# Phyre2

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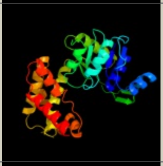
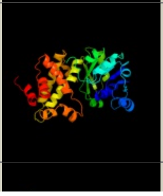
| Description | P0A9J4 |
| Date | Thu Jan 5 11:10:27 GMT 2012 |
| Unique Job ID | 75ea5dd2079ca6c0 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2ofpB_ | Alignment |  | 100.0 | 100 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ketopantoate reductase;<br>**PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate |
| 2 | c1ks9A_ | Alignment |  | 100.0 | 100 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** ketopantoate reductase from escherichia coli |
| 3 | c3g17H_ | Alignment |  | 100.0 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-reductase;<br>**PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus |
| 4 | c2ew2B_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative;<br>**PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis |
| 5 | c3egoB_ | Alignment |  | 100.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis |
| 6 | c3hn2A_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15 |
| 7 | c3i83B_ | Alignment |  | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus |
| 8 | c3hwrA_ | Alignment |  | 100.0 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution |
| 9 | c2qytA_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83 |
| 10 | c3ghyA_ | Alignment |  | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ketopantoate reductase protein;<br>**PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2 |
| 11 | c1yj8C_ | Alignment |  | 100.0 | 10 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**glycerol-3-phosphate dehydrogenase;<br>**PDBTitle:** initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase |

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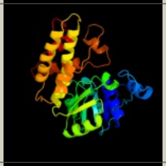
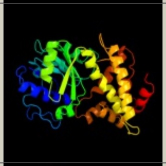
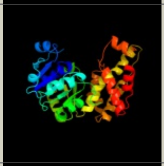
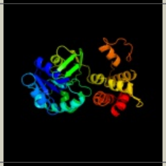
| 12 | c3k96B_ | Alignment |  | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+];<br>**PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii |
| 13 | c1z82A_ | Alignment |  | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution |
| 14 | c1wpqB_ | Alignment |  | 100.0 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad+],<br>**PDBTitle:** ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone |
| 15 | c1m67A_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine |
| 16 | c1txgA_ | Alignment |  | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+];<br>**PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus |
| 17 | c1bg6A_ | Alignment |  | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**n-(1-d-carboxylethyl)-l-norvaline dehydrogenase;<br>**PDBTitle:** crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c |
| 18 | c3c7cB_ | Alignment |  | 99.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**octopine dehydrogenase;<br>**PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine) |
| 19 | c3qhaB_ | Alignment |  | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104 |
| 20 | c3g0oA_ | Alignment |  | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase;<br>**PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium |
| 21 | c3fwnB_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating;<br>**PDBTitle:** dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate |
| 22 | c2gf2B_ | Alignment | not modelled | 99.9 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase;<br>**PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase |
| 23 | d1ks9a1 | Alignment | not modelled | 99.9 | 100 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Ketopantoate reductase PanE |
| 24 | d1ks9a2 | Alignment | not modelled | 99.9 | 100 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 25 | c3dojA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dehydrogenase-like protein;<br>**PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1) |
| 26 | c1pgjA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase;<br>**PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei |
| 27 | c2p4qA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1;<br>**PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae |
| 28 | c1yb4A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**tartronic semialdehyde reductase;<br>**PDBTitle:** crystal structure of the tartronic semialdehyde reductase |

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| | | | | | | from2 salmonella typhimurium lt2 |
| 29 | c3l6dB_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440 |
| 30 | c3ckyA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase;<br>**PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation |
| 31 | c3cumA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase;<br>**PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1 |
| 32 | c2uyyD_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**cytokine<br>**Chain:** D: **PDB Molecule:**n-pac protein;<br>**PDBTitle:** structure of the cytokine-like nuclear factor n-pac |
| 33 | c2iz1C_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating;<br>**PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data |
| 34 | c1mv8A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**gdp-mannose 6-dehydrogenase;<br>**PDBTitle:** 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa |
| 35 | c2y0dB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase;<br>**PDBTitle:** bcec mutation y10k |
| 36 | c1vpdA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase;<br>**PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2] |
| 37 | c3gg2B_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose<br>**PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate |
| 38 | c1pgqA_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**oxidoreductase (choh(d)-nadp+(a))<br>**Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase;<br>**PDBTitle:** crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism |
| 39 | c2cvzD_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase;<br>**PDBTitle:** structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8 |
| 40 | c3pduF_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein;<br>**PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+ |
| 41 | c3qsgA_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**nad-binding phosphogluconate dehydrogenase-like protein;<br>**PDBTitle:** crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius |
| 42 | c3pefA_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, nad-binding;<br>**PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+ |
| 43 | c2q3eH_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase;<br>**PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose |
| 44 | c3prjB_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase;<br>**PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase. |
| 45 | c2o3jC_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase;<br>**PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase |
| 46 | c3plnA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase;<br>**PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose |
| 47 | c2izzE_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**pyrroline-5-carboxylate reductase 1;<br>**PDBTitle:** crystal structure of human pyrroline-5-carboxylate2 reductase |
| 48 | c1dliA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**udp-glucose dehydrogenase;<br>**PDBTitle:** the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation |
| 49 | c2graA_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase 1;<br>**PDBTitle:** crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp |
| 50 | c3d1lB_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122;<br>**PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis |
| 51 | c1i36A_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747;<br>**PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases |

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| 52 | d1txga2 | Alignment | not modelled | 99.7 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 53 | c2f1kD_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase |
| 54 | c3ojlA_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cap5o;<br>**PDBTitle:** native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus |
| 55 | c3g79A_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase;<br>**PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1 |
| 56 | d1bg6a2 | Alignment | not modelled | 99.7 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 57 | d1n1ea2 | Alignment | not modelled | 99.7 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 58 | c3triB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**pyrroline-5-carboxylate reductase;<br>**PDBTitle:** structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii |
| 59 | d1jaya_ | Alignment | not modelled | 99.7 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 60 | c2ahrB_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative pyrroline carboxylate reductase;<br>**PDBTitle:** crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes |
| 61 | d2f1ka2 | Alignment | not modelled | 99.7 | 18 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 62 | c2pv7B_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**isomerase, oxidoreductase<br>**Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm)<br>**PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution |
| 63 | c2ep9A_ | Alignment | not modelled | 99.6 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase;<br>**PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form) |
| 64 | c3gt0A_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase;<br>**PDBTitle:** crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b |
| 65 | d1vpda2 | Alignment | not modelled | 99.6 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 66 | d2pgda2 | Alignment | not modelled | 99.6 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 67 | c3dttA_ | Alignment | not modelled | 99.6 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadp oxidoreductase;<br>**PDBTitle:** crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution |
| 68 | d1i36a2 | Alignment | not modelled | 99.6 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 69 | d1mv8a2 | Alignment | not modelled | 99.6 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 70 | c2rcyB_ | Alignment | not modelled | 99.6 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase;<br>**PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound |
| 71 | d3cuma2 | Alignment | not modelled | 99.6 | 14 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 72 | c2g5cD_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus |
| 73 | c3b1fA_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans |
| 74 | c2ag8A_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase;<br>**PDBTitle:** nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis |
| 75 | c3dzbA_ | Alignment | not modelled | 99.6 | 11 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus |
| 76 | d1pgja2 | Alignment | not modelled | 99.5 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains |

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|---|---|---|---|---|---|---|
| 76 | d1pgja2 | Alignment | not modelled | 99.5 | 11 | **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 77 | d2ahra2 | Alignment | not modelled | 99.5 | 15 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 78 | d1f0ya2 | Alignment | not modelled | 99.5 | 10 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 79 | c3ggpA_ | Alignment | not modelled | 99.5 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+ |
| 80 | d1dlja2 | Alignment | not modelled | 99.5 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 81 | c1m75B_ | Alignment | not modelled | 99.5 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa |
| 82 | d2cvza2 | Alignment | not modelled | 99.5 | 14 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 83 | d1yqga2 | Alignment | not modelled | 99.5 | 18 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 84 | c3c24A_ | Alignment | not modelled | 99.4 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution |
| 85 | d1wdka3 | Alignment | not modelled | 99.4 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 86 | c2vq3B_ | Alignment | not modelled | 99.4 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**metalloreductase steap3;<br>**PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle |
| 87 | c3ktdC_ | Alignment | not modelled | 99.4 | 11 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**prephenate dehydrogenase;<br>**PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution |
| 88 | c1zcjA_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme;<br>**PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase |
| 89 | c3k6jA_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence;<br>**PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans |
| 90 | c1np3B_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase;<br>**PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa |
| 91 | d2pv7a2 | Alignment | not modelled | 99.4 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 92 | c3mogA_ | Alignment | not modelled | 99.4 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655 |
| 93 | d2g5ca2 | Alignment | not modelled | 99.4 | 14 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 94 | c2i76B_ | Alignment | not modelled | 99.3 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of protein tm1727 from thermotoga maritima |
| 95 | c2x58B_ | Alignment | not modelled | 99.3 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme;<br>**PDBTitle:** the crystal structure of mfe1 liganded with coa |
| 96 | c2wtbA_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2);<br>**PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2 |
| 97 | c2d3tB_ | Alignment | not modelled | 99.2 | 11 | **PDB header:**lyase, oxidoreductase/transferase<br>**Chain:** B: **PDB Molecule:**fatty acid oxidation complex alpha subunit;<br>**PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v |
| 98 | d2i76a2 | Alignment | not modelled | 99.2 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 99 | c2rafC_ | Alignment | not modelled | 99.1 | 14 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase;<br>**PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution |
| 100 | d1np3a2 | Alignment | not modelled | 99.1 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |

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|---|---|---|---|---|---|---|
| 101 | c1zejA_ | Alignment | not modelled | 99.1 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution |
| 102 | d1uxja1 | Alignment | not modelled | 99.0 | 20 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 103 | d1gv0a1 | Alignment | not modelled | 98.9 | 21 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 104 | d1ojua1 | Alignment | not modelled | 98.9 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 105 | d1a5za1 | Alignment | not modelled | 98.9 | 21 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 106 | d1ez4a1 | Alignment | not modelled | 98.8 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 107 | d1guza1 | Alignment | not modelled | 98.8 | 21 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 108 | d9ldta1 | Alignment | not modelled | 98.8 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 109 | d1i10a1 | Alignment | not modelled | 98.8 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 110 | d1t2da1 | Alignment | not modelled | 98.7 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 111 | d1obba1 | Alignment | not modelled | 98.7 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 112 | d1hyha1 | Alignment | not modelled | 98.7 | 23 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 113 | c3dfuB_ | Alignment | not modelled | 98.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**uncharacterized protein from 6-phosphogluconate<br>**PDBTitle:** crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution |
| 114 | c8ldhA_ | Alignment | not modelled | 98.7 | 21 | **PDB header:**oxidoreductase(choh(d)-nad(a))<br>**Chain:** A: **PDB Molecule:**m4 apo-lactate dehydrogenase;<br>**PDBTitle:** refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase |
| 115 | d1ldma1 | Alignment | not modelled | 98.7 | 21 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 116 | d1i0za1 | Alignment | not modelled | 98.7 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 117 | d1y6ja1 | Alignment | not modelled | 98.7 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 118 | c1ojuA_ | Alignment | not modelled | 98.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**malate dehydrogenase;<br>**PDBTitle:** 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad. |
| 119 | c3ic5A_ | Alignment | not modelled | 98.7 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase;<br>**PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi. |
| 120 | d1llda1 | Alignment | not modelled | 98.7 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |