

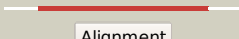

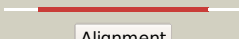




















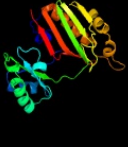



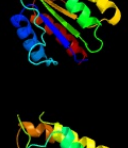
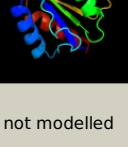


# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD0951_(sucC)_1061968_1063131 |
| Date          | Fri Jul 26 01:50:54 BST 2019    |
| Unique Job ID | c952ffc6639ed991                |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c6meIB_</a> | <br>Alignment   |    | 100.0      | 40     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> succinate--coa ligase [adp-forming] subunit beta;<br><b>PDBTitle:</b> succinyl-coa synthase from campylobacter jejuni   |
| 2  | <a href="#">c2nu9E_</a> | <br>Alignment   |    | 100.0      | 42     | <b>PDB header:</b> ligase<br><b>Chain:</b> E; <b>PDB Molecule:</b> succinyl-coa synthetase beta chain;<br><b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form                           |
| 3  | <a href="#">c1eucB_</a> | <br>Alignment   |    | 100.0      | 40     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> succinyl-coa synthetase, beta chain;<br><b>PDBTitle:</b> crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase              |
| 4  | <a href="#">c6g4qB_</a> | <br>Alignment   |    | 100.0      | 37     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> succinate--coa ligase [adp-forming] subunit beta,<br><b>PDBTitle:</b> structure of human adp-forming succinyl-coa ligase complex suclg1-2 sucla2              |
| 5  | <a href="#">c6hxxB_</a> | <br>Alignment |  | 100.0      | 30     | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> citryl-coa synthetase large subunit;<br><b>PDBTitle:</b> structure of citryl-coa synthetase from hydrogenobacter thermophilus                                  |
| 6  | <a href="#">c6mggD_</a> | <br>Alignment |  | 100.0      | 39     | <b>PDB header:</b> ligase<br><b>Chain:</b> D; <b>PDB Molecule:</b> succinate--coa ligase [adp-forming] subunit beta;<br><b>PDBTitle:</b> succinyl-coa synthase from francisella tularensis, phosphorylated, in2 complex with coa |
| 7  | <a href="#">c3ufxG_</a> | <br>Alignment |  | 100.0      | 51     | <b>PDB header:</b> ligase<br><b>Chain:</b> G; <b>PDB Molecule:</b> succinyl-coa synthetase beta subunit;<br><b>PDBTitle:</b> thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+                                  |
| 8  | <a href="#">c3mwdA_</a> | <br>Alignment |  | 100.0      | 25     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> atp-citrate synthase;<br><b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound   |
| 9  | <a href="#">c6hxiC_</a> | <br>Alignment |  | 100.0      | 23     | <b>PDB header:</b> lyase<br><b>Chain:</b> C; <b>PDB Molecule:</b> citrate lyase, subunit 1;<br><b>PDBTitle:</b> structure of atp citrate lyase from methanotherix soehngenii in complex2 with citrate and coenzyme a             |
| 10 | <a href="#">c6qfbB_</a> | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> atp-citrate synthase;<br><b>PDBTitle:</b> structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp                  |
| 11 | <a href="#">c6hxiA_</a> | <br>Alignment |  | 100.0      | 23     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> atp-citrate lyase beta-subunit;<br><b>PDBTitle:</b> structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.           |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">d1eucb2</a> | Alignment |     | 100.0 | 38 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> Succinyl-CoA synthetase, beta-chain, N-terminal domain   |
| 13 | <a href="#">d2nu7b2</a> | Alignment |    | 100.0 | 40 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> Succinyl-CoA synthetase, beta-chain, N-terminal domain   |
| 14 | <a href="#">c6no2B_</a> | Alignment |    | 100.0 | 36 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> succinate--coa ligase [adp-forming] subunit beta;<br><b>PDBTitle:</b> adp bound to k114bd mutant atp-grasp fold of blastocystis hominis2 succinyl-coa synthetase   |
| 15 | <a href="#">c1wr2A_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1789;<br><b>PDBTitle:</b> crystal structure of ph1788 from pyrococcus horikoshii ot3   |
| 16 | <a href="#">d2nu7b1</a> | Alignment |    | 100.0 | 44 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Succinyl-CoA synthetase domains<br><b>Family:</b> Succinyl-CoA synthetase domains   |
| 17 | <a href="#">c4yakD_</a> | Alignment |   | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> beta subunit of acyl-coa synthetase (ndp forming);<br><b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 in complex with coenzyme a, acetyl-coenzyme a and with3 phosphorylated phosphohistidine segment (site i orientation) |
| 18 | <a href="#">d1eucb1</a> | Alignment |  | 100.0 | 43 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Succinyl-CoA synthetase domains<br><b>Family:</b> Succinyl-CoA synthetase domains   |
| 19 | <a href="#">c4yajA_</a> | Alignment |  | 99.8  | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase<br><b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)  |
| 20 | <a href="#">d2csua3</a> | Alignment |  | 99.8  | 20 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Succinyl-CoA synthetase domains<br><b>Family:</b> Succinyl-CoA synthetase domains   |
| 21 | <a href="#">c2csuB_</a> | Alignment | not modelled  | 99.7  | 22 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein;<br><b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3   |
| 22 | <a href="#">c1m6vE_</a> | Alignment | not modelled  | 99.5  | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain;<br><b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase   |
| 23 | <a href="#">d1a9xa5</a> | Alignment | not modelled  | 99.4  | 19 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like   |
| 24 | <a href="#">c3bg5C_</a> | Alignment | not modelled  | 99.4  | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase  |
| 25 | <a href="#">c1w96B_</a> | Alignment | not modelled  | 99.4  | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase;<br><b>PDBTitle:</b> crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with sorafen a  |
| 26 | <a href="#">c1ulzA_</a> | Alignment | not modelled  | 99.3  | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain;<br><b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase   |
| 27 | <a href="#">c1vkzA_</a> | Alignment | not modelled  | 99.3  | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution  |
| 28 | <a href="#">c3q8cB_</a> | Alignment | not modelled  | 99.3  | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> biotin carboxylase;<br><b>PDBTitle:</b> crystal structure of biotin carboxylase in complex with  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | biotin,2 bicarbonate, adp and mg ion   |
| 29 | <a href="#">c2hjwA_</a> | Alignment | not modelled | 99.3 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2;<br><b>PDBTitle:</b> crystal structure of the bc domain of acc2  |
| 30 | <a href="#">c2xd4A_</a> | Alignment | not modelled | 99.3 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase;<br><b>PDBTitle:</b> nucleotide-bound structures of bacillus subtilis<br>glycinamide2 ribonucleotide synthetase                     |
| 31 | <a href="#">c2yyaB_</a> | Alignment | not modelled | 99.3 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase;<br><b>PDBTitle:</b> crystal structure of gar synthetase from aquifex aeolicus  |
| 32 | <a href="#">c3lp8A_</a> | Alignment | not modelled | 99.3 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine-glycine ligase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase<br>from2 ehrlichia chaffeensis                          |
| 33 | <a href="#">c3tw6B_</a> | Alignment | not modelled | 99.3 | 20 | <b>PDB header:</b> ligase/activator<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase protein;<br><b>PDBTitle:</b> structure of rhizobium etli pyruvate carboxylase t882a<br>with the2 allosteric activator, acetyl coenzyme-a |
| 34 | <a href="#">c3ouzA_</a> | Alignment | not modelled | 99.3 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase;<br><b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from<br>campylobacter2 jejuni   |
| 35 | <a href="#">c2dzb_</a>  | Alignment | not modelled | 99.3 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of the biotin carboxylase domain of<br>pyruvate2 carboxylase  |
| 36 | <a href="#">d1w96a3</a> | Alignment | not modelled | 99.2 | 21 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 37 | <a href="#">c5cskB_</a> | Alignment | not modelled | 99.2 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase;<br><b>PDBTitle:</b> crystal structure of yeast acetyl-coa carboxylase,<br>unbiotinylated  |
| 38 | <a href="#">c2ip4A_</a> | Alignment | not modelled | 99.2 | 31 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase;<br><b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide synthetase<br>from2 thermus thermophilus hb8                   |
| 39 | <a href="#">c3vmmA_</a> | Alignment | not modelled | 99.2 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alanine-anticapsin ligase bacd;<br><b>PDBTitle:</b> crystal structure of bacd, an l-amino acid dipeptide ligase<br>from2 bacillus subtilis                              |
| 40 | <a href="#">d1ulza3</a> | Alignment | not modelled | 99.2 | 23 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 41 | <a href="#">c5douC_</a> | Alignment | not modelled | 99.2 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase<br>[ammonia], mitochondrial;<br><b>PDBTitle:</b> crystal structure of human carbamoyl phosphate<br>synthetase i (cps1),2 ligand-bound form |
| 42 | <a href="#">c6g2dC_</a> | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase 1;<br><b>PDBTitle:</b> citrate-induced acetyl-coa carboxylase (acc-cit) filament<br>at 5.4 a2 resolution   |
| 43 | <a href="#">d1a9xa6</a> | Alignment | not modelled | 99.1 | 22 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 44 | <a href="#">d1vkza3</a> | Alignment | not modelled | 99.1 | 16 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 45 | <a href="#">c4wd3B_</a> | Alignment | not modelled | 99.1 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid ligase;<br><b>PDBTitle:</b> crystal structure of an l-amino acid ligase riza   |
| 46 | <a href="#">c2vpqA_</a> | Alignment | not modelled | 99.1 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase;<br><b>PDBTitle:</b> crystal structure of biotin carboxylase from s. aureus2<br>complexed with amppnp  |
| 47 | <a href="#">c1ehiB_</a> | Alignment | not modelled | 99.1 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine:d-lactate ligase;<br><b>PDBTitle:</b> d-alanine:d-lactate ligase (lmdl2) of vancomycin-<br>resistant2 leuconostoc mesenteroides                               |
| 48 | <a href="#">c3gidB_</a> | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase 2;<br><b>PDBTitle:</b> the biotin carboxylase (bc) domain of human acetyl-coa<br>carboxylase 22 (acc2) in complex with sorafen a                 |
| 49 | <a href="#">c5vz0D_</a> | Alignment | not modelled | 99.1 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of lactococcus lactis pyruvate<br>carboxylase g746a2 mutant in complex with cyclic-di-amp                   |
| 50 | <a href="#">d2j9ga3</a> | Alignment | not modelled | 99.1 | 20 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 51 | <a href="#">c2ys6A_</a> | Alignment | not modelled | 99.1 | 28 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase;<br><b>PDBTitle:</b> crystal structure of gar synthetase from geobacillus<br>kaustophilus  |
| 52 | <a href="#">c3ln7A_</a> | Alignment | not modelled | 99.1 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional<br>protein gshab;<br><b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase<br>from2 pasteurella multocida   |
| 53 | <a href="#">c3n6rK_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit;<br><b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa<br>carboxylase (pcc)                                 |
| 54 | <a href="#">c3wvqA_</a> | Alianment | not modelled | 99.0 | 17 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> pgm1;   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | <b>PDBTitle:</b> structure of atp grasp protein  |
| 55 | <a href="#">c2cqyA_</a> | Alignment | not modelled | 99.0 | 30 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> propionyl-coa carboxylase alpha chain,<br><b>PDBTitle:</b> solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit   |
| 56 | <a href="#">c4qslE_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase  |
| 57 | <a href="#">c3ln6A_</a> | Alignment | not modelled | 99.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab;<br><b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae  |
| 58 | <a href="#">c1kja_</a>  | Alignment | not modelled | 99.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2;<br><b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s  |
| 59 | <a href="#">c3i12A_</a> | Alignment | not modelled | 99.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a;<br><b>PDBTitle:</b> the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2   |
| 60 | <a href="#">c3dmvA_</a> | Alignment | not modelled | 99.0 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra;<br><b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli  |
| 61 | <a href="#">c2pvpB_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori   |
| 62 | <a href="#">c5mlkA_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase;<br><b>PDBTitle:</b> biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)  |
| 63 | <a href="#">d1iowa2</a> | Alignment | not modelled | 98.9 | 19 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> ATP-binding domain of peptide synthetases   |
| 64 | <a href="#">c3u9sE_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> E: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit;<br><b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex  |
| 65 | <a href="#">c2dlnA_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> ligase(peptidoglycan synthesis)<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution   |
| 66 | <a href="#">c4mamB_</a> | Alignment | not modelled | 98.9 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp |
| 67 | <a href="#">c3u9sA_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit;<br><b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex  |
| 68 | <a href="#">c5cslA_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase;<br><b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer  |
| 69 | <a href="#">c3lwbA_</a> | Alignment | not modelled | 98.9 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis   |
| 70 | <a href="#">d1ehia2</a> | Alignment | not modelled | 98.8 | 17 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> ATP-binding domain of peptide synthetases   |
| 71 | <a href="#">c2i80B_</a> | Alignment | not modelled | 98.8 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase;<br><b>PDBTitle:</b> allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies   |
| 72 | <a href="#">c2qk4A_</a> | Alignment | not modelled | 98.8 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trifunctional purine biosynthetic protein adenosine-3;<br><b>PDBTitle:</b> human glycinamide ribonucleotide synthetase  |
| 73 | <a href="#">c2gpwC_</a> | Alignment | not modelled | 98.8 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> biotin carboxylase;<br><b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.  |
| 74 | <a href="#">c4fu0B_</a> | Alignment | not modelled | 98.8 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase 7;<br><b>PDBTitle:</b> crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis   |
| 75 | <a href="#">c3hblA_</a> | Alignment | not modelled | 98.8 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of s. aureus pyruvate carboxylase t908a mutant  |
| 76 | <a href="#">d3etja3</a> | Alignment | not modelled | 98.8 | 15 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like  |
| 77 | <a href="#">c6dgiA_</a> | Alignment | not modelled | 98.8 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> the crystal structure of d-alanyl-alanine synthetase a from vibrio2 cholerae o1 biovar eltor str. n16961   |
| 78 | <a href="#">c3e5nA_</a> | Alignment | not modelled | 98.8 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a;<br><b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from2   |

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|     |                         |           |              |      |    | xanthomonas oryzae pv. oryzae kacc10331   |
| 79  | <a href="#">c1gsoA_</a> | Alignment | not modelled | 98.7 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (glycinamide ribonucleotide synthetase);<br><b>PDBTitle:</b> glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.  |
| 80  | <a href="#">c2zdaA_</a> | Alignment | not modelled | 98.7 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8   |
| 81  | <a href="#">c3qtqB_</a> | Alignment | not modelled | 98.7 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> structure of the d-alanine-d-alanine ligase from coxiella burnetii  |
| 82  | <a href="#">c1e4eB_</a> | Alignment | not modelled | 98.7 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> vancomycin/teicoplanin a-type resistance protein vana;<br><b>PDBTitle:</b> d-alanyl-d-lacate ligase  |
| 83  | <a href="#">d1e4ea2</a> | Alignment | not modelled | 98.7 | 17 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> ATP-binding domain of peptide synthetases  |
| 84  | <a href="#">c4dimA_</a> | Alignment | not modelled | 98.7 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii  |
| 85  | <a href="#">c3q2oB_</a> | Alignment | not modelled | 98.7 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase  |
| 86  | <a href="#">c2dwcB_</a> | Alignment | not modelled | 98.7 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4333aa long hypothetical phosphoribosylglycinamide formyl<br><b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp |
| 87  | <a href="#">c3orgA_</a> | Alignment | not modelled | 98.6 | 17 | <b>PDB header:</b> ligase,biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase;<br><b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp             |
| 88  | <a href="#">d2r7ka2</a> | Alignment | not modelled | 98.6 | 15 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> PurP ATP-binding domain-like   |
| 89  | <a href="#">d1kja3</a>  | Alignment | not modelled | 98.6 | 17 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like   |
| 90  | <a href="#">d2r85a2</a> | Alignment | not modelled | 98.6 | 20 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> PurP ATP-binding domain-like   |
| 91  | <a href="#">c5vevB_</a> | Alignment | not modelled | 98.6 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae   |
| 92  | <a href="#">c3se7A_</a> | Alignment | not modelled | 98.5 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> vana;<br><b>PDBTitle:</b> ancient vana   |
| 93  | <a href="#">d1oi7a2</a> | Alignment | not modelled | 98.5 | 25 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Succinyl-CoA synthetase domains<br><b>Family:</b> Succinyl-CoA synthetase domains   |
| 94  | <a href="#">d1gsoa3</a> | Alignment | not modelled | 98.5 | 28 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> BC ATP-binding domain-like   |
| 95  | <a href="#">c5dotA_</a> | Alignment | not modelled | 98.5 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial;<br><b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form   |
| 96  | <a href="#">c5i47A_</a> | Alignment | not modelled | 98.5 | 18 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> rimk domain protein atp-grasp;<br><b>PDBTitle:</b> crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745   |
| 97  | <a href="#">c5ig8A_</a> | Alignment | not modelled | 98.5 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp grasp ligase;<br><b>PDBTitle:</b> crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc   |
| 98  | <a href="#">c5ig9H_</a> | Alignment | not modelled | 98.4 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> H: <b>PDB Molecule:</b> atp grasp ligase;<br><b>PDBTitle:</b> crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc  |
| 99  | <a href="#">c3etjB_</a> | Alignment | not modelled | 98.4 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase<br><b>PDBTitle:</b> crystal structure e. coli purk in complex with mg, adp, and2 pi   |
| 100 | <a href="#">c5k2mG_</a> | Alignment | not modelled | 98.4 | 13 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> rimk-related lysine biosynthesis protein;<br><b>PDBTitle:</b> bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa  |
| 101 | <a href="#">c6hxiD_</a> | Alignment | not modelled | 98.4 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase (adp-forming) subunit alpha;<br><b>PDBTitle:</b> structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a   |
| 102 | <a href="#">c6hxiB_</a> | Alignment | not modelled | 98.4 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit;<br><b>PDBTitle:</b> structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.   |



|     |                         |           |              |      |    |   |
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| 103 | <a href="#">c1i7nA_</a> | Alignment | not modelled | 98.4 | 13 | <b>PDB header:</b> neuropeptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> synapsin ii;<br><b>PDBTitle:</b> crystal structure analysis of the c domain of synapsin ii2 from rat brain   |
| 104 | <a href="#">c3aw8A_</a> | Alignment | not modelled | 98.3 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8                     |
| 105 | <a href="#">d1uc8a2</a> | Alignment | not modelled | 98.3 | 13 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like<br><b>Family:</b> Lysine biosynthesis enzyme LysX ATP-binding domain   |
| 106 | <a href="#">c3vpbC_</a> | Alignment | not modelled | 98.3 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative acetylornithine deacetylase;<br><b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate   |
| 107 | <a href="#">d1euca2</a> | Alignment | not modelled | 98.3 | 23 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Succinyl-CoA synthetase domains<br><b>Family:</b> Succinyl-CoA synthetase domains   |
| 108 | <a href="#">c5dmxC_</a> | Alignment | not modelled | 98.3 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121  |
| 109 | <a href="#">c4qslC_</a> | Alignment | not modelled | 98.3 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase   |
| 110 | <a href="#">c3votB_</a> | Alignment | not modelled | 98.2 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid ligase, bl00235;<br><b>PDBTitle:</b> crystal structure of l-amino acid ligase from bacillus licheniformis   |
| 111 | <a href="#">c3r23B_</a> | Alignment | not modelled | 98.2 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis   |
| 112 | <a href="#">c4egqD_</a> | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei   |
| 113 | <a href="#">c3k5iB_</a> | Alignment | not modelled | 98.2 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole carboxylase;<br><b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide |
| 114 | <a href="#">c3k3pA_</a> | Alignment | not modelled | 98.2 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase;<br><b>PDBTitle:</b> crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans  |
| 115 | <a href="#">c1oi7A_</a> | Alignment | not modelled | 98.1 | 25 | <b>PDB header:</b> synthetase<br><b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain;<br><b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus   |
| 116 | <a href="#">c2r85B_</a> | Alignment | not modelled | 98.1 | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> purp protein pf1517;<br><b>PDBTitle:</b> crystal structure of purp from pyrococcus furiosus complexed with amp   |
| 117 | <a href="#">c3ax6C_</a> | Alignment | not modelled | 98.1 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima                          |
| 118 | <a href="#">c1z2pX_</a> | Alignment | not modelled | 98.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> X: <b>PDB Molecule:</b> inositol 1,3,4-trisphosphate 5/6-kinase;<br><b>PDBTitle:</b> inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3  |
| 119 | <a href="#">c4iwyA_</a> | Alignment | not modelled | 98.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein s6 modification protein;<br><b>PDBTitle:</b> semet-substituted rimk structure  |
| 120 | <a href="#">c3uvzB_</a> | Alignment | not modelled | 98.0 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria                  |