

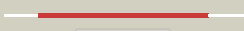


















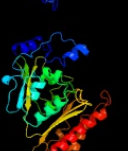






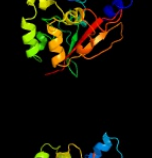




Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0375c_(-)_452295_453155 |
| Date | Tue Jul 23 14:50:44 BST 2019 |
| Unique Job ID | b5e01bd5fa70d03d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c1n62C_ |  Alignment |  | 100.0 | 39 | PDB header: oxidoreductase Chain: C: PDB Molecule: carbon monoxide dehydrogenase medium chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state |
| 2 | c1t3qF_ |  Alignment |  | 100.0 | 31 | PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86 |
| 3 | c1ffuF_ |  Alignment |  | 100.0 | 39 | PDB header: hydrolase Chain: F: PDB Molecule: cutm, flavoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor |
| 4 | c3hrdC_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase |
| 5 | c4zohB_ |  Alignment |  | 100.0 | 34 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase |
| 6 | c2w3rG_ |  Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine |
| 7 | c1rm6E_ |  Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica |
| 8 | c3b9jJ_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine |
| 9 | c3etrM_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine |
| 10 | c5y6qB_ |  Alignment |  | 100.0 | 31 | PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400 |
| 11 | c1wygA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s) |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c4uhxA | Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine |
| 13 | c5g5hB | Alignment |  | 100.0 | 29 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative xanthine dehydrogenase yags fad-binding subunit; PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant |
| 14 | c3zyvA | Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3) |
| 15 | d1n62c2 | Alignment |  | 100.0 | 43 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 16 | d1ffvc2 | Alignment |  | 100.0 | 43 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 17 | d1t3qc2 | Alignment |  | 100.0 | 33 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 18 | d1jroa4 | Alignment |  | 100.0 | 16 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 19 | d1v97a6 | Alignment |  | 100.0 | 18 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 20 | d1rm6b2 | Alignment |  | 100.0 | 28 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 21 | d3b9jb2 | Alignment | not modelled | 100.0 | 18 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like |
| 22 | d1n62c1 | Alignment | not modelled | 100.0 | 32 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 23 | d1ffvc1 | Alignment | not modelled | 100.0 | 34 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 24 | d1t3qc1 | Alignment | not modelled | 100.0 | 28 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 25 | d1jroa3 | Alignment | not modelled | 99.9 | 26 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 26 | d1v97a4 | Alignment | not modelled | 99.9 | 14 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 27 | d1rm6b1 | Alignment | not modelled | 99.9 | 20 | Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like |
| 28 | c4pytA | Alignment | not modelled | 97.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase |

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|----|--------------------------|-----------|--------------|------|----|--|
| 29 | c1hskA_ | Alignment | not modelled | 97.7 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb |
| 30 | c1mbbA_ | Alignment | not modelled | 97.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvyglucosamine PDBTitle: oxidoreductase |
| 31 | c5jzxB_ | Alignment | not modelled | 97.7 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis |
| 32 | d1hskA1 | Alignment | not modelled | 97.5 | 11 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvyglucosamine reductase (MurB), N-terminal domain |
| 33 | c4jayC_ | Alignment | not modelled | 97.3 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of p. aeruginosa murb in complex with nadp+ |
| 34 | c3i99A_ | Alignment | not modelled | 97.2 | 8 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor |
| 35 | c2gquA_ | Alignment | not modelled | 97.1 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvyglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvyglucosamine2 reductase (murb) from thermus caldophilus |
| 36 | c3tsjA_ | Alignment | not modelled | 97.0 | 14 | PDB header: allergen, oxidoreductase Chain: A: PDB Molecule: pollen allergen phl p 4; PDBTitle: crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity |
| 37 | c2wdwB_ | Alignment | not modelled | 96.8 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis |
| 38 | c5i1wD_ | Alignment | not modelled | 96.7 | 13 | PDB header: oxidoreductase Chain: D: PDB Molecule: crmk; PDBTitle: crystal structure of crmk, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis |
| 39 | d1luxyA1 | Alignment | not modelled | 96.5 | 10 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvyglucosamine reductase (MurB), N-terminal domain |
| 40 | c5d79B_ | Alignment | not modelled | 96.4 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana |
| 41 | c2ipiD_ | Alignment | not modelled | 96.4 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase |
| 42 | c5i6fA_ | Alignment | not modelled | 96.1 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose |
| 43 | c4bc9C_ | Alignment | not modelled | 96.1 | 13 | PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl |
| 44 | c2y3rC_ | Alignment | not modelled | 96.0 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: staml; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 tam1 in p21 space group |
| 45 | c3fwaA_ | Alignment | not modelled | 96.0 | 14 | PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline |
| 46 | c4ud8B_ | Alignment | not modelled | 95.9 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15 |
| 47 | c3d2hA_ | Alignment | not modelled | 95.8 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form |
| 48 | c1zr6A_ | Alignment | not modelled | 95.8 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation |
| 49 | c2uuvC_ | Alignment | not modelled | 95.7 | 14 | PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1 |
| 50 | c4ml8C_ | Alignment | not modelled | 95.6 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2) |
| 51 | c3vteA_ | Alignment | not modelled | 95.5 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa |
| 52 | c3popD_ | Alignment | not modelled | 95.4 | 15 | 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 |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c6eo5A_ | Alignment | not modelled | 95.3 | 19 | Chain: A: PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n |
| 54 | c3rjaA_ | Alignment | not modelled | 95.2 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue |
| 55 | c2vfvA_ | Alignment | not modelled | 95.2 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite |
| 56 | c3bw7A_ | Alignment | not modelled | 95.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1 |
| 57 | c4fdoA_ | Alignment | not modelled | 94.9 | 15 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319 |
| 58 | c1f0xA_ | Alignment | not modelled | 94.5 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme. |
| 59 | c6c80B_ | Alignment | not modelled | 94.3 | 15 | PDB header: immune system Chain: B: PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase |
| 60 | d1f0xa2 | Alignment | not modelled | 94.2 | 10 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 61 | c2exrA_ | Alignment | not modelled | 94.1 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482 |
| 62 | c3pm9A_ | Alignment | not modelled | 94.1 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution |
| 63 | c1wveB_ | Alignment | not modelled | 93.9 | 6 | PDB header: oxidoreductase Chain: B: PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit |
| 64 | c3js8A_ | Alignment | not modelled | 92.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase |
| 65 | d1wvfa2 | Alignment | not modelled | 92.3 | 6 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 66 | c2bvfa_ | Alignment | not modelled | 92.1 | 14 | 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) |
| 67 | c3w8wA_ | Alignment | not modelled | 91.9 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm |
| 68 | c6f73B_ | Alignment | not modelled | 91.8 | 21 | PDB header: flavoprotein Chain: B: PDB Molecule: mtvao615; PDBTitle: crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1 |
| 69 | c5fxpA_ | Alignment | not modelled | 91.1 | 9 | PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin |
| 70 | c1i19B_ | Alignment | not modelled | 90.4 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum |
| 71 | d2i0ka2 | Alignment | not modelled | 90.4 | 16 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 72 | c4oa1B_ | Alignment | not modelled | 88.9 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytokinin dehydrogenase 4; PDBTitle: crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup |
| 73 | d1w1oa2 | Alignment | not modelled | 88.2 | 15 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 74 | c5mu5A_ | Alignment | not modelled | 85.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of maf glycosyltransferase from magnetospirillum magneticum2 amb-1 |
| 75 | c6f74B_ | Alignment | not modelled | 85.5 | 8 | PDB header: flavoprotein Chain: B: PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1 |
| 76 | d1e8ga2 | Alignment | not modelled | 84.3 | 7 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 77 | c1ahuB_ | Alignment | not modelled | 84.3 | 10 | PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol |
| 78 | d1vqza1 | Alignment | not modelled | 79.3 | 12 | Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like |
| | | | | | | Fold: SufE/NifU |

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|----|-------------------------|-----------|--------------|------|----|--|
| 79 | d1x2ga1 | Alignment | not modelled | 77.8 | 19 | Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like |
| 80 | c1x2gB_ | Alignment | not modelled | 58.8 | 16 | PDB header: ligase Chain: B: PDB Molecule: lipoate-protein ligase a; PDBTitle: crystal structure of lipate-protein ligase a from2 escherichia coli |
| 81 | c5ibyA_ | Alignment | not modelled | 54.5 | 11 | PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-2) in complex with lipoic acid |
| 82 | c2e5aA_ | Alignment | not modelled | 52.4 | 6 | PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase 1; PDBTitle: crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp |
| 83 | c2yvsA_ | Alignment | not modelled | 44.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8 |
| 84 | d1li4a2 | Alignment | not modelled | 43.1 | 12 | Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase |
| 85 | c1vqzA_ | Alignment | not modelled | 34.5 | 14 | PDB header: ligase Chain: A: PDB Molecule: lipoate-protein ligase, putative; PDBTitle: crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution |
| 86 | d1v8ba2 | Alignment | not modelled | 30.6 | 10 | Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase |
| 87 | c5v96A_ | Alignment | not modelled | 29.8 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine |
| 88 | c3d64A_ | Alignment | not modelled | 27.7 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei |
| 89 | d1fmta1 | Alignment | not modelled | 27.7 | 22 | Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain |
| 90 | c1v8ba_ | Alignment | not modelled | 27.4 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase |
| 91 | c5uftA_ | Alignment | not modelled | 25.5 | 11 | PDB header: metal binding protein Chain: A: PDB Molecule: nitrogen-fixing nifu-like, n-terminal; PDBTitle: crystal structure of a nitrogen-fixing nifu-like protein (n-terminal)2 from brucella abortus |
| 92 | c3oneA_ | Alignment | not modelled | 25.3 | 14 | PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine |
| 93 | d1su0b_ | Alignment | not modelled | 24.0 | 16 | Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain |
| 94 | d1j3ka_ | Alignment | not modelled | 23.9 | 25 | Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases |
| 95 | c5ij6A_ | Alignment | not modelled | 23.8 | 17 | PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid |
| 96 | c3dhyC_ | Alignment | not modelled | 22.9 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors |
| 97 | d1wfa_ | Alignment | not modelled | 22.6 | 14 | Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain |
| 98 | c3n58D_ | Alignment | not modelled | 19.7 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form |
| 99 | d1e3db_ | Alignment | not modelled | 19.6 | 21 | Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit |