not modelled | 100.0 | 23  |
| 62 | <a href="#">c5buqA_</a> | Alignment | not modelled | 100.0 | 27  |
| 63 | <a href="#">c3ip1B_</a> | Alignment | not modelled | 100.0 | 22  |
| 64 | <a href="#">d1v25a_</a> | Alignment | not modelled | 100.0 | 18  |
| 65 | <a href="#">c3l8cA_</a> | Alignment | not modelled | 100.0 | 20  |
| 66 | <a href="#">c3g7sA_</a> | Alignment | not modelled | 100.0 | 23  |
| 67 | <a href="#">c4gr5B_</a> | Alignment | not modelled | 100.0 | 20  |
| 68 | <a href="#">c5c5hA_</a> | Alignment | not modelled | 100.0 | 28  |
| 69 | <a href="#">c3o82B_</a> | Alignment | not modelled | 100.0 | 18  |
| 70 | <a href="#">c4w8oA_</a> | Alignment | not modelled | 100.0 | 22  |
| 71 | <a href="#">c3o82A_</a> | Alignment | not modelled | 100.0 | 18  |
| 72 | <a href="#">c3qyaA_</a> | Alignment | not modelled | 100.0 | 19  |
| 73 | <a href="#">c3ivrA_</a> | Alignment | not modelled | 100.0 | 25  |
| 74 | <a href="#">c5n81B_</a> | Alignment | not modelled | 100.0 | 17  |
| 75 | <a href="#">c4lqcA_</a> | Alignment | not modelled | 100.0 | 23  |
| 76 | <a href="#">c5jipB_</a> | Alignment | not modelled | 100.0 | 22  |
| 77 | <a href="#">c3wv4B_</a> | Alignment | not modelled | 100.0 | 24  |

|     |                         |           |              |       |    |  |
|-----|-------------------------|-----------|--------------|-------|----|--|
| 78  | <a href="#">c5oe3C</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> anthranilate--coa ligase;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of pqsa in complex with2 anthraniloyl-amp (crystal form 1)   |
| 79  | <a href="#">c3t5cA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable chain-fatty-acid-coa ligase fadd13;<br><b>PDBTitle:</b> crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2   |
| 80  | <a href="#">c5burB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase;<br><b>PDBTitle:</b> o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion  |
| 81  | <a href="#">c5jipC</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nonribosomal peptide synthase;<br><b>PDBTitle:</b> crystal structure of cmis6   |
| 82  | <a href="#">c6abhG</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase;<br><b>PDBTitle:</b> structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)  |
| 83  | <a href="#">c3e53A</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty-acid-coa ligase fadd28;<br><b>PDBTitle:</b> crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis   |
| 84  | <a href="#">c2y4oA</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase;<br><b>PDBTitle:</b> crystal structure of paak2 in complex with phenylacetyl adenylate  |
| 85  | <a href="#">c4gs5A</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like<br><b>PDBTitle:</b> the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053                   |
| 86  | <a href="#">c2y27B</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase;<br><b>PDBTitle:</b> crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia  |
| 87  | <a href="#">c3qovD</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase;<br><b>PDBTitle:</b> crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution   |
| 88  | <a href="#">c3hguB</a>  | Alignment | not modelled | 99.8  | 17 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ehpf;<br><b>PDBTitle:</b> structure of phenazine antibiotic biosynthesis protein  |
| 89  | <a href="#">c3laxA</a>  | Alignment | not modelled | 99.6  | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase;<br><b>PDBTitle:</b> the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482  |
| 90  | <a href="#">c5kodA</a>  | Alignment | not modelled | 98.8  | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5;<br><b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana   |
| 91  | <a href="#">c4ep1A</a>  | Alignment | not modelled | 98.3  | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> jasmonic acid-amido synthetase jar1;<br><b>PDBTitle:</b> crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile  |
| 92  | <a href="#">c4b2gB</a>  | Alignment | not modelled | 98.3  | 14 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme;<br><b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis   |
| 93  | <a href="#">c6avhA</a>  | Alignment | not modelled | 97.8  | 14 | <b>PDB header:</b> ligase, plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase;<br><b>PDBTitle:</b> gh3.15 acyl acid amido synthetase   |
| 94  | <a href="#">c4ewvB</a>  | Alignment | not modelled | 97.1  | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4-substituted benzoates-glutamate ligase gh3.12;<br><b>PDBTitle:</b> crystal structure of gh3.12 in complex with ampcpp   |
| 95  | <a href="#">c3smaD</a>  | Alignment | not modelled | 68.3  | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> frbf;<br><b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf   |
