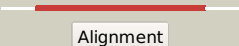



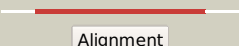





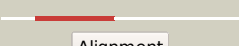













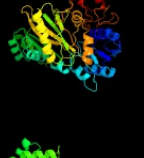
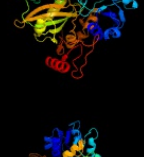




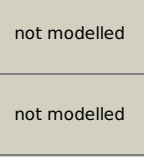


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1384_(carB)_1557107_1560454 |
| Date | Wed Jul 31 22:05:49 BST 2019 |
| Unique Job ID | 8c433e0a620fa500 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c5douC_ |  Alignment |  | 100.0 | 39 | PDB header: ligase Chain: C; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form |
| 2 | c1m6vE_ |  Alignment |  | 100.0 | 54 | PDB header: ligase Chain: E; PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase |
| 3 | c5dotA_ |  Alignment |  | 100.0 | 39 | PDB header: ligase Chain: A; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form |
| 4 | c5vz0D_ |  Alignment |  | 100.0 | 20 | PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp |
| 5 | c3u9sE_ |  Alignment |  | 100.0 | 17 | PDB header: ligase Chain: E; PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex |
| 6 | c5cskB_ |  Alignment |  | 100.0 | 18 | PDB header: ligase Chain: B; PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated |
| 7 | c6g2dC_ |  Alignment |  | 100.0 | 18 | PDB header: ligase Chain: C; PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution |
| 8 | c3tw6B_ |  Alignment |  | 100.0 | 19 | PDB header: ligase/activator Chain: B; PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a |
| 9 | c3bg5C_ |  Alignment |  | 100.0 | 21 | PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase |
| 10 | c4qslE_ |  Alignment |  | 100.0 | 21 | PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase |
| 11 | c1w96B_ |  Alignment |  | 100.0 | 16 | PDB header: ligase Chain: B; PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a |

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|----|--------------------------|-----------|---|-------|----|---|
| 12 | c4qslC_ | Alignment |  | 100.0 | 21 | PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase |
| 13 | c3hblA_ | Alignment |  | 100.0 | 21 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant |
| 14 | c5cslA_ | Alignment |  | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer |
| 15 | c2hjlwA_ | Alignment |  | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2 |
| 16 | c3g8cB_ | Alignment |  | 100.0 | 21 | PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion |
| 17 | c2vpqA_ | Alignment |  | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp |
| 18 | c3n6rK_ | Alignment |  | 100.0 | 20 | PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) |
| 19 | c3u9sA_ | Alignment |  | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex |
| 20 | c1ulzA_ | Alignment |  | 100.0 | 22 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase |
| 21 | c3ouza_ | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni |
| 22 | c5mlkA_ | Alignment | not modelled | 100.0 | 21 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285) |
| 23 | c2dzdB_ | Alignment | not modelled | 100.0 | 21 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase |
| 24 | c2gpwC_ | Alignment | not modelled | 100.0 | 21 | PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli. |
| 25 | c3gidB_ | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with sorafen a |
| 26 | c3u9sl_ | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: I: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex |
| 27 | c5ks8B_ | Alignment | not modelled | 100.0 | 21 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus |
| 28 | d1a9xa5 | Alignment | not modelled | 100.0 | 64 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c4rcnA | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase |
| 30 | c5h80A | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase |
| 31 | c3jzfA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series |
| 32 | c5mlkB | Alignment | not modelled | 100.0 | 21 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285) |
| 33 | c1kijA | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s |
| 34 | c3va7A | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase |
| 35 | c4qskB | Alignment | not modelled | 100.0 | 23 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp |
| 36 | c2qf7A | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli |
| 37 | c5i8iD | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase |
| 38 | c2xd4A | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase |
| 39 | c3lp8A | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis |
| 40 | c2qk4A | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase |
| 41 | d1a9xa6 | Alignment | not modelled | 100.0 | 53 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 42 | c4hmvB | Alignment | not modelled | 100.0 | 22 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase |
| 43 | c2ip4A | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8 |
| 44 | c3bg5B | Alignment | not modelled | 100.0 | 23 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase |
| 45 | c2yyaB | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus |
| 46 | c1vkzA | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution |
| 47 | c2ys6A | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus |
| 48 | c3q2oB | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase |
| 49 | d1a9xa1 | Alignment | not modelled | 100.0 | 39 | Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain |
| 50 | c3orgA | Alignment | not modelled | 100.0 | 15 | PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp |
| 51 | c3ax6C | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima |
| 52 | c1gsoA | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli. PDB header: transferase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 53 | c2dwcB | Alignment | not modelled | 100.0 | 18 | Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp |
| 54 | c3vmmA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis |
| 55 | c4mamB | Alignment | not modelled | 100.0 | 15 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp |
| 56 | c4dimA | Alignment | not modelled | 100.0 | 15 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii |
| 57 | c4ffnA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp |
| 58 | c3uvzB | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria |
| 59 | c4wd3B | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza |
| 60 | c2r85B | Alignment | not modelled | 100.0 | 18 | PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp |
| 61 | c3k5iB | Alignment | not modelled | 100.0 | 15 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide |
| 62 | c3aw8A | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8 |
| 63 | c3etjB | Alignment | not modelled | 100.0 | 12 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi |
| 64 | c1ehiB | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides |
| 65 | c5vevB | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae |
| 66 | c4fu0B | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis |
| 67 | c3votB | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase, bl00235; PDBTitle: crystal structure of l-amino acid ligase from bacillus licheniformis |
| 68 | c3i12A | Alignment | not modelled | 100.0 | 17 | PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 69 | d1w96a3 | Alignment | not modelled | 100.0 | 15 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 70 | c3lwbA | Alignment | not modelled | 100.0 | 22 | PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis |
| 71 | c2i80B | Alignment | not modelled | 100.0 | 15 | PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies |
| 72 | c2dlnA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution |
| 73 | c1e4eB | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase |
| 74 | c6dgiA | Alignment | not modelled | 100.0 | 14 | PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: the crystal structure of d-alanyl-alanine synthetase a from vibrio2 cholerae o1 biovar eltor str. n16961 |
| 75 | c2z04A | Alignment | not modelled | 100.0 | 17 | PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus |
| 76 | c3e5nA | Alignment | not modelled | 100.0 | 10 | PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 76 | c3e31A | Alignment | not modelled | 100.0 | 19 | PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331 PDB header: ligase |
| 77 | c3r23B | Alignment | not modelled | 100.0 | 19 | Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis |
| 78 | c2pvpB | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori |
| 79 | c5dmxC | Alignment | not modelled | 100.0 | 25 | PDB header: ligase Chain: C: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121 |
| 80 | c4egqD | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei |
| 81 | c3se7A | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana |
| 82 | c2zdqA | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8 |
| 83 | c3k3pA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans |
| 84 | d1a9xa3 | Alignment | not modelled | 100.0 | 61 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |
| 85 | c2pn1A | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution |
| 86 | c3tqtB | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii |
| 87 | c2yvqA | Alignment | not modelled | 100.0 | 26 | PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens |
| 88 | c4egjD | Alignment | not modelled | 100.0 | 25 | PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans |
| 89 | d1a9xa2 | Alignment | not modelled | 100.0 | 31 | Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain |
| 90 | d2j9ga3 | Alignment | not modelled | 100.0 | 22 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 91 | c4iwyA | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure |
| 92 | d1a9xa4 | Alignment | not modelled | 100.0 | 70 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |
| 93 | d1ulza3 | Alignment | not modelled | 100.0 | 24 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 94 | c5ig9H | Alignment | not modelled | 100.0 | 14 | PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc |
| 95 | c3wvqA | Alignment | not modelled | 100.0 | 16 | PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein |
| 96 | d1vkza3 | Alignment | not modelled | 100.0 | 17 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 97 | c5i47A | Alignment | not modelled | 100.0 | 23 | PDB header: biosynthetic protein Chain: A: PDB Molecule: rimk domain protein atp-grasp; PDBTitle: crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745 |
| 98 | d1kjqz3 | Alignment | not modelled | 100.0 | 19 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 99 | c3df7A | Alignment | not modelled | 100.0 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative atp-grasp superfamily protein; PDBTitle: crystal structure of a putative atp-grasp superfamily protein from2 archaeoglobus fulgidus |
| 100 | d2r7ka2 | Alignment | not modelled | 100.0 | 22 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like |
| 101 | c3vpbC | Alignment | not modelled | 100.0 | 16 | PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate |
| 102 | c5k2mC | Alignment | not modelled | 100.0 | 18 | PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 102 | c3k2mg | Alignment | not modelled | 100.0 | 10 | PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa PDB header: ligase |
| 103 | c5ig8A | Alignment | not modelled | 100.0 | 11 | Chain: A; PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc |
| 104 | d3etja3 | Alignment | not modelled | 100.0 | 12 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 105 | c1uc8B | Alignment | not modelled | 100.0 | 24 | PDB header: biosynthetic protein Chain: B; PDB Molecule: lysine biosynthesis enzyme; PDBTitle: crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8 |
| 106 | d1ehia2 | Alignment | not modelled | 100.0 | 17 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 107 | d2r85a2 | Alignment | not modelled | 99.9 | 17 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like |
| 108 | d1iowa2 | Alignment | not modelled | 99.9 | 19 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 109 | d1e4ea2 | Alignment | not modelled | 99.9 | 19 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 110 | c1i7nA | Alignment | not modelled | 99.9 | 14 | PDB header: neuropeptide Chain: A; PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain |
| 111 | d1gsoa3 | Alignment | not modelled | 99.9 | 17 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 112 | c2p0aA | Alignment | not modelled | 99.9 | 15 | PDB header: neuropeptide Chain: A; PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp |
| 113 | c1pk8D | Alignment | not modelled | 99.9 | 13 | PDB header: membrane protein Chain: D; PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp |
| 114 | c3ln6A | Alignment | not modelled | 99.9 | 20 | PDB header: ligase Chain: A; PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae |
| 115 | d1uc8a2 | Alignment | not modelled | 99.9 | 21 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain |
| 116 | c1z2pX | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: X; PDB Molecule: inositol 1,3,4-trisphosphate 5/6-kinase; PDBTitle: inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3 |
| 117 | c3ln7A | Alignment | not modelled | 99.9 | 22 | PDB header: ligase Chain: A; PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida |
| 118 | d1wo8a1 | Alignment | not modelled | 99.9 | 19 | Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA |
| 119 | c6f2cK | Alignment | not modelled | 99.9 | 16 | PDB header: lyase Chain: K; PDB Molecule: methylglyoxal synthase; PDBTitle: methylglyoxal synthase mgsa from bacillus subtilis |
| 120 | d1pk8a2 | Alignment | not modelled | 99.9 | 11 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain |