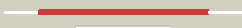



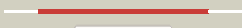








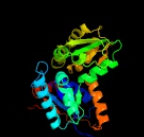










Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1338_(murl)_1505081_1505896 |
| Date | Wed Jul 31 22:05:43 BST 2019 |
| Unique Job ID | dfc5dab1c4482e5a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c5ijwA_ |  Alignment |  | 100.0 | 87 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction |
| 2 | c2jfoB_ |  Alignment |  | 100.0 | 40 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate |
| 3 | c3hfrA_ |  Alignment |  | 100.0 | 41 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes |
| 4 | c2dwaA_ |  Alignment |  | 100.0 | 40 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis |
| 5 | c2gzmB_ |  Alignment |  | 100.0 | 39 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus anthracis |
| 6 | c2jfqA_ |  Alignment |  | 100.0 | 38 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate racemase in2 complex with d- glutamate |
| 7 | c2ohoA_ |  Alignment |  | 100.0 | 36 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor |
| 8 | c3outC_ |  Alignment |  | 100.0 | 33 | PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate. |
| 9 | c1zuwA_ |  Alignment |  | 100.0 | 42 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu |
| 10 | c5w16D_ |  Alignment |  | 100.0 | 45 | PDB header: isomerase Chain: D: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate |
| 11 | c2jfnA_ |  Alignment |  | 100.0 | 31 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c3uhfB_ | Alignment | | 100.0 | 32 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni |
| 13 | c1b74A_ | Alignment | | 100.0 | 36 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus |
| 14 | c2fzB_ | Alignment | | 100.0 | 30 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor |
| 15 | c5b19A_ | Alignment | | 100.0 | 16 | PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: picrophilus torridus aspartate racemase |
| 16 | d1b74a1 | Alignment | | 100.0 | 42 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 17 | c5wxzA_ | Alignment | | 100.0 | 15 | PDB header: isomerase Chain: A: PDB Molecule: mcyf; PDBTitle: crystal structure of microcystis aeruginosa pcc 7806 aspartate2 racemase in complex with d-aspartate |
| 18 | c2zskA_ | Alignment | | 100.0 | 16 | PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3 |
| 19 | c5elmB_ | Alignment | | 100.0 | 14 | PDB header: isomerase Chain: B: PDB Molecule: asp/glu_racemase family protein; PDBTitle: crystal structure of l-aspartate/glutamate specific racemase in2 complex with l-glutamate |
| 20 | c3s81A_ | Alignment | | 100.0 | 17 | PDB header: isomerase Chain: A: PDB Molecule: putative aspartate racemase; PDBTitle: crystal structure of putative aspartate racemase from salmonella2 typhimurium |
| 21 | c3ojcD_ | Alignment | not modelled | 100.0 | 16 | PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis |
| 22 | c2dx7B_ | Alignment | not modelled | 100.0 | 20 | PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid |
| 23 | d1b74a2 | Alignment | not modelled | 100.0 | 31 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 24 | c3qviB_ | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae |
| 25 | c2vlbC_ | Alignment | not modelled | 99.9 | 17 | PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase |
| 26 | c5lg5F_ | Alignment | not modelled | 99.9 | 15 | PDB header: isomerase Chain: F: PDB Molecule: allantoin racemase; PDBTitle: crystal structure of allantoin racemase from pseudomonas fluorescens2 allr |
| 27 | c2eq5D_ | Alignment | not modelled | 99.9 | 20 | PDB header: isomerase Chain: D: PDB Molecule: 228aa long hypothetical hydantoin racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3 |
| 28 | c2dgdD_ | Alignment | not modelled | 99.8 | 10 | PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | from2 sulfobolus tokodaii |
| 29 | c5b19B | Alignment | not modelled | 99.8 | 14 | PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: microphilus torridus aspartate racemase |
| 30 | d1jfla2 | Alignment | not modelled | 99.8 | 20 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 31 | d2dx7a1 | Alignment | not modelled | 99.7 | 18 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 32 | d1jfla1 | Alignment | not modelled | 99.3 | 21 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 33 | c4ix1B | Alignment | not modelled | 98.9 | 13 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205 |
| 34 | c4fq5B | Alignment | not modelled | 98.5 | 13 | PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate |
| 35 | c2xecD | Alignment | not modelled | 98.5 | 17 | PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris |
| 36 | c5tpwB | Alignment | not modelled | 94.5 | 10 | PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor ionotropic, nmda 2a; PDBTitle: crystal structure of amino terminal domains of the nmda receptor2 subunit glun1 and glun2a in complex with zinc at the glun2a |
| 37 | d1m3ua | Alignment | not modelled | 94.0 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB |
| 38 | c5uowB | Alignment | not modelled | 93.9 | 12 | PDB header: membrane protein Chain: B: PDB Molecule: n-methyl-d-aspartate receptor subunit nr2a; PDBTitle: triheteromeric nmda receptor glun1/glun2a/glun2b in complex with2 glycine, glutamate, mk-801 and a glun2b-specific fab, at ph 6.5 |
| 39 | c5kc9B | Alignment | not modelled | 92.3 | 15 | PDB header: signaling protein Chain: B: PDB Molecule: glutamate receptor ionotropic, delta-1; PDBTitle: crystal structure of the amino-terminal domain (atd) of iglur delta-12 (glud1) |
| 40 | c3ez4B | Alignment | not modelled | 92.2 | 12 | PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei |
| 41 | c2wjxA | Alignment | not modelled | 91.6 | 11 | PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution |
| 42 | d1o66a | Alignment | not modelled | 91.4 | 12 | Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB |
| 43 | c2oblA | Alignment | not modelled | 90.7 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: escn; PDBTitle: structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria |
| 44 | c2h31A | Alignment | not modelled | 90.0 | 14 | PDB header: ligase, lyase Chain: A: PDB Molecule: multifunctional protein ade2; PDBTitle: crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis |
| 45 | d1o5oa | Alignment | not modelled | 88.6 | 20 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 46 | c3gkaB | Alignment | not modelled | 88.6 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei |
| 47 | d1qcza | Alignment | not modelled | 88.6 | 15 | Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 48 | c4nphA | Alignment | not modelled | 88.3 | 20 | PDB header: protein transport Chain: A: PDB Molecule: probable secretion system apparatus atp synthase ssan; PDBTitle: crystal structure of ssan from salmonella enterica |
| 49 | c4ja0A | Alignment | not modelled | 88.2 | 16 | PDB header: protein binding Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase; PDBTitle: crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution |
| 50 | c6npjC | Alignment | not modelled | 88.1 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: translocator escn; PDBTitle: structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system |
| 51 | c3p3wC | Alignment | not modelled | 88.0 | 16 | PDB header: transport protein Chain: C: PDB Molecule: glutamate receptor 3; PDBTitle: structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution |
| 52 | c5ideA | Alignment | not modelled | 87.7 | 12 | PDB header: signaling protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: cryo-em structure of glua2/3 ampa receptor heterotetramer (model i) PDB header: lyase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c3lp6D_ | Alignment | not modelled | 87.5 | 15 | Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution |
| 54 | c3kg2A_ | Alignment | not modelled | 87.5 | 13 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775 |
| 55 | d1skyb3 | Alignment | not modelled | 87.0 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 56 | c6qkzA_ | Alignment | not modelled | 86.6 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: glua1; PDBTitle: full length glua1/2-gamma8 complex |
| 57 | c2fw9A_ | Alignment | not modelled | 86.3 | 15 | PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8 |
| 58 | d1e5qa1 | Alignment | not modelled | 86.0 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 59 | d1u11a_ | Alignment | not modelled | 85.8 | 15 | Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 60 | c3orsD_ | Alignment | not modelled | 85.6 | 15 | PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus |
| 61 | c2dpyA_ | Alignment | not modelled | 85.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: flagellum-specific atp synthase; PDBTitle: crystal structure of the flagellar type iii atpase fliii |
| 62 | c5bo5B_ | Alignment | not modelled | 84.2 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: neq263; PDBTitle: structure of a unique atp synthase subunit neqb from nanoarchaeum2 equitans |
| 63 | c5cjjA_ | Alignment | not modelled | 84.1 | 17 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168 |
| 64 | c2ywrA_ | Alignment | not modelled | 84.1 | 20 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus |
| 65 | d1oy0a_ | Alignment | not modelled | 84.1 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB |
| 66 | c3tqrA_ | Alignment | not modelled | 83.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii |
| 67 | c5eoxB_ | Alignment | not modelled | 83.7 | 29 | PDB header: peptide binding protein Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp |
| 68 | d1jkxa_ | Alignment | not modelled | 83.6 | 16 | Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase |
| 69 | c3h5lB_ | Alignment | not modelled | 83.0 | 16 | PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc transporter; PDBTitle: crystal structure of a putative branched-chain amino acid abc2 transporter from silicibacter pomeroyi |
| 70 | c6irfD_ | Alignment | not modelled | 82.9 | 10 | PDB header: membrane protein Chain: D: PDB Molecule: glutamate receptor ionotropic, nmda 2a; PDBTitle: structure of the human glun1/glun2a nmda receptor in the2 glutamate/glycine-bound state at ph 6.3, class i |
| 71 | c4ew6A_ | Alignment | not modelled | 82.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli |
| 72 | c4grdA_ | Alignment | not modelled | 82.3 | 21 | PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315 |
| 73 | d1meoa_ | Alignment | not modelled | 82.0 | 17 | Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase |
| 74 | c5syrA_ | Alignment | not modelled | 81.9 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp synthase spa/mxib; PDBTitle: crystal structure of atpase delta1-79 spa47 r350a |
| 75 | c1dkrB_ | Alignment | not modelled | 81.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation. PDB header: ribosomal protein |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 76 | c3cpqB | Alignment | not modelled | 81.6 | 10 | Chain: B; PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044) |
| 77 | d1xmpa | Alignment | not modelled | 80.9 | 21 | Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 78 | c3p9xB | Alignment | not modelled | 80.8 | 29 | PDB header: transferase Chain: B; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans |
| 79 | c5dmnA | Alignment | not modelled | 80.7 | 19 | PDB header: transferase Chain: A; PDB Molecule: homocysteine s-methyltransferase; PDBTitle: crystal structure of the homocysteine methyltransferase mmum from2 escherichia coli, apo form |
| 80 | c3trhI | Alignment | not modelled | 80.7 | 17 | PDB header: lyase Chain: I; PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii |
| 81 | c4b4kK | Alignment | not modelled | 80.6 | 21 | PDB header: isomerase Chain: K; PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure |
| 82 | c3bolB | Alignment | not modelled | 80.1 | 24 | PDB header: transferase Chain: B; PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+ |
| 83 | d1i5ea | Alignment | not modelled | 79.9 | 19 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 84 | c3sg0A | Alignment | not modelled | 79.7 | 13 | PDB header: signaling protein Chain: A; PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodospseudomonas palustris haa2 |
| 85 | c6o55B | Alignment | not modelled | 79.4 | 15 | PDB header: isomerase Chain: B; PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila |
| 86 | d1w41a1 | Alignment | not modelled | 79.3 | 16 | Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins |
| 87 | c2c61A | Alignment | not modelled | 78.8 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: a-type atp synthase non-catalytic subunit b; PDBTitle: crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazel go1 |
| 88 | c3av3A | Alignment | not modelled | 78.7 | 22 | PDB header: transferase Chain: A; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus |
| 89 | d1lt7a | Alignment | not modelled | 78.4 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase |
| 90 | c5b0oB | Alignment | not modelled | 78.4 | 17 | PDB header: hydrolase/motor protein Chain: B; PDB Molecule: flagellum-specific atp synthase; PDBTitle: structure of the flih-flii complex |
| 91 | c3a5dM | Alignment | not modelled | 77.5 | 18 | PDB header: hydrolase Chain: M; PDB Molecule: v-type atp synthase beta chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase |
| 92 | d2bo1a1 | Alignment | not modelled | 77.5 | 21 | Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins |
| 93 | c4s1nA | Alignment | not modelled | 77.4 | 15 | PDB header: transferase Chain: A; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4 |
| 94 | d1umya | Alignment | not modelled | 77.3 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase |
| 95 | c1u9yD | Alignment | not modelled | 77.2 | 12 | PDB header: transferase Chain: D; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii |
| 96 | d1o4va | Alignment | not modelled | 77.1 | 14 | Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 97 | c6focB | Alignment | not modelled | 77.0 | 16 | PDB header: hydrolase Chain: B; PDB Molecule: atp synthase subunit alpha,atp synthase subunit alpha,atp PDBTitle: f1-atpase from mycobacterium smegmatis |
| 98 | c4mwaA | Alignment | not modelled | 76.4 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis |
| 99 | c5ereA | Alignment | not modelled | 75.9 | 16 | PDB header: signaling protein Chain: A; PDB Molecule: extracellular ligand-binding receptor; PDBTitle: extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692 |
| 100 | c4a3uB | Alignment | not modelled | 74.8 | 11 | PDB header: oxidoreductase Chain: B; PDB Molecule: nadh:\flavin oxidoreductase/nadh oxidase; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 100 | c9a3ub | Alignment | not modelled | 74.8 | 11 | PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr) PDB header: lyase |
| 101 | c3lwzC | Alignment | not modelled | 74.4 | 37 | Chain: C; PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinatase2 dehydratase (arog) from yersinia pestis |
| 102 | d1t0kb | Alignment | not modelled | 74.0 | 17 | Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins |
| 103 | d1skye3 | Alignment | not modelled | 73.9 | 12 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 104 | c2gr2A | Alignment | not modelled | 73.9 | 26 | PDB header: oxidoreductase Chain: A; PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form) |
| 105 | c2pjuD | Alignment | not modelled | 73.5 | 17 | PDB header: transcription Chain: D; PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr |
| 106 | d1uqra | Alignment | not modelled | 73.4 | 26 | Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase |
| 107 | c3zu0A | Alignment | not modelled | 72.7 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadm) |
| 108 | c6re7U | Alignment | not modelled | 72.5 | 19 | PDB header: proton transport Chain: U; PDB Molecule: atp synthase subunit alpha; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2c,2 focussed refinement of f1 head and rotor |
| 109 | c1nhqA | Alignment | not modelled | 72.4 | 20 | PDB header: oxidoreductase (h2o2(a)) Chain: A; PDB Molecule: nadh peroxidase; PDBTitle: crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303 |
| 110 | d1gqoa | Alignment | not modelled | 72.1 | 31 | Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase |
| 111 | c3lpnB | Alignment | not modelled | 72.0 | 11 | PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp). |
| 112 | c2o14A | Alignment | not modelled | 71.9 | 16 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein yxim; PDBTitle: x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595 |
| 113 | c2v3cC | Alignment | not modelled | 71.8 | 18 | PDB header: signaling protein Chain: C; PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii |
| 114 | c4a1dG | Alignment | not modelled | 71.7 | 11 | PDB header: ribosome Chain: G; PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4. |
| 115 | d2cvza2 | Alignment | not modelled | 71.3 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 116 | c3j21Z | Alignment | not modelled | 71.1 | 13 | PDB header: ribosome Chain: Z; PDB Molecule: 50s ribosomal protein l30e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 117 | c5ocsB | Alignment | not modelled | 71.0 | 20 | PDB header: flavoprotein Chain: B; PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans |
| 118 | c3wb9A | Alignment | not modelled | 70.9 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum |
| 119 | c3cr8C | Alignment | not modelled | 70.3 | 18 | PDB header: transferase Chain: C; PDB Molecule: sulfate adenyltransferase, adenylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans |
| 120 | c2qe7C | Alignment | not modelled | 70.1 | 16 | PDB header: hydrolase Chain: C; PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1 |