| 96  | <a href="#">d2ayia1</a> | Alignment | not modelled | 67.6  | 14 | <b>Fold:</b> Thermophilic metalloprotease-like<br><b>Superfamily:</b> Thermophilic metalloprotease-like<br><b>Family:</b> Thermophilic metalloprotease (M29)   |
| 97  | <a href="#">c5u18A</a>  | Alignment | not modelled | 63.8  | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-3" methyltransferase;<br><b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin   |
| 98  | <a href="#">d2nyga1</a> | Alignment | not modelled | 61.0  | 20 | <b>Fold:</b> TTHA0583/YokD-like<br><b>Superfamily:</b> TTHA0583/YokD-like<br><b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like  |
| 99  | <a href="#">c6bc3A</a>  | Alignment | not modelled | 59.9  | 23 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein;<br><b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via   |
| 100 | <a href="#">c3e4fB</a>  | Alignment | not modelled | 55.0  | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase;<br><b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis   |
| 101 | <a href="#">c5ht0B</a>  | Alignment | not modelled | 54.4  | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005;<br><b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a |
|     |                         |           |              |       |    | <b>PDB header:</b> transferase   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 102 | <a href="#">c6mb6A_</a> | Alignment | not modelled | 54.4 | 25 | <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein;<br><b>PDBTitle:</b> aac-iiib binary with coash  |
| 103 | <a href="#">d1z7wa1</a> | Alignment | not modelled | 52.4 | 19 | <b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes  |
| 104 | <a href="#">d1piwa2</a> | Alignment | not modelled | 49.7 | 13 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain  |
| 105 | <a href="#">c3u5rG_</a> | Alignment | not modelled | 48.1 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a hypothetical protein smc02350 from2 sinorhizobium meliloti 1021  |
| 106 | <a href="#">c6mn5A_</a> | Alignment | not modelled | 46.9 | 23 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva;<br><b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a                            |
| 107 | <a href="#">d1e3ja2</a> | Alignment | not modelled | 45.2 | 15 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain  |
| 108 | <a href="#">c4k2bA_</a> | Alignment | not modelled | 44.9 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda;<br><b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine  |
| 109 | <a href="#">d1ilga2</a> | Alignment | not modelled | 40.5 | 14 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Dimeric alpha+beta barrel<br><b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain  |
| 110 | <a href="#">c4z1oB_</a> | Alignment | not modelled | 40.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyltransferase;<br><b>PDBTitle:</b> hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium |
| 111 | <a href="#">c2ywiA_</a> | Alignment | not modelled | 39.4 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein;<br><b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus  |
| 112 | <a href="#">d1kola2</a> | Alignment | not modelled | 38.1 | 17 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain  |
| 113 | <a href="#">c6dt0D_</a> | Alignment | not modelled | 36.4 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial calcium uniporter;<br><b>PDBTitle:</b> cryo-em structure of a mitochondrial calcium uniporter  |
| 114 | <a href="#">d1udxa3</a> | Alignment | not modelled | 36.1 | 37 | <b>Fold:</b> Obg GTP-binding protein C-terminal domain<br><b>Superfamily:</b> Obg GTP-binding protein C-terminal domain<br><b>Family:</b> Obg GTP-binding protein C-terminal domain  |
| 115 | <a href="#">c5f1yA_</a> | Alignment | not modelled | 31.8 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mccc family protein;<br><b>PDBTitle:</b> crystal structure of ba3275, the member of s66 family of serine2 peptidases   |
| 116 | <a href="#">d1pl8a2</a> | Alignment | not modelled | 31.0 | 19 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain  |
| 117 | <a href="#">c5vogA_</a> | Alignment | not modelled | 30.6 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoribosyltransferase;<br><b>PDBTitle:</b> crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pppp  |
| 118 | <a href="#">c3ippA_</a> | Alignment | not modelled | 30.5 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynje;<br><b>PDBTitle:</b> crystal structure of sulfur-free ynje   |
| 119 | <a href="#">c4lmaA_</a> | Alignment | not modelled | 28.4 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase;<br><b>PDBTitle:</b> crystal structure analysis of o-acetylserine sulphydrylase cysk1 from2 microcystis aeruginosa 7806  |
| 120 | <a href="#">c2zy3A_</a> | Alignment | not modelled | 28.4 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase;<br><b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase   |