





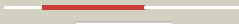


























| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3dmyA_ |  Alignment |  | 100.0 | 96 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli |
| 2 | c2csuB_ |  Alignment |  | 100.0 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3 |
| 3 | c3mwdB_ |  Alignment |  | 100.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound |
| 4 | c2nu8D_ |  Alignment |  | 100.0 | 18 | PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase |
| 5 | c2fpgA_ |  Alignment |  | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp |
| 6 | c2yv2A_ |  Alignment |  | 100.0 | 21 | PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1 |
| 7 | c2yv1A_ |  Alignment |  | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661 |
| 8 | c1oi7A_ |  Alignment |  | 100.0 | 18 | PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus |
| 9 | d1euca2 |  Alignment |  | 100.0 | 20 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 10 | d2nu7a2 |  Alignment |  | 100.0 | 19 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 11 | d1oi7a2 |  Alignment |  | 100.0 | 23 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | d2csua2 | Alignment |  | 100.0 | 20 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 13 | d2csua3 | Alignment |  | 99.9 | 14 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 14 | d2nu7b1 | Alignment |  | 99.6 | 16 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 15 | d1eucb1 | Alignment |  | 99.5 | 20 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 16 | c2duwA | Alignment |  | 99.4 | 17 | PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae |
| 17 | d2csua1 | Alignment |  | 99.4 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 18 | c2nu9E | Alignment |  | 99.3 | 17 | PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form |
| 19 | d1iuka | Alignment |  | 99.2 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 20 | d1y81a1 | Alignment |  | 99.2 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 21 | c1eucB | Alignment | not modelled | 99.1 | 22 | PDB header: ligase Chain: B: PDB Molecule: succinyl-coa synthetase, beta chain; PDBTitle: crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase |
| 22 | d2nu7a1 | Alignment | not modelled | 99.1 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 23 | d1euca1 | Alignment | not modelled | 99.1 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 24 | d1oi7a1 | Alignment | not modelled | 99.1 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 25 | d2d59a1 | Alignment | not modelled | 99.0 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 26 | c3ff4A | Alignment | not modelled | 98.6 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412 |
| 27 | c3e18A | Alignment | not modelled | 97.4 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua |
| 28 | c3moiA | Alignment | not modelled | 97.4 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50 |
| 29 | c3m2tA | Alignment | not modelled | 97.4 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3m2A | Alignment | not modelled | 97.4 | 14 | PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae |
| 30 | c3dtyA | Alignment | not modelled | 97.3 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae |
| 31 | c3fd8A | Alignment | not modelled | 97.3 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis |
| 32 | c3oqbF | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110 |
| 33 | c2q4eB | Alignment | not modelled | 97.2 | 9 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670 |
| 34 | c3rbvA | Alignment | not modelled | 97.2 | 21 | PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata in complex with nadp |
| 35 | c3q2kB | Alignment | not modelled | 97.2 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaC |
| 36 | c3f4lF | Alignment | not modelled | 97.1 | 22 | PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647 |
| 37 | c3btuD | Alignment | not modelled | 97.1 | 15 | PDB header: transcription protein Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k] |
| 38 | c3evnA | Alignment | not modelled | 97.1 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r |
| 39 | c2ixaA | Alignment | not modelled | 97.1 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetyl galactosaminidase; PDBTitle: a-zyme, n-acetyl galactosaminidase |
| 40 | d1lc0a1 | Alignment | not modelled | 97.1 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 41 | c3ec7C | Alignment | not modelled | 97.1 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2 |
| 42 | d1h6da1 | Alignment | not modelled | 97.1 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 43 | c2o48X | Alignment | not modelled | 97.1 | 16 | PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase |
| 44 | c3kuxA | Alignment | not modelled | 97.1 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis |
| 45 | c3db2C | Alignment | not modelled | 97.0 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfotobacterium hafniense dcb-2 at 1.70 a3 resolution |
| 46 | c2p2sA | Alignment | not modelled | 97.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution |
| 47 | c3e9mC | Alignment | not modelled | 97.0 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis |
| 48 | c3e82A | Alignment | not modelled | 97.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae |
| 49 | c1zh8B | Alignment | not modelled | 97.0 | 9 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution |
| 50 | c1lc3A | Alignment | not modelled | 96.9 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex |
| 51 | c3ip3D | Alignment | not modelled | 96.9 | 12 | PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima |
| 52 | c1h6dL | Alignment | not modelled | 96.9 | 18 | PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol |
| 53 | c1ofgF | Alignment | not modelled | 96.9 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c1drwA_ | Alignment | not modelled | 96.9 | 10 | Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex |
| 55 | c3gfgB_ | Alignment | not modelled | 96.9 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form |
| 56 | c2glxD_ | Alignment | not modelled | 96.9 | 24 | PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase |
| 57 | c3nt5B_ | Alignment | not modelled | 96.9 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose |
| 58 | c3fhIC_ | Alignment | not modelled | 96.9 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343 |
| 59 | c3ezyB_ | Alignment | not modelled | 96.8 | 10 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima |
| 60 | c1evjC_ | Alignment | not modelled | 96.8 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d |
| 61 | d1ydw1 | Alignment | not modelled | 96.8 | 8 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 62 | c3c1aB_ | Alignment | not modelled | 96.8 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution |
| 63 | c2ho3D_ | Alignment | not modelled | 96.7 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/ldh/moca family from2 streptococcus pneumoniae |
| 64 | c1xeaD_ | Alignment | not modelled | 96.7 | 12 | PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of a gfo/ldh/moca family oxidoreductase2 from vibrio cholerae |
| 65 | c1e5IA_ | Alignment | not modelled | 96.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea |
| 66 | c3euwB_ | Alignment | not modelled | 96.6 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032 |
| 67 | d1ryda1 | Alignment | not modelled | 96.6 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 68 | c3mwdA_ | Alignment | not modelled | 96.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound |
| 69 | d1zh8a1 | Alignment | not modelled | 96.4 | 9 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 70 | c3bioB_ | Alignment | not modelled | 96.4 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/ldh/moca family member) from2 porphyromonas gingivalis w83 |
| 71 | c3oa2B_ | Alignment | not modelled | 96.4 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution |
| 72 | c3oa0B_ | Alignment | not modelled | 96.3 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: lipopolysaccharide biosynthesis protein wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glnaca |
| 73 | c3v5nA_ | Alignment | not modelled | 96.3 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti |
| 74 | d1xeaa1 | Alignment | not modelled | 96.3 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 75 | c2dc1A_ | Alignment | not modelled | 96.3 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus |
| 76 | c3ceaA_ | Alignment | not modelled | 96.2 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution |
| 77 | c3ijpA_ | Alignment | not modelled | 96.2 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution |
| 78 | d2nvwa1 | Alignment | not modelled | 96.1 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| | | | | | | PDB header: oxidoreductase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 79 | c2axqA | Alignment | not modelled | 96.0 | 15 | Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae |
| 80 | d1diha1 | Alignment | not modelled | 96.0 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 81 | d1j5pa4 | Alignment | not modelled | 95.9 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 82 | c3do5A | Alignment | not modelled | 95.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution |
| 83 | c3uuwB | Alignment | not modelled | 95.5 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile. |
| 84 | c3dapB | Alignment | not modelled | 95.4 | 8 | PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline |
| 85 | c1j5pA | Alignment | not modelled | 95.2 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution |
| 86 | d1tita1 | Alignment | not modelled | 95.2 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 87 | c2vt2A | Alignment | not modelled | 95.0 | 12 | PDB header: transcription Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: structure and functional properties of the bacillus2 subtilis transcriptional repressor rex |
| 88 | c1titB | Alignment | not modelled | 95.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog) |
| 89 | d2g0ta1 | Alignment | not modelled | 94.9 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 90 | c2z2vA | Alignment | not modelled | 94.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii |
| 91 | c2dt5A | Alignment | not modelled | 94.7 | 11 | PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8 |
| 92 | d1f06a1 | Alignment | not modelled | 94.6 | 8 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 93 | c2nvwB | Alignment | not modelled | 94.4 | 14 | PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluyveromyces lactis |
| 94 | c3ketA | Alignment | not modelled | 94.1 | 15 | PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator |
| 95 | d2dt5a2 | Alignment | not modelled | 93.6 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain |
| 96 | c3bezC | Alignment | not modelled | 92.9 | 22 | PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals |
| 97 | c1pgiA | Alignment | not modelled | 92.3 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei |
| 98 | c3ic5A | Alignment | not modelled | 92.2 | 7 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi. |
| 99 | c2iexA | Alignment | not modelled | 92.0 | 18 | PDB header: lyase Chain: A: PDB Molecule: dihydroxynapthoic acid synthetase; PDBTitle: crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426 |
| 100 | c1yl7F | Alignment | not modelled | 90.9 | 10 | PDB header: oxidoreductase Chain: F: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c) |
| 101 | c2obnA | Alignment | not modelled | 90.7 | 16 | PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution |
| 102 | d1ebfa1 | Alignment | not modelled | 90.5 | 9 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| | | | | | | PDB header: oxidoreductase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 103 | c2p4qA_ | Alignment | not modelled | 90.5 | 13 | Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae |
| 104 | c1vm6B_ | Alignment | not modelled | 90.3 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution |
| 105 | dlq52a_ | Alignment | not modelled | 89.6 | 16 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 106 | d1vm6a3 | Alignment | not modelled | 89.5 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 107 | c3mtjA_ | Alignment | not modelled | 89.4 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a |
| 108 | d1yl7a1 | Alignment | not modelled | 89.2 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 109 | d1rjma_ | Alignment | not modelled | 89.0 | 16 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 110 | c2iz1C_ | Alignment | not modelled | 88.8 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data |
| 111 | c3fwnB_ | Alignment | not modelled | 88.7 | 16 | 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 |
| 112 | c1pggA_ | Alignment | not modelled | 88.4 | 16 | 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 |
| 113 | c3h02F_ | Alignment | not modelled | 88.3 | 20 | PDB header: lyase Chain: F: PDB Molecule: naphthoate synthase; PDBTitle: 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium. |
| 114 | c2ejwB_ | Alignment | not modelled | 87.5 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8 |
| 115 | c3p5mB_ | Alignment | not modelled | 86.6 | 20 | PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium |
| 116 | c2ozpA_ | Alignment | not modelled | 85.9 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tha1904) from thermus thermophilus |
| 117 | c2vbiF_ | Alignment | not modelled | 85.3 | 13 | PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus |
| 118 | c3rsiA_ | Alignment | not modelled | 85.3 | 18 | PDB header: isomerase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196 |
| 119 | c1zpdA_ | Alignment | not modelled | 85.3 | 17 | PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis |
| 120 | c3p21D_ | Alignment | not modelled | 85.2 | 12 | PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis |