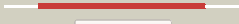



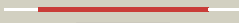



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1470_(trxA)_1658986_1659360
 Date Fri Aug 2 13:30:05 BST 2019
 Unique Job ID c22afdda0b522a1f

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2pptA_ |  Alignment |  | 99.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2 |
| 2 | c6ib1B_ |  Alignment |  | 99.9 | 23 | PDB header: immune system Chain: B: PDB Molecule: thioredoxin 1,beta-1 adrenergic receptor; PDBTitle: activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80 |
| 3 | c3p2aB_ |  Alignment |  | 99.9 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis |
| 4 | c2l6dA_ |  Alignment |  | 99.9 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of desulfthioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form |
| 5 | c3p2aA_ |  Alignment |  | 99.9 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis |
| 6 | c3hz4A_ |  Alignment |  | 99.9 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina mazei |
| 7 | c2e0qA_ |  Alignment |  | 99.9 | 28 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7 |
| 8 | c5zf2A_ |  Alignment |  | 99.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (h-type,trx-h); PDBTitle: crystal structure of trlxp from edwardsiella tarda eib202 |
| 9 | c3gniD_ |  Alignment |  | 99.9 | 24 | PDB header: structural genomics, unknown function Chain: D: PDB Molecule: thioredoxin domain protein; PDBTitle: the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb |
| 10 | c6ckpA_ |  Alignment |  | 99.9 | 30 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin domain 2 from brucella melitensis2 at 1.15 angstrom resolution |
| 11 | c6gd1B_ |  Alignment |  | 99.9 | 24 | PDB header: rna binding protein Chain: B: PDB Molecule: thioredoxin 1,elav-like protein 1; PDBTitle: structure of hur rrm3 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3dxbE_ | Alignment | | 99.9 | 24 | PDB header: splicing, transcription Chain: E: PDB Molecule: thioredoxin n-terminally fused to puf60(uhm); PDBTitle: structure of the uhm domain of puf60 fused to thioredoxin |
| 13 | d1gh2a_ | Alignment | | 99.9 | 21 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 14 | c6bkbB_ | Alignment | | 99.9 | 27 | PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27) |
| 15 | c2i4aA_ | Alignment | | 99.9 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti |
| 16 | d1dbya_ | Alignment | | 99.9 | 26 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 17 | c3qdnA_ | Alignment | | 99.9 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium |
| 18 | c2vocA_ | Alignment | | 99.9 | 25 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin a active site mutants form mixed disulfide dimers that2 resemble enzyme-substrate reaction intermediate |
| 19 | c6esxC_ | Alignment | | 99.9 | 29 | PDB header: cell cycle Chain: C: PDB Molecule: thioredoxin 1; PDBTitle: caulobacter crescentus trx1 |
| 20 | c3vfiA_ | Alignment | | 99.9 | 19 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a metagenomic thioredoxin |
| 21 | c2wz9A_ | Alignment | not modelled | 99.9 | 19 | PDB header: protein binding Chain: A: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the thioredoxin domain of human txn2 |
| 22 | c3tcoA_ | Alignment | not modelled | 99.9 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (trxa-1); PDBTitle: crystallographic and spectroscopic characterization of sulfobolus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability |
| 23 | c5jy5A_ | Alignment | not modelled | 99.9 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution |
| 24 | c4ruvA_ | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325 |
| 25 | d1thxa_ | Alignment | not modelled | 99.9 | 23 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 26 | c2o7kA_ | Alignment | not modelled | 99.9 | 25 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: s. aureus thioredoxin |
| 27 | c4xhmB_ | Alignment | not modelled | 99.9 | 33 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin (trx-3); PDBTitle: archaeoglobus fulgidus thioredoxin 3 m60h |
| 28 | c1x5dA_ | Alignment | not modelled | 99.9 | 23 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a6; PDBTitle: the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6 |
| | | | | | | PDB header: protein binding |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2diyA_ | Alignment | not modelled | 99.9 | 20 | Chain: A; PDB Molecule: thioredoxin-like protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2 |
| 30 | d1r26a_ | Alignment | not modelled | 99.9 | 23 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 31 | c6mzaA_ | Alignment | not modelled | 99.9 | 25 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of a putative thioredoxin (trxa) in the reduced2 state from rickettsia prowazekii, the etiological agent responsible3 for typhus. seattle structural genomics center for infectious disease4 target ripra.00029.a |
| 32 | c4cw9A_ | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thiredoxin c34s mutant |
| 33 | d2trxa_ | Alignment | not modelled | 99.9 | 25 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 34 | d1nw2a_ | Alignment | not modelled | 99.9 | 33 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 35 | c6gn9A_ | Alignment | not modelled | 99.9 | 27 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution |
| 36 | c2vfvA_ | Alignment | not modelled | 99.9 | 23 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin h isoform 2.;; PDBTitle: crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state |
| 37 | c4tw5A_ | Alignment | not modelled | 99.9 | 11 | PDB header: isomerase Chain: A; PDB Molecule: eps1p; PDBTitle: structure of the first two thioredoxin domains of saccharomyces2 cerevisiae eps1p |
| 38 | d1syra_ | Alignment | not modelled | 99.9 | 28 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 39 | d1ep7a_ | Alignment | not modelled | 99.9 | 24 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 40 | c4kndA_ | Alignment | not modelled | 99.9 | 25 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: thioredoxin from anaeromyxobacter dehalogenans. |
| 41 | c1w89E_ | Alignment | not modelled | 99.9 | 33 | PDB header: electron transport Chain: E; PDB Molecule: thioredoxin; PDBTitle: structure of the reduced form of human thioredoxin 2 |
| 42 | d1xfla_ | Alignment | not modelled | 99.9 | 25 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 43 | c2yzuA_ | Alignment | not modelled | 99.9 | 25 | PDB header: electron transport Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8 |
| 44 | c1t00A_ | Alignment | not modelled | 99.9 | 29 | PDB header: electron transport Chain: A; PDB Molecule: thioredoxin; PDBTitle: the structure of thioredoxin from s. coelicolor |
| 45 | d1fb6a_ | Alignment | not modelled | 99.9 | 21 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 46 | c3zzxB_ | Alignment | not modelled | 99.9 | 28 | PDB header: oxidoreductase Chain: B; PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaeus vannamei |
| 47 | c5e37A_ | Alignment | not modelled | 99.9 | 22 | PDB header: oxidoreductase Chain: A; PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii |
| 48 | c3wgeA_ | Alignment | not modelled | 99.9 | 26 | PDB header: isomerase Chain: A; PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx2 |
| 49 | c2vm2C_ | Alignment | not modelled | 99.9 | 22 | PDB header: oxidoreductase Chain: C; PDB Molecule: thioredoxin h isoform 1.;; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant |
| 50 | c2dj1A_ | Alignment | not modelled | 99.9 | 25 | PDB header: isomerase Chain: A; PDB Molecule: protein disulfide-isomerase a4; PDBTitle: the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4 |
| 51 | c2lrcA_ | Alignment | not modelled | 99.9 | 21 | PDB header: oxidoreductase Chain: A; PDB Molecule: probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form |
| 52 | c2oe0B_ | Alignment | not modelled | 99.9 | 28 | PDB header: electron transport Chain: B; PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae |
| 53 | d1ti3a_ | Alignment | not modelled | 99.9 | 29 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 54 | c2nbsA_ | Alignment | not modelled | 99.9 | 14 | PDB header: unknown function Chain: A; PDB Molecule: e_1r26; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26 |
| 55 | d1m7ta_ | Alignment | not modelled | 99.9 | 24 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like |

| | | | | | Family:Thioltransferase |
|----|-------------------------|-----------|--------------|------|--|
| 56 | c2i1uA | Alignment | not modelled | 99.9 | 30 PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: mycobacterium tuberculosis thioredoxin c |
| 57 | c4tveA | Alignment | not modelled | 99.9 | 16 PDB header: isomerase Chain: A: PDB Molecule: naumovozyma dairenensis eps1p; PDBTitle: structure of the first two thioredoxin domains of naumovozyma2 dairenensis eps1p |
| 58 | c2vimA | Alignment | not modelled | 99.9 | 30 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: x-ray structure of fasciola hepatica thioredoxin |
| 59 | d1f9ma | Alignment | not modelled | 99.9 | 24 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 60 | c2r2jA | Alignment | not modelled | 99.9 | 19 PDB header: chaperone Chain: A: PDB Molecule: thioredoxin domain-containing protein 4; PDBTitle: crystal structure of human erp44 |
| 61 | c2l5lA | Alignment | not modelled | 99.9 | 21 PDB header: transport protein Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of thioredoxin from bacteroides vulgatus |
| 62 | d1a8la2 | Alignment | not modelled | 99.9 | 14 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like |
| 63 | c3d22A | Alignment | not modelled | 99.9 | 20 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant, ptxrh4c61s |
| 64 | c2j23A | Alignment | not modelled | 99.9 | 26 PDB header: immune protein Chain: A: PDB Molecule: thioredoxin; PDBTitle: cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family |
| 65 | c2yoiA | Alignment | not modelled | 99.9 | 30 PDB header: oxidoreductase Chain: A: PDB Molecule: leca thioredoxin; PDBTitle: crystal structure of ancestral thioredoxin relative to last eukaryotes2 common ancestor (leca) from the precambrian period |
| 66 | c5dbqA | Alignment | not modelled | 99.9 | 22 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of insect thioredoxin at 1.95 angstroms |
| 67 | c3hypB | Alignment | not modelled | 99.9 | 24 PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant |
| 68 | d1j08a2 | Alignment | not modelled | 99.9 | 14 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like |
| 69 | c2mcsA | Alignment | not modelled | 99.9 | 29 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of a putative thioredoxin (ech_0218) in the2 reduced state from ehrlichia chaffeensis, the etiological agent3 responsible for human monocytic ehrlichiosis. seattle structural4 genomics center for infectious disease target ehcha.00546.a |
| 70 | c3emxB | Alignment | not modelled | 99.9 | 19 PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix |
| 71 | c2i9hA | Alignment | not modelled | 99.9 | 32 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1) |
| 72 | c2albA | Alignment | not modelled | 99.9 | 25 PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a3; PDBTitle: nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57 |
| 73 | c2yj7A | Alignment | not modelled | 99.9 | 28 PDB header: oxidoreductase Chain: A: PDB Molecule: lpbca thioredoxin; PDBTitle: crystal structure of a hyperstable protein from the precambrian2 period |
| 74 | c3wgdD | Alignment | not modelled | 99.9 | 30 PDB header: isomerase Chain: D: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx1 |
| 75 | d1oaza | Alignment | not modelled | 99.9 | 24 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 76 | d1xwaa | Alignment | not modelled | 99.9 | 24 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 77 | c3f8uA | Alignment | not modelled | 99.9 | 26 PDB header: immune system/isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a3erp57; PDBTitle: tapasin/erp57 heterodimer |
| 78 | c6g61A | Alignment | not modelled | 99.9 | 27 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin o1, mitochondrial; PDBTitle: crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state |
| 79 | c2vafA | Alignment | not modelled | 99.9 | 15 PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin-2; PDBTitle: crystal structure of human cardiac calsequestrin |
| 80 | c2b5eA | Alignment | not modelled | 99.9 | 18 PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of yeast protein disulfide isomerase |
| 81 | c5nvmA | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein 2.1; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 81 | c3lyt1A | Alignment | not modelled | 99.9 | 13 | PDBTitle: crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state |
| 82 | d2ifqa1 | Alignment | not modelled | 99.9 | 31 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 83 | c4i8bA | Alignment | not modelled | 99.9 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from schistosoma japonicum |
| 84 | c1a8yA | Alignment | not modelled | 99.9 | 13 | PDB header: calcium-binding protein Chain: A: PDB Molecule: calsequestrin; PDBTitle: crystal structure of calsequestrin from rabbit skeletal muscle2 sarcoplasmic reticulum at 2.4 a resolution |
| 85 | d1qgva | Alignment | not modelled | 99.9 | 15 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd |
| 86 | c5xf7A | Alignment | not modelled | 99.9 | 20 | PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase-like protein of the testis; PDBTitle: crystal structure of human protein disulfide isomerase-like protein of2 the testis |
| 87 | c3ed3A | Alignment | not modelled | 99.9 | 25 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase mpd1; PDBTitle: crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p |
| 88 | c2xbqB | Alignment | not modelled | 99.9 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom |
| 89 | c2dj0A | Alignment | not modelled | 99.9 | 26 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-related transmembrane protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2 |
| 90 | c6i1cB | Alignment | not modelled | 99.9 | 22 | PDB header: electron transport Chain: B: PDB Molecule: thioredoxin f2; PDBTitle: crystal structure of chlamydomonas reinhardtii thioredoxin f2 |
| 91 | c2dizA | Alignment | not modelled | 99.9 | 28 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5 |
| 92 | c1sjjA | Alignment | not modelled | 99.8 | 16 | PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin, cardiac muscle isoform; PDBTitle: comparing skeletal and cardiac calsequestrin structures and their2 calcium binding: a proposed mechanism for coupled calcium binding and3 protein polymerization |
| 93 | c3ul3A | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery |
| 94 | c1xbsA | Alignment | not modelled | 99.8 | 16 | PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein |
| 95 | d1a8ya1 | Alignment | not modelled | 99.8 | 11 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Calsequestrin |
| 96 | c1v98A | Alignment | not modelled | 99.8 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure analysis of thioredoxin from thermus thermophilus |
| 97 | d1zmaa1 | Alignment | not modelled | 99.8 | 13 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 98 | c2f51B | Alignment | not modelled | 99.8 | 25 | PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: structure of trichomonas vaginalis thioredoxin |
| 99 | c1x5eA | Alignment | not modelled | 99.8 | 19 | PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain containing protein 1; PDBTitle: the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein |
| 100 | c4e11A | Alignment | not modelled | 99.8 | 26 | PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of oxidized hpdi (abb'xa') |
| 101 | c4i6xA | Alignment | not modelled | 99.8 | 12 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a5; PDBTitle: crystal structure of non-catalytic domain of protein disulfide2 isomerase-related (pdir) protein |
| 102 | c2I57A | Alignment | not modelled | 99.8 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens |
| 103 | c3apsA | Alignment | not modelled | 99.8 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of trx4 domain of erdj5 |
| 104 | c2dj2A | Alignment | not modelled | 99.8 | 27 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a4; PDBTitle: the solution structure of the second thioredoxin domain of2 mouse protein disulfide-isomerase a4 |
| 105 | c2dm1A | Alignment | not modelled | 99.8 | 25 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a6; PDBTitle: the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6 |
| 106 | c2dbcA | Alignment | not modelled | 99.8 | 17 | PDB header: signaling protein Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2) |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 107 | d2b5ea4 | Alignment | not modelled | 99.8 | 18 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like |
| 108 | c3apoA | Alignment | not modelled | 99.8 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5 |
| 109 | c5ganD | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: D: PDB Molecule: spliceosomal protein dib1; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom |
| 110 | c2qsiB | Alignment | not modelled | 99.8 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009 |
| 111 | c3t59D | Alignment | not modelled | 99.8 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: c76a/c455s mutant of mouse qsox1 containing an interdomain disulfide |
| 112 | c3cxgA | Alignment | not modelled | 99.8 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: crystal structure of plasmodium falciparum thioredoxin, pfi0790w |
| 113 | c3q6oA | Alignment | not modelled | 99.8 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: oxidoreductase fragment of human qsox1 |
| 114 | d1mekA | Alignment | not modelled | 99.8 | 25 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like |
| 115 | c2qc7A | Alignment | not modelled | 99.8 | 13 | PDB header: chaperone Chain: A: PDB Molecule: endoplasmic reticulum protein erp29; PDBTitle: crystal structure of the protein-disulfide isomerase related chaperone2 erp29 |
| 116 | c3idvA | Alignment | not modelled | 99.8 | 27 | PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a4; PDBTitle: crystal structure of the a0a fragment of erp72 |
| 117 | d2hfda1 | Alignment | not modelled | 99.8 | 14 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like |
| 118 | d1a8la1 | Alignment | not modelled | 99.8 | 13 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like |
| 119 | c3qd9D | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: qsox from trypanosoma brucei (tbqsox); PDBTitle: c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide |
| 120 | c1b9xC | Alignment | not modelled | 99.8 | 19 | PDB header: signaling protein Chain: C: PDB Molecule: protein (phosducin); PDBTitle: structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin |