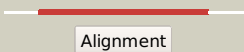

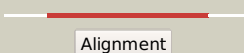

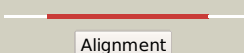

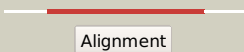

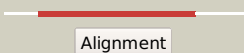

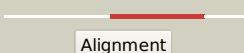

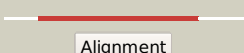





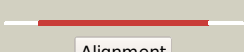

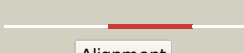












Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2411c_(-)_2708320_2709975 |
| Date | Wed Aug 7 12:50:03 BST 2019 |
| Unique Job ID | acb8399189061750 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3n6xA_ |  Alignment |  | 100.0 | 51 | PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution |
| 2 | c2ioaA_ |  Alignment |  | 99.7 | 18 | PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine PDBTitle: e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor |
| 3 | c2vpmB_ |  Alignment |  | 99.5 | 14 | PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase |
| 4 | d2io8a3 |  Alignment |  | 98.6 | 22 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Glutathionylspermidine synthase ATP-binding domain-like |
| 5 | c1m0tB_ |  Alignment |  | 98.3 | 14 | PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase; PDBTitle: yeast glutathione synthase |
| 6 | c1gshA_ |  Alignment |  | 98.1 | 17 | PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5 |
| 7 | c5oesD_ |  Alignment |  | 97.9 | 16 | PDB header: plant protein Chain: D: PDB Molecule: glutathione synthetase; PDBTitle: the structure of a glutathione synthetase (stgss1) from solanum2 tuberosum in adp and y-ec bound closed conformation. |
| 8 | c5oetB_ |  Alignment |  | 97.8 | 13 | PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase-like effector 30 (gpa-gss30-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss30) from2 globodera pallida in apoform. |
| 9 | c2hgsA_ |  Alignment |  | 97.7 | 15 | PDB header: amine/carboxylate ligase Chain: A: PDB Molecule: protein (glutathione synthetase); PDBTitle: human glutathione synthetase |
| 10 | c3kalB_ |  Alignment |  | 97.7 | 14 | PDB header: ligase Chain: B: PDB Molecule: homoglutathione synthetase; PDBTitle: structure of homoglutathione synthetase from glycine max in2 closed conformation with homoglutathione, adp, a sulfate3 ion, and three magnesium ions bound |
| 11 | c4iwyA_ |  Alignment |  | 96.8 | 16 | PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c2wyoC | Alignment |  | 96.8 | 17 | PDB header: ligase Chain: C: PDB Molecule: glutathione synthetase; PDBTitle: trypanosoma brucei glutathione synthetase |
| 13 | c1i7nA | Alignment |  | 96.7 | 14 | PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain |
| 14 | c1kjiA | Alignment |  | 96.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s |
| 15 | c3lp8A | Alignment |  | 96.6 | 16 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis |
| 16 | c3kakB | Alignment |  | 96.5 | 15 | PDB header: ligase Chain: B: PDB Molecule: homogluthione synthetase; PDBTitle: structure of homogluthione synthetase from glycine max in2 open conformation with gamma-glutamyl-cysteine bound. |
| 17 | c5i47A | Alignment |  | 96.5 | 17 | 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 |
| 18 | c2p0aA | Alignment |  | 96.4 | 14 | PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp |
| 19 | c5oevD | Alignment |  | 96.0 | 14 | PDB header: transferase Chain: D: PDB Molecule: glutathione synthetase-like effector 22 (gpa-gss22-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform. |
| 20 | c2xd4A | Alignment |  | 95.9 | 18 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase |
| 21 | c3ln7A | Alignment | not modelled | 95.9 | 9 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida |
| 22 | d1gsaa2 | Alignment | not modelled | 95.6 | 23 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 23 | c3tinA | Alignment | not modelled | 95.2 | 24 | PDB header: ligase Chain: A: PDB Molecule: ttl protein; PDBTitle: tubulin tyrosine ligase |
| 24 | c2yyaB | Alignment | not modelled | 95.1 | 14 | PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus |
| 25 | c1vkzA | Alignment | not modelled | 95.1 | 18 | 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 |
| 26 | c1pk8D | Alignment | not modelled | 95.1 | 15 | PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp |
| 27 | c2ip4A | Alignment | not modelled | 94.7 | 14 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8 |
| 28 | c3ln6A | Alignment | not modelled | 94.4 | 17 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase |

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|----|--------------------------|-----------|--------------|------|----|--|
| | | | | | | from2 streptococcus agalactiae |
| 29 | c4y1rA_ | Alignment | not modelled | 94.2 | 19 | PDB header: ligase Chain: A: PDB Molecule: tubulin polyglutamylase ttl17; PDBTitle: tubulin glutamylase |
| 30 | c1ehiB_ | Alignment | not modelled | 93.6 | 14 | PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides |
| 31 | c4wd3B_ | Alignment | not modelled | 92.9 | 13 | PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza |
| 32 | c3qtqB_ | Alignment | not modelled | 92.5 | 17 | PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii |
| 33 | c5oevB_ | Alignment | not modelled | 92.4 | 12 | PDB header: transferase Chain: B: PDB Molecule: glutathione synthetase-like effector 22 (gpa-gss22-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform. |
| 34 | c3i12A_ | Alignment | not modelled | 91.8 | 11 | 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 |
| 35 | c3wvqA_ | Alignment | not modelled | 91.5 | 15 | PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein |
| 36 | c3qg8cB_ | Alignment | not modelled | 91.3 | 16 | 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 |
| 37 | c3ouzA_ | Alignment | not modelled | 91.0 | 10 | PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni |
| 38 | d1e4ea2 | Alignment | not modelled | 90.8 | 13 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 39 | c4mamB_ | Alignment | not modelled | 90.7 | 16 | 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 |
| 40 | d1i7na2 | Alignment | not modelled | 90.6 | 20 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain |
| 41 | d1a9xa5 | Alignment | not modelled | 90.5 | 13 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 42 | c2dzdB_ | Alignment | not modelled | 89.2 | 13 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase |
| 43 | c4fu0B_ | Alignment | not modelled | 89.2 | 17 | 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 |
| 44 | d1ehia2 | Alignment | not modelled | 89.1 | 12 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 45 | c6dgiA_ | Alignment | not modelled | 89.0 | 9 | 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 |
| 46 | d1pk8a2 | Alignment | not modelled | 88.9 | 20 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain |
| 47 | c4ijjF_ | Alignment | not modelled | 88.7 | 22 | PDB header: cell cycle Chain: F: PDB Molecule: tubulin tyrosine ligase, ttl; PDBTitle: crystal structure of tubulin-stathmin-ttl-apo complex |
| 48 | c1uc8B_ | Alignment | not modelled | 88.2 | 16 | 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 |
| 49 | c3vmmA_ | Alignment | not modelled | 87.7 | 16 | 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 |
| 50 | c2qb5B_ | Alignment | not modelled | 86.8 | 27 | PDB header: transferase Chain: B: PDB Molecule: inositol-tetrakisphosphate 1-kinase; PDBTitle: crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+ |
| 51 | c2pvpB_ | Alignment | not modelled | 86.0 | 10 | PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori |
| 52 | d1iowa2 | Alignment | not modelled | 85.0 | 10 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases |
| 53 | c5ig8A_ | Alignment | not modelled | 84.6 | 14 | PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc |
| | | | | | | PDB header: ligase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c3lwbA_ | Alignment | not modelled | 82.6 | 15 | Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis |
| 55 | c2vpqA_ | Alignment | not modelled | 82.3 | 13 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp |
| 56 | c2cqyA_ | Alignment | not modelled | 81.7 | 10 | PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit |
| 57 | c1e4eB_ | Alignment | not modelled | 80.3 | 14 | PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase |
| 58 | c5ig9H_ | Alignment | not modelled | 80.2 | 20 | 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 |
| 59 | c3e5nA_ | Alignment | not modelled | 77.1 | 10 | PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331 |
| 60 | c1ulzA_ | Alignment | not modelled | 76.6 | 14 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase |
| 61 | c1w96B_ | Alignment | not modelled | 76.5 | 15 | 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 |
| 62 | c2zdqA_ | Alignment | not modelled | 76.5 | 17 | 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 |
| 63 | c5k2mG_ | Alignment | not modelled | 76.2 | 20 | PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa |
| 64 | c3uvzB_ | Alignment | not modelled | 74.5 | 12 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria |
| 65 | d2j9ga3 | Alignment | not modelled | 74.1 | 22 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 66 | c2dlnA_ | Alignment | not modelled | 73.8 | 9 | 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 |
| 67 | c3vpbC_ | Alignment | not modelled | 72.8 | 15 | PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate |
| 68 | d1kjqA3 | Alignment | not modelled | 71.1 | 13 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 69 | d1uc8a2 | Alignment | not modelled | 71.0 | 18 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain |
| 70 | c1m6vE_ | Alignment | not modelled | 70.3 | 13 | 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 |
| 71 | d1vkza3 | Alignment | not modelled | 70.3 | 14 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 72 | d1w96a3 | Alignment | not modelled | 69.2 | 17 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 73 | d1m0wa2 | Alignment | not modelled | 69.0 | 16 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Eukaryotic glutathione synthetase ATP-binding domain |
| 74 | d2r85a2 | Alignment | not modelled | 66.5 | 18 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like |
| 75 | c2i80B_ | Alignment | not modelled | 65.9 | 13 | 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 |
| 76 | c2hjwA_ | Alignment | not modelled | 65.6 | 18 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2 |
| 77 | c3orqA_ | Alignment | not modelled | 65.2 | 8 | 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 |
| 78 | d1gsoa3 | Alignment | not modelled | 63.1 | 25 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 79 | c2ys6A_ | Alignment | not modelled | 59.3 | 13 | PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | kaustophilus |
| 80 | c3gidB_ | Alignment | not modelled | 58.6 | 14 | 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 soraphen a |
| 81 | c4egqD_ | Alignment | not modelled | 58.5 | 27 | 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 |
| 82 | c3df7A_ | Alignment | not modelled | 58.0 | 26 | 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 |
| 83 | d2r7ka2 | Alignment | not modelled | 57.1 | 15 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like |
| 84 | c1z2pX_ | Alignment | not modelled | 54.3 | 31 | 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 |
| 85 | d2hgsa4 | Alignment | not modelled | 53.7 | 16 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Eukaryotic glutathione synthetase ATP-binding domain |
| 86 | d1l8na1 | Alignment | not modelled | 50.9 | 15 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain |
| 87 | d1ulza3 | Alignment | not modelled | 50.2 | 18 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 88 | c3r23B_ | Alignment | not modelled | 48.8 | 25 | PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis |
| 89 | c3tw6B_ | Alignment | not modelled | 47.0 | 25 | 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 |
| 90 | c3bg5C_ | Alignment | not modelled | 46.1 | 15 | PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase |
| 91 | c3t9aA_ | Alignment | not modelled | 46.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: inositol pyrophosphate kinase; PDBTitle: crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0 |
| 92 | c5dmxC_ | Alignment | not modelled | 42.0 | 38 | 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 |
| 93 | c4eacC_ | Alignment | not modelled | 41.9 | 17 | PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12 |
| 94 | d2gxfa1 | Alignment | not modelled | 37.8 | 18 | Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like |
| 95 | c4yakD_ | Alignment | not modelled | 37.0 | 14 | PDB header: ligase Chain: D: PDB Molecule: beta subunit of acyl-coa synthetase (ndp forming); PDBTitle: 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) |
| 96 | c2z04A_ | Alignment | not modelled | 35.2 | 13 | PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus |
| 97 | d1eucb2 | Alignment | not modelled | 35.0 | 15 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain |
| 98 | c3soyA_ | Alignment | not modelled | 31.7 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 99 | d3etja3 | Alignment | not modelled | 31.2 | 18 | Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like |
| 100 | c3q2oB_ | Alignment | not modelled | 28.9 | 15 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase |
| 101 | c5vlqA_ | Alignment | not modelled | 28.5 | 18 | PDB header: ligase Chain: A: PDB Molecule: loc100158544 protein; PDBTitle: structure of the ttl13 glycolase |
| 102 | d7reqb2 | Alignment | not modelled | 28.3 | 8 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 103 | c3etjB_ | Alignment | not modelled | 27.8 | 20 | PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 104 | c4ffnA_ | Alignment | not modelled | 27.8 | 28 | PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp |
| 105 | c3ax6C_ | Alignment | not modelled | 27.6 | 23 | PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima |
| 106 | c3k3pA_ | Alignment | not modelled | 27.5 | 21 | 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 |
| 107 | c1gsoA_ | Alignment | not modelled | 27.3 | 28 | PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli. |
| 108 | d1gsaa1 | Alignment | not modelled | 27.0 | 16 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain |
| 109 | c4egjD_ | Alignment | not modelled | 26.6 | 27 | PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans |
| 110 | c5j1bB_ | Alignment | not modelled | 25.0 | 14 | PDB header: signaling protein Chain: B: PDB Molecule: cell wall assembly regulator smi1; PDBTitle: structure of the core domaine of knr4, an intrinsically disordered2 protein from saccharomyces cerevisiae - wt. |
| 111 | c3se7A_ | Alignment | not modelled | 24.9 | 14 | PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana |
| 112 | c4s2uA_ | Alignment | not modelled | 24.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli |
| 113 | d1pqua1 | Alignment | not modelled | 23.4 | 6 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 114 | c2r85B_ | Alignment | not modelled | 22.4 | 18 | PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp |
| 115 | c2cmgA_ | Alignment | not modelled | 22.2 | 14 | PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of spermidine synthase from helicobacter2 pylori |
| 116 | d1wb9a4 | Alignment | not modelled | 22.1 | 14 | Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I |
| 117 | c1ik6A_ | Alignment | not modelled | 21.2 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum |
| 118 | c2pn1A_ | Alignment | not modelled | 20.9 | 26 | 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 |
| 119 | c1mqrA_ | Alignment | not modelled | 20.7 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6 |
| 120 | c5kciA_ | Alignment | not modelled | 20.6 | 4 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ypl067c; PDBTitle: crystal structure of htc1 |