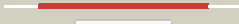



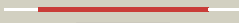




























Phyre2

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|------------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3552_(-)_3990950_3991702 |
| Date | Fri Aug 9 18:20:23 BST 2019 |
| Unique Job ID | f95b8a86819c6fe2 |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|--------------------------|---|---|------------|--------|---|
| 1 | c6conF_ |  Alignment |  | 100.0 | 100 | PDB header: hydrolase Chain: F: PDB Molecule: coa-transferase subunit beta; PDBTitle: crystal structure of mycobacterium tuberculosis ipdab |
| 2 | c6co6B_ |  Alignment |  | 100.0 | 69 | PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab |
| 3 | d1poib_ |  Alignment |  | 100.0 | 23 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like |
| 4 | c5n02B_ |  Alignment |  | 100.0 | 27 | PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant |
| 5 | d2ahua1 |  Alignment |  | 100.0 | 18 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like |
| 6 | d1ooya1 |  Alignment |  | 100.0 | 17 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like |
| 7 | c2ahvC_ |  Alignment |  | 100.0 | 18 | PDB header: transferase Chain: C: PDB Molecule: putative enzyme ydif; PDBTitle: crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1 |
| 8 | c3cdkD_ |  Alignment |  | 100.0 | 16 | PDB header: transferase Chain: D: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis |
| 9 | c3rrrID_ |  Alignment |  | 100.0 | 18 | PDB header: transferase Chain: D: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit b; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695 |
| 10 | c1ooyA_ |  Alignment |  | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase, PDBTitle: succinyl-coa:3-ketoacid coa transferase from pig heart |
| 11 | c4kqbB_ |  Alignment |  | 100.0 | 14 | PDB header: transferase Chain: B: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase; PDBTitle: structure of succinyl-coa: 3-ketoacid coa transferase from drosophila2 melanogaster |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | c5dbnD | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: D: PDB Molecule: acetate coa-transferase subunit beta; PDBTitle: crystal structure of atoda complex |
| 13 | c2hj0A | Alignment |  | 99.7 | 17 | PDB header: lyase Chain: A: PDB Molecule: putative citrate lyase, alfa subunit; PDBTitle: crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 . |
| 14 | c3eh7A | Alignment |  | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83 |
| 15 | c4eu4A | Alignment |  | 99.6 | 17 | PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:acetate coenzyme a transferase; PDBTitle: succinyl-coa: acetate coa-transferase (aarch6) in complex with coa2 (hexagonal lattice) |
| 16 | c1xr4B | Alignment |  | 99.6 | 18 | PDB header: hydrolase/transferase Chain: B: PDB Molecule: putative citrate lyase alpha chain/citrate-acp transferase; PDBTitle: x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium] |
| 17 | c2oasA | Alignment |  | 99.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coenzyme a transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119. |
| 18 | c3gk7A | Alignment |  | 99.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum |
| 19 | c2g39A | Alignment |  | 99.5 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: acetyl-coa hydrolase; PDBTitle: crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa |
| 20 | c2nvvF | Alignment |  | 99.5 | 19 | PDB header: hydrolase Chain: F: PDB Molecule: acetyl-coa hydrolase/transferase family protein; PDBTitle: crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16. |
| 21 | c3qk1B | Alignment | not modelled | 99.4 | 14 | PDB header: transferase Chain: B: PDB Molecule: coenzyme a transferase; PDBTitle: crystal structure of ripa from yersinia pestis |
| 22 | d1xr4a2 | Alignment | not modelled | 99.3 | 17 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 23 | d2g39a2 | Alignment | not modelled | 99.2 | 18 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 24 | c3d3uA | Alignment | not modelled | 99.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26 |
| 25 | c5vitP | Alignment | not modelled | 98.7 | 16 | PDB header: transferase Chain: P: PDB Molecule: mdca; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate |
| 26 | c3l7oB | Alignment | not modelled | 98.0 | 17 | PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159 |
| 27 | c4gmkB | Alignment | not modelled | 97.9 | 12 | PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118 |
| 28 | c1k5C | Alignment | not modelled | 97.9 | 18 | PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c6j1kA | Alignment | not modelled | 97.9 | 16 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from ochrobactrum2 sp. csl1 |
| 30 | c3hheA | Alignment | not modelled | 97.9 | 14 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae |
| 31 | c6eepA | Alignment | not modelled | 97.9 | 17 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila |
| 32 | c3kwmC | Alignment | not modelled | 97.8 | 10 | PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a |
| 33 | c1m0sA | Alignment | not modelled | 97.7 | 12 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21) |
| 34 | c5uf2A | Alignment | not modelled | 97.7 | 13 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae |
| 35 | c1lkzB | Alignment | not modelled | 97.7 | 10 | PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli. |
| 36 | c1uj6A | Alignment | not modelled | 97.6 | 16 | PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate |
| 37 | c2f8mB | Alignment | not modelled | 97.5 | 15 | PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum |
| 38 | d1m0sa1 | Alignment | not modelled | 97.5 | 14 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 39 | d1lk5a1 | Alignment | not modelled | 97.4 | 19 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 40 | c2pjmA | Alignment | not modelled | 97.1 | 15 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii |
| 41 | d1uj4a1 | Alignment | not modelled | 97.0 | 15 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 42 | c3cdkA | Alignment | not modelled | 96.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis |
| 43 | c3rrlC | Alignment | not modelled | 96.6 | 17 | PDB header: transferase Chain: C: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695 |
| 44 | d1ooya2 | Alignment | not modelled | 96.1 | 17 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 45 | c4nmIA | Alignment | not modelled | 96.0 | 15 | PDB header: isomerase Chain: A: PDB Molecule: ribulose 5-phosphate isomerase; PDBTitle: 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid |
| 46 | c3u7jA | Alignment | not modelled | 95.9 | 17 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis |
| 47 | d1k6da | Alignment | not modelled | 95.5 | 15 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 48 | c1xtzA | Alignment | not modelled | 95.4 | 21 | PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes |
| 49 | c4x84C | Alignment | not modelled | 95.4 | 16 | PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa |
| 50 | c5mzyA | Alignment | not modelled | 94.5 | 21 | PDB header: lyase Chain: A: PDB Molecule: glutaconate coa-transferase family, subunit a; PDBTitle: crystal structure of the decarboxylase aiba/aibb in complex with a2 possible transition state analog |
| 51 | d2g39a1 | Alignment | not modelled | 93.9 | 19 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 52 | d1o8bb1 | Alignment | not modelled | 93.7 | 10 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 53 | c6a34B | Alignment | not modelled | 89.3 | 8 | PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | d1poia_ | Alignment | not modelled | 84.0 | 15 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 55 | c3ecsD_ | Alignment | not modelled | 83.7 | 14 | PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha |
| 56 | c6i7tB_ | Alignment | not modelled | 83.4 | 12 | PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex |
| 57 | c3af5A_ | Alignment | not modelled | 80.5 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii |
| 58 | c2ycbA_ | Alignment | not modelled | 70.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor; PDBTitle: structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus |
| 59 | d1vb5a_ | Alignment | not modelled | 66.2 | 15 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like |
| 60 | d1xr4a1 | Alignment | not modelled | 65.0 | 15 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 61 | d1t5oa_ | Alignment | not modelled | 64.2 | 14 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like |
| 62 | c2xr1A_ | Alignment | not modelled | 60.9 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei |
| 63 | c2yvka_ | Alignment | not modelled | 58.6 | 14 | PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis |
| 64 | d1o8ba1 | Alignment | not modelled | 57.5 | 14 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 65 | c6co9A_ | Alignment | not modelled | 56.4 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: probable coa-transferase alpha subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab coeaa-coa complex |
| 66 | c3a11D_ | Alignment | not modelled | 49.0 | 13 | PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1 |
| 67 | c2xr1B_ | Alignment | not modelled | 43.5 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei |
| 68 | c6i3mD_ | Alignment | not modelled | 43.2 | 9 | PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52. |
| 69 | c4zemB_ | Alignment | not modelled | 34.6 | 12 | PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum |
| 70 | c2eo0A_ | Alignment | not modelled | 32.3 | 4 | PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein st1444; PDBTitle: crystal structure of holliday junction resolvase st1444 |
| 71 | d2ahua2 | Alignment | not modelled | 29.2 | 7 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 72 | c4zeoH_ | Alignment | not modelled | 28.2 | 10 | PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum |
| 73 | c6ezoD_ | Alignment | not modelled | 25.3 | 15 | PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib |
| 74 | c5b04B_ | Alignment | not modelled | 23.9 | 14 | PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe |
| 75 | c2w48D_ | Alignment | not modelled | 21.9 | 10 | PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae |
| 76 | c2gezF_ | Alignment | not modelled | 21.3 | 23 | PDB header: hydrolase Chain: F: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase |
| | | | | | | PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b |

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|----|-------------------------|-----------|--------------|------|----|--|
| 77 | c5b04G | Alignment | not modelled | 21.1 | 9 | subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe |
| 78 | c2gacD | Alignment | not modelled | 20.3 | 20 | PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |
| 79 | c4wt3A | Alignment | not modelled | 18.7 | 27 | PDB header: chaperone Chain: A: PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana |
| 80 | c2bvfa | Alignment | not modelled | 18.4 | 15 | PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1) |
| 81 | d1gefa | Alignment | not modelled | 17.8 | 9 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like |
| 82 | d1t9ka | Alignment | not modelled | 16.9 | 16 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like |
| 83 | c1p4vA | Alignment | not modelled | 16.2 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: n(4)-(beta-n-acetylglucosaminy)-l-asparaginase PDBTitle: crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine |
| 84 | d1ob8a | Alignment | not modelled | 15.0 | 4 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like |
| 85 | d1knx2 | Alignment | not modelled | 14.6 | 12 | Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: HPr kinase HPrK C-terminal domain |
| 86 | c2a8B | Alignment | not modelled | 14.5 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human caspase1 (t234a mutant) |
| 87 | d2a0ua1 | Alignment | not modelled | 13.9 | 13 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like |
| 88 | c2zakB | Alignment | not modelled | 12.9 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase precursor; PDBTitle: orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (eca3ii) with active-site t179a mutation |
| 89 | c4ml8C | Alignment | not modelled | 12.6 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2) |
| 90 | c1jqsb | Alignment | not modelled | 11.8 | 50 | PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of I11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog |
| 91 | c1apzB | Alignment | not modelled | 11.7 | 15 | PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product |
| 92 | c4pv3D | Alignment | not modelled | 11.5 | 26 | PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations |
| 93 | c4go1A | Alignment | not modelled | 11.0 | 13 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lssr; PDBTitle: crystal structure of full length transcription repressor lssr from e.2 coli. |
| 94 | d1h2ba2 | Alignment | not modelled | 11.0 | 9 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 95 | c5d79B | Alignment | not modelled | 10.7 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana |
| 96 | c3pm9A | Alignment | not modelled | 9.9 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodospseudomonas palustris cga009 at 2.57 a resolution |
| 97 | c3popD | Alignment | not modelled | 9.8 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis |
| 98 | c2wj0B | Alignment | not modelled | 9.7 | 13 | PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate |
| 99 | d2okga1 | Alignment | not modelled | 9.6 | 10 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like |