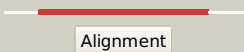

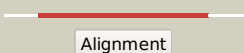

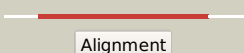

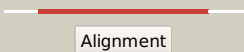

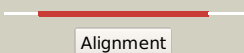

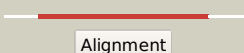

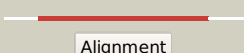





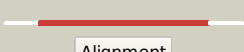

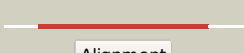












Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0952_(sucD)_1063144_1064055 |
| Date | Fri Jul 26 01:50:54 BST 2019 |
| Unique Job ID | 4069498e1523b181 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2fpgA_ |  Alignment |  | 100.0 | 49 | PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp |
| 2 | c2nu8D_ |  Alignment |  | 100.0 | 52 | PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase |
| 3 | c6melA_ |  Alignment |  | 100.0 | 49 | PDB header: ligase Chain: A: PDB Molecule: succinate--coa ligase subunit alpha; PDBTitle: succinyl-coa synthase from campylobacter jejuni |
| 4 | c4yajA_ |  Alignment |  | 100.0 | 19 | PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form) |
| 5 | c6hxiD_ |  Alignment |  | 100.0 | 27 | PDB header: lyase Chain: D: PDB Molecule: succinyl-coa ligase (adp-forming) subunit alpha; PDBTitle: structure of atp citrate lyase from methanothrix soehngenii in complex2 with citrate and coenzyme a |
| 6 | c6hxqA_ |  Alignment |  | 100.0 | 34 | PDB header: lyase Chain: A: PDB Molecule: citryl-coa synthetase small subunit; PDBTitle: structure of citryl-coa synthetase from hydrogenobacter thermophilus |
| 7 | c3mwdB_ |  Alignment |  | 100.0 | 25 | PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound |
| 8 | c2yv2A_ |  Alignment |  | 100.0 | 47 | 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 |
| 9 | c2csuB_ |  Alignment |  | 100.0 | 23 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3 |
| 10 | c1oi7A_ |  Alignment |  | 100.0 | 46 | 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 |
| 11 | c6hxiB_ |  Alignment |  | 100.0 | 29 | PDB header: lyase Chain: B: PDB Molecule: atp-citrate lyase alpha-subunit; PDBTitle: structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a. |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | c2yv1A_ | Alignment |  | 100.0 | 50 | 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 |
| 13 | c6qfbB_ | Alignment |  | 100.0 | 31 | PDB header: lyase Chain: B; PDB Molecule: atp-citrate synthase; PDBTitle: structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp |
| 14 | c3dmyA_ | Alignment |  | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli |
| 15 | d1euca2 | Alignment |  | 100.0 | 47 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 16 | d2nu7a2 | Alignment |  | 100.0 | 55 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 17 | d1oi7a2 | Alignment |  | 100.0 | 47 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 18 | d2csua2 | Alignment |  | 100.0 | 18 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 19 | d2csua1 | Alignment |  | 100.0 | 22 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 20 | d2d59a1 | Alignment |  | 99.9 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 21 | c2duwA_ | Alignment | not modelled | 99.9 | 21 | PDB header: ligand binding protein Chain: A; PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae |
| 22 | d1y81a1 | Alignment | not modelled | 99.9 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 23 | d1euca1 | Alignment | not modelled | 99.9 | 51 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 24 | d1iuka_ | Alignment | not modelled | 99.9 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 25 | d2nu7a1 | Alignment | not modelled | 99.9 | 48 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 26 | d1oi7a1 | Alignment | not modelled | 99.9 | 46 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 27 | c3ff4A_ | Alignment | not modelled | 99.8 | 9 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412 |
| 28 | c5z2fa_ | Alignment | not modelled | 99.1 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14 |
| 29 | c5ugjC_ | Alignment | not modelled | 98.9 | 15 | PDB header: oxidoreductase Chain: C; PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | meningitidis |
| 30 | c5kt0A | Alignment | not modelled | 98.8 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis. |
| 31 | c4f3yA | Alignment | not modelled | 98.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis |
| 32 | c1drwA | Alignment | not modelled | 98.7 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex |
| 33 | c3wg9D | Alignment | not modelled | 98.6 | 18 | PDB header: transcription Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of rsp, a rex-family repressor |
| 34 | c4ywjB | Alignment | not modelled | 98.6 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa |
| 35 | c5tenH | Alignment | not modelled | 98.5 | 17 | PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag |
| 36 | c3ijpA | Alignment | not modelled | 98.5 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution |
| 37 | c3ketA | Alignment | not modelled | 98.5 | 21 | 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 |
| 38 | d1eucb1 | Alignment | not modelled | 98.5 | 20 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 39 | c3wb9A | Alignment | not modelled | 98.5 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum |
| 40 | d2nu7b1 | Alignment | not modelled | 98.5 | 21 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 41 | c5zz5D | Alignment | not modelled | 98.5 | 19 | PDB header: gene regulation Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: redox-sensing transcriptional repressor rex |
| 42 | d1dih1 | Alignment | not modelled | 98.4 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 43 | c6iaqA | Alignment | not modelled | 98.4 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis |
| 44 | c3bioB | Alignment | not modelled | 98.4 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83 |
| 45 | c2dt5A | Alignment | not modelled | 98.4 | 15 | 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 |
| 46 | d2csua3 | Alignment | not modelled | 98.4 | 21 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 47 | c2dc1A | Alignment | not modelled | 98.3 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus |
| 48 | c5wo1A | Alignment | not modelled | 98.3 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii |
| 49 | c3ufxG | Alignment | not modelled | 98.2 | 10 | PDB header: ligase Chain: G: PDB Molecule: succinyl-coa synthetase beta subunit; PDBTitle: thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+ |
| 50 | c3e18A | Alignment | not modelled | 98.2 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua |
| 51 | c6norB | Alignment | not modelled | 98.2 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad |
| 52 | c3db2C | Alignment | not modelled | 98.1 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution |
| | | | | | | Fold: NAD(P)-binding Rossmann-fold domains |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | d1ydwa1 | Alignment | not modelled | 98.1 | 13 | Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 54 | c3evnA | Alignment | not modelled | 98.1 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r |
| 55 | c3wgzB | Alignment | not modelled | 98.1 | 9 | PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate dehydrogenase; PDBTitle: crystal structure of meso-dapdh q154l/t173l/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88 |
| 56 | d1f06a1 | Alignment | not modelled | 98.1 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 57 | c6me1B | Alignment | not modelled | 98.0 | 24 | PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: succinyl-coa synthase from campylobacter jejuni |
| 58 | c2nu9E | Alignment | not modelled | 98.0 | 20 | PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form |
| 59 | c5u5iA | Alignment | not modelled | 98.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: htpa reductase; PDBTitle: the dimeric crystal structure of the selenomethionine derivative of2 htpa reductase from sellaginella moellendorffii |
| 60 | c3dapB | Alignment | not modelled | 98.0 | 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 |
| 61 | c5b3uB | Alignment | not modelled | 98.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803 |
| 62 | d2dt5a2 | Alignment | not modelled | 98.0 | 12 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain |
| 63 | c3euwB | Alignment | not modelled | 98.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032 |
| 64 | c5ua0B | Alignment | not modelled | 98.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase 2, PDBTitle: dimeric crystal structure of htpa reductase from arabidopsis thaliana |
| 65 | c1yl7F | Alignment | not modelled | 98.0 | 23 | 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) |
| 66 | c6g1mA | Alignment | not modelled | 98.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form |
| 67 | c5eesA | Alignment | not modelled | 98.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dapb in complex with nadp+ from corynebacterium2 glutamicum |
| 68 | c1eucB | Alignment | not modelled | 98.0 | 21 | 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 |
| 69 | c5uibA | Alignment | not modelled | 98.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium |
| 70 | c1t4bB | Alignment | not modelled | 98.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: 1.6 angstrom structure of escherichia coli aspartate-2 semialdehyde dehydrogenase. |
| 71 | c3q2kB | Alignment | not modelled | 97.9 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna |
| 72 | d1yl7a1 | Alignment | not modelled | 97.9 | 22 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 73 | c6iauB | Alignment | not modelled | 97.9 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine |
| 74 | c6g4qB | Alignment | not modelled | 97.9 | 19 | PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase complex suc1g1-2 suc1a2 |
| 75 | c2vt2A | Alignment | not modelled | 97.9 | 28 | PDB header: transcription Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: structure and functional properties of the bacillus subtilis2 transcriptional repressor rex |
| 76 | c4miyB | Alignment | not modelled | 97.9 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 77 | c2glxD_ | Alignment | not modelled | 97.9 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase |
| 78 | c2p2sA_ | Alignment | not modelled | 97.9 | 15 | 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 |
| 79 | c4gmfD_ | Alignment | not modelled | 97.9 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3) |
| 80 | c3e9mC_ | Alignment | not modelled | 97.8 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis |
| 81 | c2q4eB_ | Alignment | not modelled | 97.8 | 14 | 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 |
| 82 | c3fhIC_ | Alignment | not modelled | 97.8 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343 |
| 83 | c3c1aB_ | Alignment | not modelled | 97.8 | 9 | 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 |
| 84 | c3ceaA_ | Alignment | not modelled | 97.8 | 16 | 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 |
| 85 | c3ec7C_ | Alignment | not modelled | 97.8 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2 |
| 86 | c3f4IF_ | Alignment | not modelled | 97.8 | 13 | 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 |
| 87 | c3ezyB_ | Alignment | not modelled | 97.8 | 10 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima |
| 88 | c4hktA_ | Alignment | not modelled | 97.8 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312) |
| 89 | c2o48X_ | Alignment | not modelled | 97.8 | 16 | PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase |
| 90 | d1lc0a1 | Alignment | not modelled | 97.7 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 91 | c3oa2B_ | Alignment | not modelled | 97.7 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: wbpb; PDBTitle: crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution |
| 92 | c3wycB_ | Alignment | not modelled | 97.7 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp |
| 93 | c3rbvA_ | Alignment | not modelled | 97.7 | 12 | 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 |
| 94 | c1zh8B_ | Alignment | not modelled | 97.7 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution |
| 95 | c4wojB_ | Alignment | not modelled | 97.7 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate semialdehyde dehydrogenase; PDBTitle: aspartate semialdehyde dehydrogenase from francisella tularensis |
| 96 | c3e82A_ | Alignment | not modelled | 97.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae |
| 97 | c3kuxA_ | Alignment | not modelled | 97.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis |
| 98 | c3gfgB_ | Alignment | not modelled | 97.7 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form |
| 99 | c4gqaC_ | Alignment | not modelled | 97.6 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae |
| 100 | c3moiA_ | Alignment | not modelled | 97.6 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50 |
| 101 | c3uw3A_ | Alignment | not modelled | 97.6 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 102 | c3u3xj_ | Alignment | not modelled | 97.6 | 16 | PDB header: oxidoreductase Chain: J: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021 |
| 103 | c2ixaA_ | Alignment | not modelled | 97.6 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase |
| 104 | c4mkzA_ | Alignment | not modelled | 97.6 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k |
| 105 | c4fb5A_ | Alignment | not modelled | 97.6 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a probable oxidoreductase protein |
| 106 | c1mb4B_ | Alignment | not modelled | 97.6 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase from vibrio2 cholerae with nadp and s-methyl-l-cysteine sulfoxide |
| 107 | c6jnkA_ | Alignment | not modelled | 97.6 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p(+))); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form) |
| 108 | c3btuD_ | Alignment | not modelled | 97.6 | 15 | PDB header: transcription 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] |
| 109 | c1lc3A_ | Alignment | not modelled | 97.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex |
| 110 | c1j5pA_ | Alignment | not modelled | 97.6 | 9 | PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution |
| 111 | c3nt5B_ | Alignment | not modelled | 97.6 | 17 | 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 |
| 112 | d2nvwa1 | Alignment | not modelled | 97.6 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 113 | c2nvwB_ | Alignment | not modelled | 97.6 | 16 | PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal scture of transcriptional regulator gal80p from2 kluyveromyces lactis |
| 114 | c4h3vA_ | Alignment | not modelled | 97.6 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: oxidoreductase domain protein; PDBTitle: crystal structure of oxidoreductase domain protein from kribbella2 flavida |
| 115 | c3m2tA_ | Alignment | not modelled | 97.6 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum |
| 116 | c3v5nA_ | Alignment | not modelled | 97.5 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti |
| 117 | c6a3fB_ | Alignment | not modelled | 97.5 | 9 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative dehydrogenase; PDBTitle: levoglucosan dehydrogenase, apo form |
| 118 | c5a06E_ | Alignment | not modelled | 97.5 | 8 | PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol |
| 119 | c1h6dL_ | Alignment | not modelled | 97.5 | 12 | PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose PDBTitle: oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol |
| 120 | c1ofgF_ | Alignment | not modelled | 97.5 | 12 | PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase |