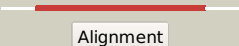



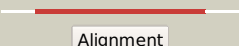





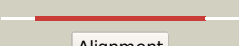













Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0770 (-) _863259_864146 |
| Date | Fri Jul 26 01:50:35 BST 2019 |
| Unique Job ID | 28751b946c1bdb16 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3cumA_ |  Alignment |  | 100.0 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1 |
| 2 | c3qhaB_ |  Alignment |  | 100.0 | 70 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104 |
| 3 | c1yb4A_ |  Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2 |
| 4 | c4dlIB_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxy-3-oxopropionate reductase; PDBTitle: crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666 |
| 5 | c3w6uA_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding protein; PDBTitle: crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum calidifontis |
| 6 | c1vpdA_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2] |
| 7 | c3ckyA_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation |
| 8 | c2gf2B_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase |
| 9 | c3g0oA_ |  Alignment |  | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium |
| 10 | c2uyyD_ |  Alignment |  | 100.0 | 22 | PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac |
| 11 | c2cvzD_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8 |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c3pefA_ | Alignment | | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+ |
| 13 | c3dojA_ | Alignment | | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1) |
| 14 | c4gjbB_ | Alignment | | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans |
| 15 | c5y8mA_ | Alignment | | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba) |
| 16 | c5u5gC_ | Alignment | | 100.0 | 24 | PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp |
| 17 | c5ojIA_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]zajepine |
| 18 | c5a9tA_ | Alignment | | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline |
| 19 | c5je8A_ | Alignment | | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad |
| 20 | c3pduF_ | Alignment | | 100.0 | 28 | PDB header: oxidoreductase Chain: F: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase family protein; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+ |
| 21 | c4d3sA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardioptis halophila |
| 22 | c3l6dB_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440 |
| 23 | c5g6sD_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline |
| 24 | c4e21B_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens |
| 25 | c4d3fB_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph |
| 26 | c5ocmA_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: nad_gly3p_dh, nad-dependent glycerol-3-phosphate PDBTitle: imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate |
| 27 | c6grIA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate PDBTitle: structure of imine reductase (apo form) at 1.6 a resolution from2 saccharomonospora xinjiangensis |
| | | Alignment | | | | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 28 | c2p4qA_ | Alignment | not modelled | 100.0 | 19 | decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae |
| 29 | c1pgjA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei |
| 30 | c4oqyA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase |
| 31 | c3fwnB_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate |
| 32 | c4oqzA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase |
| 33 | c3zhbC_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp. |
| 34 | c1pggA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism |
| 35 | c2iz1C_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data |
| 36 | c4ezbA_ | Alignment | not modelled | 100.0 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein from2 sinorhizobium meliloti 1021 |
| 37 | c6fqzB_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate |
| 38 | c3qsgA_ | Alignment | not modelled | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-binding phosphogluconate dehydrogenase-like protein; PDBTitle: crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius |
| 39 | c4wb1B_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cals8 from micromonospora echinospora (p294s2 mutant) |
| 40 | c2y0dB_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k |
| 41 | c3vtfA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum |
| 42 | c1mv8A_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa |
| 43 | c3gg2B_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate |
| 44 | c4a7pA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea |
| 45 | c2q3eH_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose |
| 46 | c3prjB_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase. |
| 47 | c4r16A_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic PDBTitle: structure of udp-d-mannac dehdrogeanse from pyrococcus horikoshii |
| 48 | c3k96B_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii |
| 49 | c1i36A_ | Alignment | not modelled | 100.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases |
| 50 | c3plnA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose |
| 51 | c2o3jC_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose |

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|----|-------------------------|-----------|--------------|-------|----|--|
| | | | | | | dehydrogenase |
| 52 | c1m67A_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine |
| 53 | c3g79A_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; PDBTitle: crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1 |
| 54 | c3ojlA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus |
| 55 | c4edfC_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e |
| 56 | c1bg6A_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c |
| 57 | c1dliA_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation |
| 58 | c1txgA_ | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus |
| 59 | c3wffD_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh |
| 60 | c2ofpB_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate |
| 61 | c5zikC_ | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa |
| 62 | c4ol9A_ | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate |
| 63 | c2ew2B_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase, putative; PDBTitle: crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis |
| 64 | d1vpda2 | Alignment | not modelled | 99.9 | 35 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 65 | c3hwrA_ | Alignment | not modelled | 99.9 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution |
| 66 | c1z82A_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution |
| 67 | c5ayvB_ | Alignment | not modelled | 99.9 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate |
| 68 | c1ks9A_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli |
| 69 | c3hn2A_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15 |
| 70 | d3cuma2 | Alignment | not modelled | 99.9 | 39 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 71 | c6c4jA_ | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution |
| 72 | c2graA_ | Alignment | not modelled | 99.9 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp |
| 73 | c3ghyA_ | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2 |
| 74 | c2izzE_ | Alignment | not modelled | 99.9 | 11 | PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase |
| 75 | c3g17H_ | Alignment | not modelled | 99.9 | 13 | PDB header: structural genomics, unknown function Chain: H: PDB Molecule: similar to 2-dehydropantoate 2-reductase; PDBTitle: structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 76 | c1vj8C_ | Alignment | not modelled | 99.9 | 10 | Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase |
| 77 | c5bseF_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: F: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of medicago truncatula (delta)1-pyrroline-5-2 carboxylate reductase (mtp5cr) |
| 78 | c1wpqB_ | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad+]; PDBTitle: ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone |
| 79 | c3triB_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii |
| 80 | c3egoB_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of probable 2-dehydropantoate 2-reductase pane from2 bacillus subtilis |
| 81 | c5t57A_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: semialdehyde dehydrogenase nad-binding protein; PDBTitle: crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad |
| 82 | d1pgja2 | Alignment | not modelled | 99.9 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 83 | c2ahrB_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes |
| 84 | d2cvza2 | Alignment | not modelled | 99.9 | 30 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 85 | c2ep9A_ | Alignment | not modelled | 99.9 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form) |
| 86 | c3d1B_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis |
| 87 | d2pgda2 | Alignment | not modelled | 99.9 | 24 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 88 | c2qytA_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83 |
| 89 | c4fgwA_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae |
| 90 | c4wjiA_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cyclohexadienyl dehydrogenase and adh prephenate PDBTitle: crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 melliloti in complex with nadp and tyrosine |
| 91 | c2rcyB_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound |
| 92 | c2pv7B_ | Alignment | not modelled | 99.9 | 14 | PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution |
| 93 | c2f1kD_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase |
| 94 | c3b1fA_ | Alignment | not modelled | 99.8 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans |
| 95 | d1i36a2 | Alignment | not modelled | 99.8 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 96 | c3dzba_ | Alignment | not modelled | 99.8 | 11 | PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus |
| 97 | c3i83B_ | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus |
| 98 | c5t8xA_ | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean |
| 99 | c4xdzB_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans |
| | | | | | | PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 100 | c3gt0A_ | Alignment | not modelled | 99.8 | 16 | PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b |
| 101 | c5n2iC_ | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound |
| 102 | c2ag8A_ | Alignment | not modelled | 99.8 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis |
| 103 | c2g5cD_ | Alignment | not modelled | 99.8 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus |
| 104 | c4ypoB_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+ |
| 105 | c4j0eB_ | Alignment | not modelled | 99.8 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhadbitis elegans in p1 space group |
| 106 | c3c7cB_ | Alignment | not modelled | 99.8 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine) |
| 107 | c4kqxB_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor |
| 108 | c4e12A_ | Alignment | not modelled | 99.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase |
| 109 | d1mv8a2 | Alignment | not modelled | 99.8 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 110 | c6c4iC_ | Alignment | not modelled | 99.8 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: yersinopine dehydrogenase; PDBTitle: yersinopine dehydrogenase (ypodh) - apo |
| 111 | c4xdyB_ | Alignment | not modelled | 99.8 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean |
| 112 | d2f1ka2 | Alignment | not modelled | 99.8 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 113 | c3ggpA_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+ |
| 114 | c1np3B_ | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa |
| 115 | c6c4nB_ | Alignment | not modelled | 99.7 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: pseudopaline dehydrogenase; PDBTitle: pseudopaline dehydrogenase (paodh) - nadp+ bound |
| 116 | c4om8B_ | Alignment | not modelled | 99.7 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 5-formly-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase. |
| 117 | d1jaya_ | Alignment | not modelled | 99.7 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 118 | c2yzc_ | Alignment | not modelled | 99.7 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: metalloreductase steap4; PDBTitle: rat steap4 oxidoreductase domain complexed with nadp |
| 119 | c6aajB_ | Alignment | not modelled | 99.7 | 13 | PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity. |
| 120 | d1n1ea2 | Alignment | not modelled | 99.7 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |