
































Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1205_(-)_1348725_1349288 |
| Date | Wed Jul 31 22:05:29 BST 2019 |
| Unique Job ID | 2dde4a84485fb0a7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | d1ydha_ |  Alignment |  | 100.0 | 27 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 2 | c5zbjA_ |  Alignment |  | 100.0 | 42 | PDB header: hydrolase Chain: A: PDB Molecule: putative cytokinin riboside 5'-monophosphate PDBTitle: crystal strcuture of type-i log from pseudomonas aeruginosa pao1 |
| 3 | c5itsD_ |  Alignment |  | 100.0 | 33 | PDB header: hydrolase Chain: D: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of log from corynebacterium glutamicum |
| 4 | d1t35a_ |  Alignment |  | 100.0 | 28 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 5 | c2q4dB_ |  Alignment |  | 100.0 | 28 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950 |
| 6 | c3quaA_ |  Alignment |  | 100.0 | 73 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis |
| 7 | c3sbxC_ |  Alignment |  | 100.0 | 83 | PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp |
| 8 | c5ajtA_ |  Alignment |  | 100.0 | 32 | PDB header: hydrolase Chain: A: PDB Molecule: phosphoribohydrolase lonely guy; PDBTitle: crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea |
| 9 | d2q4oa1 |  Alignment |  | 100.0 | 30 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 10 | c2q4oA_ |  Alignment |  | 100.0 | 30 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210 |
| 11 | c5zi9B_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from streptomyces coelicolor a3 |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | d1weka_ | Alignment |  | 100.0 | 26 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 13 | c5wq3A_ | Alignment |  | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from corynebacterium glutamicum |
| 14 | d1weha_ | Alignment |  | 100.0 | 29 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 15 | c3bq9A_ | Alignment |  | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145 |
| 16 | c6gfmA_ | Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase pppn (pppgpp-2 form) |
| 17 | c3gh1A_ | Alignment |  | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae |
| 18 | c1rcuB_ | Alignment |  | 100.0 | 22 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein vt76; PDBTitle: x-ray structure of tm1055 northeast structural genomics2 consortium target vt76 |
| 19 | d1rcua_ | Alignment |  | 100.0 | 22 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like |
| 20 | c2iz6A_ | Alignment |  | 100.0 | 28 | PDB header: metal transport Chain: A: PDB Molecule: molybdenum cofactor carrier protein; PDBTitle: structure of the chlamydomonas reinhardtii moco carrier2 protein |
| 21 | c3uqzB_ | Alignment | not modelled | 99.6 | 20 | PDB header: dna binding protein Chain: B: PDB Molecule: dna processing protein dpra; PDBTitle: x-ray structure of dna processing protein a (dpra) from streptococcus2 pneumoniae |
| 22 | c3majA_ | Alignment | not modelled | 99.6 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009 |
| 23 | c4ljkA_ | Alignment | not modelled | 99.6 | 18 | PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a (dpra); PDBTitle: structural insights into the unique single-stranded dna binding mode2 of dna processing protein a from helicobacter pylori |
| 24 | d2nx2a1 | Alignment | not modelled | 98.5 | 17 | Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like |
| 25 | c6d73C_ | Alignment | not modelled | 97.4 | 24 | PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+ |
| 26 | c6mizC_ | Alignment | not modelled | 97.4 | 25 | PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state |
| 27 | c6d73B_ | Alignment | not modelled | 97.2 | 24 | PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+ |
| 28 | c6co7C_ | Alignment | not modelled | 97.2 | 23 | PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | PDBTitle: structure of the nvtrpm2 channel in complex with ca2+ |
| 29 | c6bcqB_ | Alignment | not modelled | 96.9 | 24 | PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with long coiled coil at2 3.3 angstrom resolution |
| 30 | c6bcoD_ | Alignment | not modelled | 96.9 | 24 | PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with short coiled coil2 at 2.9 angstrom resolution |
| 31 | c6drkD_ | Alignment | not modelled | 96.7 | 25 | PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel, subfamily m, PDBTitle: structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state |
| 32 | c3imkA_ | Alignment | not modelled | 96.5 | 16 | PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution |
| 33 | c6nr3D_ | Alignment | not modelled | 93.4 | 16 | PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium |
| 34 | c6nr3C_ | Alignment | not modelled | 93.4 | 16 | PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium |
| 35 | c6nr3B_ | Alignment | not modelled | 93.4 | 16 | PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium |
| 36 | c6nr3A_ | Alignment | not modelled | 93.4 | 16 | PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium |
| 37 | c5vtoA_ | Alignment | not modelled | 93.4 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: blasticidin m; PDBTitle: solution structure of blsm |
| 38 | c4jenB_ | Alignment | not modelled | 93.2 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: cmp n-glycosidase; PDBTitle: structure of clostridium botulinum cmp n-glycosidase, bcmb |
| 39 | c6evsA_ | Alignment | not modelled | 92.4 | 17 | PDB header: transferase Chain: A: PDB Molecule: n-deoxyribosyltransferase; PDBTitle: characterization of 2-deoxyribosyltransferase from psychrotolerant2 bacterium bacillus psychrosaccharolyticus: a suitable biocatalyst for3 the industrial synthesis of antiviral and antitumoral nucleosides |
| 40 | c2khzB_ | Alignment | not modelled | 92.2 | 19 | PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl |
| 41 | c6nr2B_ | Alignment | not modelled | 91.8 | 19 | PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2 |
| 42 | c6nr2C_ | Alignment | not modelled | 91.8 | 19 | PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2 |
| 43 | c6nr2D_ | Alignment | not modelled | 91.8 | 19 | PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2 |
| 44 | c6nr2A_ | Alignment | not modelled | 91.8 | 19 | PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2 |
| 45 | d2nu7b1 | Alignment | not modelled | 91.3 | 18 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 46 | c5nbrB_ | Alignment | not modelled | 88.7 | 18 | PDB header: transferase Chain: B: PDB Molecule: deoxyribosyltransferase; PDBTitle: 2-desoxiribosyltransferase from leishmania mexicana |
| 47 | c3bgkA_ | Alignment | not modelled | 88.0 | 19 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of hypothetic protein smu.573 from streptococcus2 mutans |
| 48 | c2r3bA_ | Alignment | not modelled | 87.6 | 17 | PDB header: transferase Chain: A: PDB Molecule: yjef-related protein; PDBTitle: crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution |
| 49 | c4jemA_ | Alignment | not modelled | 86.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: cmp/hydroxymethyl cmp hydrolase; PDBTitle: crystal structure of milb complexed with cytidine 5'-monophosphate |
| 50 | c3zlbA_ | Alignment | not modelled | 81.2 | 17 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae PDB header: ligase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 51 | c4qjIB_ | Alignment | not modelled | 79.1 | 16 | Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis |
| 52 | d1f8ya_ | Alignment | not modelled | 77.4 | 23 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase |
| 53 | d1u0ta_ | Alignment | not modelled | 76.3 | 23 | Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like |
| 54 | c2jzcA_ | Alignment | not modelled | 75.6 | 12 | PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1 |
| 55 | c2bonB_ | Alignment | not modelled | 74.6 | 26 | PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs) |
| 56 | c1zrsB_ | Alignment | not modelled | 72.3 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: wild-type ld-carboxypeptidase |
| 57 | c1zmrA_ | Alignment | not modelled | 72.3 | 18 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase |
| 58 | c6efwA_ | Alignment | not modelled | 72.2 | 19 | PDB header: lyase Chain: A: PDB Molecule: atp-dependent (s)-nad(p)h-hydrate dehydratase; PDBTitle: crystal structure of a yjef family protein from cryptococcus2 neoformans var. grubii serotype a |
| 59 | d2auna2 | Alignment | not modelled | 72.1 | 29 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like |
| 60 | d1phpa_ | Alignment | not modelled | 67.3 | 18 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 61 | c3q3vA_ | Alignment | not modelled | 66.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni. |
| 62 | d1yoba1 | Alignment | not modelled | 65.4 | 24 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 63 | c3ehdA_ | Alignment | not modelled | 63.6 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved protein from enterococcus faecalis v583 |
| 64 | c4ng4B_ | Alignment | not modelled | 60.0 | 16 | PDB header: transferase Chain: B: PDB Molecule: phosphoglycerate kinase; PDBTitle: structure of phosphoglycerate kinase (cbu_1782) from coxiella burnetii |
| 65 | c3s40C_ | Alignment | not modelled | 57.2 | 24 | PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne |
| 66 | c2qv7A_ | Alignment | not modelled | 57.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg |
| 67 | c4as2D_ | Alignment | not modelled | 55.9 | 25 | PDB header: hydrolase Chain: D: PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form |
| 68 | d2jgra1 | Alignment | not modelled | 54.1 | 26 | Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like |
| 69 | d2bona1 | Alignment | not modelled | 53.7 | 26 | Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like |
| 70 | d1v6sa_ | Alignment | not modelled | 52.4 | 13 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 71 | c3d3jA_ | Alignment | not modelled | 51.2 | 17 | PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p |
| 72 | d1s2da_ | Alignment | not modelled | 51.2 | 10 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase |
| 73 | c4e5sC_ | Alignment | not modelled | 51.1 | 14 | PDB header: hydrolase Chain: C: PDB Molecule: mccflike protein (ba_5613); PDBTitle: crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames |
| 74 | d1e4ea1 | Alignment | not modelled | 50.5 | 22 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain |
| 75 | d1fw8a_ | Alignment | not modelled | 50.1 | 19 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 76 | d2f62a1 | Alignment | not modelled | 49.7 | 20 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 77 | c4dg5A | Alignment | not modelled | 48.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of staphylococcal phosphoglycerate kinase |
| 78 | c4h1hB | Alignment | not modelled | 47.3 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e |
| 79 | d1iowa1 | Alignment | not modelled | 45.1 | 22 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain |
| 80 | c6fsiA | Alignment | not modelled | 45.0 | 12 | PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution) |
| 81 | c6bpqD | Alignment | not modelled | 44.8 | 11 | PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8 |
| 82 | c6bpqB | Alignment | not modelled | 44.8 | 11 | PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8 |
| 83 | c6bpqC | Alignment | not modelled | 44.8 | 11 | PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8 |
| 84 | c6bpqA | Alignment | not modelled | 44.8 | 11 | PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8 |
| 85 | c3d3kD | Alignment | not modelled | 44.8 | 18 | PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p |
| 86 | c5f2kA | Alignment | not modelled | 44.7 | 31 | PDB header: transferase Chain: A: PDB Molecule: fatty acid o-methyltransferase; PDBTitle: crystal structure of mycobacterial fatty acid o-methyltransferase in2 complex with sah and octanoate |
| 87 | c2wc1A | Alignment | not modelled | 43.5 | 19 | PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a |
| 88 | c3c5yD | Alignment | not modelled | 43.0 | 13 | PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution |
| 89 | d1qpga | Alignment | not modelled | 42.6 | 19 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 90 | d2p1ra1 | Alignment | not modelled | 42.3 | 21 | Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like |
| 91 | c2dg2D | Alignment | not modelled | 42.2 | 17 | PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding protein |
| 92 | d1hdia | Alignment | not modelled | 41.2 | 15 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 93 | d1ehia1 | Alignment | not modelled | 41.1 | 23 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain |
| 94 | c2i80B | Alignment | not modelled | 40.8 | 19 | 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 |
| 95 | c5ohxB | Alignment | not modelled | 40.7 | 17 | PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera |
| 96 | d2qv7a1 | Alignment | not modelled | 39.5 | 15 | Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like |
| 97 | c2duwA | Alignment | not modelled | 39.4 | 13 | PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae |
| 98 | c5b3kA | Alignment | not modelled | 39.3 | 19 | PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa |
| 99 | c3gndC | Alignment | not modelled | 38.8 | 15 | PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 100 | d1u7za | Alignment | not modelled | 38.6 | 16 | Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like |
| 101 | c4ei8A | Alignment | not modelled | 38.3 | 8 | PDB header: replication Chain: A: PDB Molecule: plasmid replication protein repx; PDBTitle: crystal structure of bacillus cereus tubz, apo-form |
| | | | | | | PDB header: transport protein |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 102 | c4nguA_ | Alignment | not modelled | 38.3 | 6 | Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio alaskensis</i> g20 (dde_1548), target efi-510103, with 3 bound d-ala-d-ala |
| 103 | c3hy5A_ | Alignment | not modelled | 37.6 | 12 | PDB header: transport protein Chain: A: PDB Molecule: retinaldehyde-binding protein 1; PDBTitle: crystal structure of cralbp |
| 104 | c5dmxC_ | Alignment | not modelled | 37.0 | 24 | PDB header: ligase Chain: C: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from <i>Acinetobacter baumannii</i> , space group p212121 |
| 105 | d1ag9a_ | Alignment | not modelled | 36.9 | 27 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 106 | c3k3pA_ | Alignment | not modelled | 36.2 | 19 | 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 <i>Streptococcus mutans</i> |
| 107 | c4fu0B_ | Alignment | not modelled | 35.8 | 19 | PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vng d-ala:d-ser ligase from <i>Enterococcus faecalis</i> |
| 108 | c4imrA_ | Alignment | not modelled | 34.7 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from <i>Agrobacterium tumefaciens</i> c58 with nadp3 bound |
| 109 | c6odmC_ | Alignment | not modelled | 34.6 | 36 | PDB header: viral protein Chain: C: PDB Molecule: capsid vertex component 1; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit |
| 110 | c4heqB_ | Alignment | not modelled | 34.4 | 9 | PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from <i>Desulfovibrio gigas</i> |
| 111 | d1m6ex_ | Alignment | not modelled | 34.2 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Salicylic acid carboxyl methyltransferase (SAMT) |
| 112 | d2fcra_ | Alignment | not modelled | 34.1 | 19 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 113 | d1ja1a2 | Alignment | not modelled | 33.9 | 15 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 114 | c3imfA_ | Alignment | not modelled | 33.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from <i>Bacillus anthracis</i> str. 'ames ancestor' |
| 115 | c3tlgB_ | Alignment | not modelled | 33.6 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state |
| 116 | c6c8rA_ | Alignment | not modelled | 33.4 | 15 | PDB header: transferase Chain: A: PDB Molecule: loganic acid o-methyltransferase; PDBTitle: loganic acid o-methyltransferase complexed with sah and loganic acid |
| 117 | c3qjgD_ | Alignment | not modelled | 33.4 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from <i>Staphylococcus aureus</i> |
| 118 | d16pka_ | Alignment | not modelled | 32.9 | 16 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 119 | d1vmea1 | Alignment | not modelled | 32.8 | 14 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 120 | c3nywD_ | Alignment | not modelled | 32.8 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a betaketoacyl-[acp] reductase (fabg) from <i>Bacteroides thetaiotaomicron</i> |