

Phyre²

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| Email | mdejesus@rockefeller.edu |
| Description | RVBD1869c_(-)_2119467_2120702 |
| Date | Fri Aug 2 13:30:48 BST 2019 |
| Unique Job ID | da14e56f3e5fb6d9 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|------------------------|---|---|------------|--------|---|
| 1 | c3lxdA |  |  | 100.0 | 39 | PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans |
| 2 | c3fg2P |  |  | 100.0 | 33 | PDB header: oxidoreductase Chain: P: PDB Molecule: putative rubredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodopseudomonas palustris |
| 3 | c1q1wA |  |  | 100.0 | 37 | PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from2 pseudomonas putida |
| 4 | c2gr2A |  |  | 100.0 | 37 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form) |
| 5 | c3ef6A |  |  | 100.0 | 34 | PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin-nad(+) PDBTitle: crystal structure of toluene 2,3-dioxygenase reductase |
| 6 | c3ntaA |  |  | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase |
| 7 | c3icrA |  |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd |
| 8 | c2cdub |  |  | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadph oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis |
| 9 | c1nhqA |  |  | 100.0 | 20 | PDB header: oxidoreductase (h2o2(a)) Chain: A: PDB Molecule: nahd peroxidase; PDBTitle: crystallographic analyses of nahd peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303 |
| 10 | c3oc4A |  |  | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, pyridine nucleotide-disulfide family; PDBTitle: crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583 |
| 11 | c5jciA |  |  | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: os09g0567300 protein; PDBTitle: structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica |

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|----|------------------------|-----------|---|-------|----|--|
| 12 | c1gv4A | Alignment |  | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif) |
| 13 | c2bcpA | Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide |
| 14 | c1yqzA | Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution |
| 15 | c3iwaA | Alignment |  | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris |
| 16 | c3kd9B | Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii |
| 17 | c5er0D | Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: D: PDB Molecule: nadh oxidase; PDBTitle: water-forming nadh oxidase from lactobacillus brevis (lbnox) |
| 18 | c5w1jA | Alignment |  | 100.0 | 21 | PDB header: signaling protein Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: echinococcus granulosus thioredoxin glutathione reductas (egtgr) |
| 19 | c3cgdB | Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase, class i; PDBTitle: pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity |
| 20 | c1m6iA | Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif) |
| 21 | c3kljA | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal) PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum |
| 22 | c2v3aA | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin reductase; PDBTitle: crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa. |
| 23 | c2v6oA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr) |
| 24 | c4dnaA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable glutathione reductase; PDBTitle: crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021 |
| 25 | c2qaeA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase |
| 26 | c1tytA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase, oxidized form; PDBTitle: crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution |
| 27 | c2eq7B | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo |
| 28 | c3ubrh | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; |

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|----|------------------------|-----------|--------------|-------|----|---|
| 28 | c5qntD | Alignment | not modelled | 100.0 | 20 | PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021 PDB header: oxidoreductase |
| 29 | c1zmcG | Alignment | not modelled | 100.0 | 19 | Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+ |
| 30 | c6aonB | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad |
| 31 | c2c3dB | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxopropyl-com reductase; PDBTitle: 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site |
| 32 | c1ojtA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase |
| 33 | c1lvIA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution |
| 34 | c2w0hA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph |
| 35 | c1dxIC | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum |
| 36 | c1ndaD | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state |
| 37 | c6bz0C | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from acinetobacter baumannii in complex with fad. |
| 38 | c1ebdB | Alignment | not modelled | 100.0 | 21 | PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase |
| 39 | c5v36A | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad |
| 40 | c1xdia | Alignment | not modelled | 100.0 | 23 | PDB header: unknown function Chain: A: PDB Molecule: rv3303c-lpda; PDBTitle: crystal structure of lpda (rv3303c) from mycobacterium tuberculosis |
| 41 | c1v59B | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+ |
| 42 | c4jdrB | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli |
| 43 | c1lpfB | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties |
| 44 | c1zx9A | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera |
| 45 | c6du7C | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae |
| 46 | c2nvkX | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster |
| 47 | c2eq8E | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp |
| 48 | c2r9zB | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile |
| 49 | c3dgzA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation |
| 50 | c1zkqA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2 |
| 51 | c1geuA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site |
| 52 | c4j56A | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex |
| 53 | c3ic9D | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; |

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| 53 | c3ic5D | Alignment | not modelled | 100.0 | 19 | PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h. PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus |
| 54 | c3I8KB | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad |
| 55 | c6b4oB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate |
| 56 | c1bwca | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae |
| 57 | c3o0hA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae |
| 58 | c4ywoA | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: mercuric reductase from metallosphaera sedula |
| 59 | c1onfA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase |
| 60 | c2a8xA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis |
| 61 | c2cfyB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1 |
| 62 | c2hqmb | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae |
| 63 | c5x1yC | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: mercuric reductase; PDBTitle: structure of mercuric reductase from lysinibacillus sphaericus |
| 64 | c4b1bB | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom |
| 65 | c1xhcA | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase /nitrite reductase; PDBTitle: nadh oxidase /nitrite reductase from pyrococcus furiosus pfu-1140779-2 001 |
| 66 | c5jwca | Alignment | not modelled | 100.0 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: nadh dehydrogenase, putative; PDBTitle: structure of ndh2 from plasmodium falciparum in complex with ryl-552 |
| 67 | c6mp5B | Alignment | not modelled | 100.0 | 16 | PDB header: membrane protein, oxidoreductase Chain: B: PDB Molecule: sulfide:quinone oxidoreductase, mitochondrial; PDBTitle: crystal structure of native human sulfide:quinone oxidoreductase |
| 68 | c3hyxC | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: sulfide:quinone reductase; PDBTitle: 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c |
| 69 | c4xdbC | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase, membrane protein, flavop Chain: C: PDB Molecule: nadh dehydrogenase-like protein saouhsc_00878; PDBTitle: nadh:quinone oxidoreductase (ndh-ii) from staphylococcus aureus -2 holoprotein structure |
| 70 | c4nwzA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus thermarum at 2.5a resolution |
| 71 | c5n1tA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-binding subunit of sulfide dehydrogenase; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus |
| 72 | c1hyuA | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf |
| 73 | c1fcdb | Alignment | not modelled | 100.0 | 18 | PDB header: electron transport(flavocytochrome) Chain: B: PDB Molecule: flavocytochrome c sulfide dehydrogenase (flavin- PDBTitle: the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3.2 angstroms resolution |
| 74 | c3kpgA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: sulfide:quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone |
| 75 | c4g6gB | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: rotenone-insensitive nadh-ubiquinone oxidoreductase, PDBTitle: crystal structure of ndh with trt |
| 76 | c4gapB | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: rotenone-insensitive nadh-ubiquinone oxidoreductase; PDBTitle: structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+ |
| 77 | c1gthD | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary |

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| | | | | | | complex with2 nadph and 5-iodouracil |
| 78 | c5jcaL | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (fnri) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (fnri)2 from pyrococcus furiosus |
| 79 | c2zbwA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8 |
| 80 | c3k30B | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex |
| 81 | c4gcmB | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution |
| 82 | c5jriA | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803 |
| 83 | c5uwYA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005 |
| 84 | c5odeA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: glI2934 protein; PDBTitle: structure of a novel oxidoreductase from gloeobacter violaceus |
| 85 | c5niiB | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of the atypical thioredoxin reductase tri from2 desulfovibrio vulgaris hildenborough |
| 86 | c6qkgB | Alignment | not modelled | 100.0 | 19 | PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr) |
| 87 | c5w4cA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation) |
| 88 | c4ylfD | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase subunit a; PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure |
| 89 | c3r9uA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni. |
| 90 | c4jnqA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a thioredoxin reductase from brucella melitensis |
| 91 | c6gnCA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution |
| 92 | c3h8IA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism |
| 93 | c1djnB | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylphilus methylotrophicus (sp.3 w3a1) |
| 94 | c4ntdA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi |
| 95 | c4fk1D | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: putative thioredoxin reductase; PDBTitle: crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis |
| 96 | c1vdca | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase |
| 97 | c6de6B | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9 |
| 98 | c1ps9A | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase |
| 99 | c3ab1B | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase |
| 100 | c6gndG | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: G: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of the complex of a ferredoxin-flavin thioredoxin2 reductase and a thioredoxin from clostridium acetobutylicum at 2.9 a3 resolution |
| 101 | c1fl2A | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli |
| 102 | c3ctyA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; |

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| | | | | | | PDBTitle: crystal structure of t. acidophilum thioredoxin reductase |
| 103 | c5yqqB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris |
| 104 | c4ntcA | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: glit; PDBTitle: crystal structure of glit |
| 105 | c5mjkC | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of lactococcus lactis thioredoxin reductase (f02 conformation) |
| 106 | c6garB | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus |
| 107 | c5twcA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form |
| 108 | c5xhuA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ygct from bacillus subtilis |
| 109 | c2vdcl | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 Å resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. |
| 110 | c1f6mF | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin reductase,2 thioredoxin, and the nadp+ analog, aadp+ |
| 111 | c4a5lB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of the thioredoxin reductase from entamoeba2 histolytica |
| 112 | d1gv4a1 | Alignment | not modelled | 100.0 | 31 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 113 | c3lzxB | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii) |
| 114 | c3f8rD | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules |
| 115 | c5j60B | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: structure of a thioredoxin reductase from gloeobacter violaceus |
| 116 | c3d8xB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae ndpph dependent2 thioredoxin reductase 1 |
| 117 | c4jnaA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: deph; PDBTitle: crystal structure of the deph complex with dimethyl-fk228 |
| 118 | c4usqA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of flavin-containing monooxygenase from2 cellvibrio sp. br |
| 119 | c3d1cA | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing putative monooxygenase; PDBTitle: crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 Å resolution |
| 120 | c2q7vA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin reductase |