

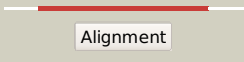

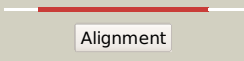

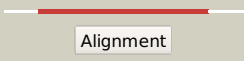

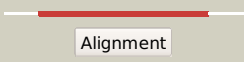
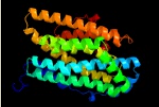
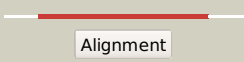

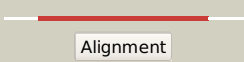

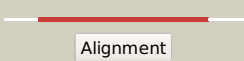
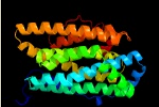
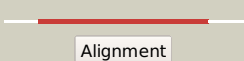

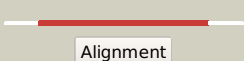

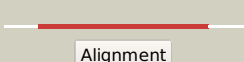



Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1981c_(nrdF)_2224228_2225196 |
| Date | Mon Aug 5 13:25:08 BST 2019 |
| Unique Job ID | 0055e60ce88df95b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1oquc_ |  Alignment |  | 100.0 | 63 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 2 | c6gp2A_ |  Alignment |  | 100.0 | 45 | PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside-diphosphate reductase beta chain; PDBTitle: ribonucleotide reductase class ie r2 from mesoplasma florum, dopa-2 active form |
| 3 | c4n83F_ |  Alignment |  | 100.0 | 52 | PDB header: oxidoreductase Chain: F; PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: x-ray crystal structure of streptococcus sanguinis dimanganese(ii)-2 nrdf |
| 4 | d1r2fa_ |  Alignment |  | 100.0 | 65 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 5 | c1r2fB_ |  Alignment |  | 100.0 | 65 | PDB header: oxidoreductase Chain: B; PDB Molecule: protein (ribonucleotide reductase r2); PDBTitle: ribonucleotide reductase r2f protein from salmonella2 typhimurium |
| 6 | d3dhza1 |  Alignment |  | 100.0 | 65 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 7 | d1uzra_ |  Alignment |  | 100.0 | 71 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 8 | c4bmtB_ |  Alignment |  | 100.0 | 43 | PDB header: oxidoreductase Chain: B; PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: crystal structure of ribonucleotide reductase di-iron nrd2 from bacillus cereus |
| 9 | c4dr0A_ |  Alignment |  | 100.0 | 45 | PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: crystal structure of bacillus subtilis dimanganese(ii) nrdf |
| 10 | c1yfdA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside-diphosphate reductase 1 beta chain; PDBTitle: crystal structure of the y122h mutant of ribonucleotide reductase r22 protein from e. coli |
| 11 | c6cwqA_ |  Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleotide reductase; PDBTitle: x-ray crystal structure of flavobacterium johnsoniae dimanganese(ii)2 ribonucleotide reductase beta subunit (as-isolated) |

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|----|--------------------------|-----------|--------------|-------|----|---|
| 12 | c2rccC_ | Alignment | | 100.0 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: crystal structure of putative class i ribonucleotide reductase2 (np_241368.1) from bacillus halodurans at 1.90 a resolution |
| 13 | d1mxra_ | Alignment | | 100.0 | 24 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 14 | d1smsa_ | Alignment | | 100.0 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 15 | d1syya_ | Alignment | | 100.0 | 20 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 16 | c1syyaA_ | Alignment | | 100.0 | 20 | PDB header: replication,oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase beta chain; PDBTitle: crystal structure of the r2 subunit of ribonucleotide reductase from2 chlamydia trachomatis |
| 17 | c5olkD_ | Alignment | | 100.0 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase, beta subunit 1; PDBTitle: crystal structure of the atp-cone-containing nrdb from2 leeuwenhoekiella blandensis |
| 18 | d1jk0a_ | Alignment | | 100.0 | 20 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 19 | c1h0oA_ | Alignment | | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; cobalt substitution of mouse r2 ribonucleotide reductase to2 model the reactive diferrous state |
| 20 | d1w68a_ | Alignment | | 100.0 | 18 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 21 | c1smqD_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase small chain PDBTitle: structure of the ribonucleotide reductase rnr2 homodimer2 from saccharomyces cerevisiae |
| 22 | c3hf1B_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase subunit m2 b; PDBTitle: crystal structure of human p53r2 |
| 23 | c2o1zA_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase subunit r2; PDBTitle: plasmodium vivax ribonucleotide reductase subunit r2 (pv086155) |
| 24 | c2p1iA_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, small chain; PDBTitle: plasmodium yoelii ribonucleotide reductase subunit r2 (py03671) |
| 25 | c2vuxB_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase subunit m2 b; PDBTitle: human ribonucleotide reductase, subunit m2 b |
| 26 | d1jk0b_ | Alignment | not modelled | 100.0 | 14 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 27 | c4a58B_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase small chain; PDBTitle: crystal structure of a monometal state of the2 ribonucleotide-reductase small subunit from epstein-barr virus in3 orthorhombic space group |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 28 | c3ee4A_ | Alignment | not modelled | 100.0 | 17 | Chain: A: PDB Molecule: probable ribonucleoside-diphosphate reductase; PDBTitle: r2-like ligand binding mn/fe oxidase from m. tuberculosis PDB header: oxidoreductase |
| 29 | c4hr0A_ | Alignment | not modelled | 100.0 | 16 | Chain: A: PDB Molecule: ribonucleotide reductase small subunit; PDBTitle: r2-like ligand-binding oxidase with aerobically reconstituted metal2 cofactor PDB header: oxidoreductase |
| 30 | c6qrzA_ | Alignment | not modelled | 100.0 | 18 | Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: crystal structure of r2-like ligand-binding oxidase from sulfobolus2 acidocaldarius solved by 3d micro-crystal electron diffraction PDB header: lyase |
| 31 | c5uxgB_ | Alignment | not modelled | 100.0 | 12 | Chain: B: PDB Molecule: aldehyde deformylating oxygenase; PDBTitle: protein 84 with aldehyde deformylating oxygenase activity from2 sulfobolus tokodaii (monoclinic) PDB header: lyase |
| 32 | c6d9fA_ | Alignment | not modelled | 100.0 | 14 | Chain: A: PDB Molecule: putative vlbm homolog; PDBTitle: protein 60 with aldehyde deformylating oxidase activity from2 kitasatospora setae PDB header: lyase |
| 33 | d1mhyd_ | Alignment | not modelled | 99.0 | 14 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 34 | d1mtyd_ | Alignment | not modelled | 99.0 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 35 | d2inca1 | Alignment | not modelled | 99.0 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 36 | c5hyhA_ | Alignment | not modelled | 98.9 | 12 | PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: cmli (chemically reduced state), arylamine oxygenase of2 chloramphenicol biosynthetic pathway PDB header: oxidoreductase |
| 37 | c3dhiA_ | Alignment | not modelled | 98.9 | 15 | Chain: A: PDB Molecule: toluene 4-monooxygenase hydroxylase alpha subunit; PDBTitle: crystal structure of reduced toluene 4-monooxygenase hydroxylase2 complexed with effector protein PDB header: oxidoreductase |
| 38 | c3chtA_ | Alignment | not modelled | 98.8 | 12 | Chain: A: PDB Molecule: p-aminobenzoate n-oxygenase; PDBTitle: crystal structure of di-iron aurf with partially bound ligand PDB header: oxidoreductase |
| 39 | c4mudA_ | Alignment | not modelled | 98.4 | 11 | Chain: A: PDB Molecule: ring oxydation complex/ phenylacetic acid degradation PDBTitle: crystal structure of a ring oxydation complex/ phenylacetic acid2 degradation-like protein (sso1313) from sulfobolus solfataricus p2 at3 2.43 a resolution PDB header: oxidoreductase |
| 40 | c2innA_ | Alignment | not modelled | 98.3 | 13 | Chain: A: PDB Molecule: phenol hydroxylase component phn; PDBTitle: structure of the phenol hydroxylase-regulatory protein complex PDB header: oxidoreductase |
| 41 | d1za0a1 | Alignment | not modelled | 98.1 | 18 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 42 | d1afra_ | Alignment | not modelled | 98.0 | 9 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 43 | c2inpD_ | Alignment | not modelled | 98.0 | 12 | PDB header: oxidoreductase Chain: D: PDB Molecule: phenol hydroxylase component phl; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex PDB header: oxidoreductase |
| 44 | c3dhgB_ | Alignment | not modelled | 97.8 | 12 | Chain: B: PDB Molecule: toluene 4-monooxygenase hydroxylase beta subunit; PDBTitle: crystal structure of toluene 4-monooxygenase hydroxylase PDB header: oxidoreductase |
| 45 | d2incb1 | Alignment | not modelled | 97.8 | 14 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 46 | c3pw1A_ | Alignment | not modelled | 97.2 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: phenylacetic acid degradation protein paaa; PDBTitle: the phenylacetyl-coa monooxygenase paaac subcomplex with phenylacetyl-2 coa PDB header: oxidoreductase |
| 47 | d2fzfa1 | Alignment | not modelled | 96.3 | 10 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 48 | d1mhyb_ | Alignment | not modelled | 95.8 | 11 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 49 | c3pm5B_ | Alignment | not modelled | 95.6 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: benzoyl-coa oxygenase component b; PDBTitle: crystal structure of boxb in mixed valent state with bound benzoyl-coa PDB header: hydrolase |
| 50 | c2rd3A_ | Alignment | not modelled | 95.6 | 11 | Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of tena homologue (hp1287) from helicobacter pylori PDB header: metal transport |
| 51 | c3qhbA_ | Alignment | not modelled | 95.2 | 13 | Chain: A: PDB Molecule: symerythrin; PDBTitle: crystal structure of oxidized symerythrin from cyanophora paradoxa PDB header: hydrolase |
| 52 | c2qcxA_ | Alignment | not modelled | 95.0 | 10 | Chain: A: PDB Molecule: transcriptional activator tena; PDBTitle: crystal structure of bacillus subtilis tena y112f mutant complexed2 with formyl aminomethyl pyrimidine PDB header: lyase |
| 53 | c4gwwA_ | Alignment | not modelled | 94.3 | 15 | Chain: A: PDB Molecule: aldehyde decarbonylase; PDB header: lyase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c3quwA | Alignment | not modelled | 94.3 | 10 | PDBTitle: crystal structure of the apo form of cyanobacterial aldehyde-2 deformylating oxygenase PDB header: unknown function Chain: B; PDB Molecule: tena/thi-4 protein, domain of unknown function with a heme |
| 54 | c3ddeB | Alignment | not modelled | 94.1 | 11 | PDBTitle: crystal structure of a domain of unknown function with a heme2 oxygenase-like fold (sden_3740) from shewanella denitrificans os2173 at 2.30 a resolution PDB header: transferase |
| 55 | c3bjdA | Alignment | not modelled | 92.0 | 15 | Chain: A; PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) synthase; PDBTitle: crystal structure of putative 3-oxoacyl-(acyl-carrier-protein)2 synthase from pseudomonas aeruginosa |
| 56 | c2hr5B | Alignment | not modelled | 91.9 | 13 | PDB header: metal binding protein Chain: B; PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form |
| 57 | d1lkoa1 | Alignment | not modelled | 91.5 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 58 | c4di0B | Alignment | not modelled | 89.4 | 13 | PDB header: oxidoreductase Chain: B; PDB Molecule: rubrerythrin; PDBTitle: the structure of rubrerythrin from burkholderia pseudomallei |
| 59 | c5uwzA | Alignment | not modelled | 89.2 | 14 | PDB header: lyase Chain: A; PDB Molecule: aldehyde decarbonylase; PDBTitle: protein 12 with aldehyde deformylating oxygenase activity from2 gloeobacter violaceus |
| 60 | d1otka | Alignment | not modelled | 88.2 | 11 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 61 | c5n5eM | Alignment | not modelled | 87.8 | 16 | PDB header: oxidoreductase Chain: M; PDB Molecule: pfc_05175; PDBTitle: crystal structure of encapsulated ferritin domain from pyrococcus2 furiosus pfc_05175 |
| 62 | d1j30a | Alignment | not modelled | 87.7 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 63 | d1nnqa1 | Alignment | not modelled | 87.7 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 64 | d1jkva | Alignment | not modelled | 87.4 | 9 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Manganese catalase (T-catalase) |
| 65 | c4r42B | Alignment | not modelled | 87.3 | 14 | PDB header: oxidoreductase Chain: B; PDB Molecule: alr3090 protein; PDBTitle: crystal structure of katb, a manganese catalase from anabaena pcc7120 |
| 66 | d1udda | Alignment | not modelled | 87.1 | 8 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4 |
| 67 | d1rtwa | Alignment | not modelled | 86.1 | 8 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4 |
| 68 | d1rcwa | Alignment | not modelled | 85.4 | 12 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqqC-like |
| 69 | c1to9A | Alignment | not modelled | 85.0 | 10 | PDB header: biosynthetic protein Chain: A; PDB Molecule: thi-4 protein; PDBTitle: crystal structure of thi-4 protein from bacillus subtilis |
| 70 | d1to9a | Alignment | not modelled | 85.0 | 10 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4 |
| 71 | c5ux2B | Alignment | not modelled | 84.7 | 13 | PDB header: lyase Chain: B; PDB Molecule: aldehyde decarbonylase; PDBTitle: protein 19 with aldehyde deformylating oxidase activity from2 synechococcus |
| 72 | d1yv1a1 | Alignment | not modelled | 84.4 | 7 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 73 | d1vjxa | Alignment | not modelled | 81.8 | 12 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 74 | c3oqlB | Alignment | not modelled | 81.6 | 9 | PDB header: transcription Chain: B; PDB Molecule: tena homolog; PDBTitle: crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution |
| 75 | d1z72a1 | Alignment | not modelled | 81.4 | 11 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4 |
| 76 | c3bknB | Alignment | not modelled | 81.2 | 14 | PDB header: metal binding protein Chain: B; PDB Molecule: bacterioferritin; PDBTitle: the structure of mycobacterial bacterioferritin |
| 77 | d2oc5a1 | Alignment | not modelled | 80.7 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: PMT1231-like |
| 78 | c1dvbA | Alignment | not modelled | 79.5 | 13 | PDB header: electron transport Chain: A; PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin |
| 79 | c1yuzB | Alignment | not modelled | 79.3 | 13 | PDB header: oxidoreductase Chain: B; PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c4fn6B | Alignment | not modelled | 79.1 | 8 | PDB header: transcription Chain: B: PDB Molecule: thiaminase-2; PDBTitle: structural characterization of thiaminase type ii tena from2 staphylococcus aureus |
| 81 | c3gvyC | Alignment | not modelled | 78.2 | 11 | PDB header: metal binding protein Chain: C: PDB Molecule: bacterioferritin; PDBTitle: crystal structure of bacterioferritin from r.sphaeroides |
| 82 | c5xx9A | Alignment | not modelled | 78.0 | 11 | PDB header: metal transport Chain: A: PDB Molecule: bacterioferritin; PDBTitle: crystal structure of bacterioferritin |
| 83 | c2qqyA | Alignment | not modelled | 75.6 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sigma b operon; PDBTitle: crystal structure of ferritin like, diiron-carboxylate proteins from2 bacillus anthracis str. ames |
| 84 | c3oghB | Alignment | not modelled | 73.9 | 9 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ycie; PDBTitle: crystal structure of ycie protein from e. coli cft073, a member of2 ferritin-like superfamily of diiron-containing four-helix-bundle3 proteins |
| 85 | c4lqxB | Alignment | not modelled | 72.9 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: tena/thi-4 domain-containing protein; PDBTitle: crystal structure of a tena/thi-4 domain-containing protein (sso2700)2 from sulfobolus solfataricus p2 at 2.34 a resolution |
| 86 | d2oh3a1 | Alignment | not modelled | 71.1 | 12 | Fold: Ferritin-like Superfamily: Ferritin-like Family: AMB4284-like |
| 87 | c3oqlA | Alignment | not modelled | 68.6 | 9 | PDB header: transcription Chain: A: PDB Molecule: tena homolog; PDBTitle: crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution |
| 88 | d1nf4a | Alignment | not modelled | 67.6 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 89 | d2fkza1 | Alignment | not modelled | 67.1 | 10 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 90 | d2gm8a1 | Alignment | not modelled | 66.3 | 9 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4 |
| 91 | d2cwa1 | Alignment | not modelled | 66.3 | 14 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Manganese catalase (T-catalase) |
| 92 | c3no6B | Alignment | not modelled | 63.7 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: transcriptional activator tena; PDBTitle: crystal structure of a putative thiaminase ii (se1693) from2 staphylococcus epidermidis atcc 12228 at 1.65 a resolution |
| 93 | c5vrdD | Alignment | not modelled | 61.0 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: crystal structure for methylobacterium extorquens pqqcd (natural2 fusion) |
| 94 | d1jgca | Alignment | not modelled | 60.6 | 10 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 95 | d2htna1 | Alignment | not modelled | 59.1 | 12 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 96 | c3q4nA | Alignment | not modelled | 58.5 | 10 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0754; PDBTitle: crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661 |
| 97 | c3mvuA | Alignment | not modelled | 56.4 | 11 | PDB header: transcription regulator Chain: A: PDB Molecule: tena family transcriptional regulator; PDBTitle: crystal structure of a tena family transcription regulator2 (tm1040_3656) from silicibacter sp. tm1040 at 1.80 a resolution |
| 98 | c3rm5B | Alignment | not modelled | 51.5 | 9 | PDB header: transferase Chain: B: PDB Molecule: hydroxymethylpyrimidine/phosphomethylpyrimidine kinase PDBTitle: structure of trifunctional thi20 from yeast |
| 99 | d1zpya1 | Alignment | not modelled | 48.2 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: half-ferritin |
| 100 | c2vzbA | Alignment | not modelled | 47.5 | 13 | PDB header: metal transport Chain: A: PDB Molecule: putative bacterioferritin-related protein; PDBTitle: a dodecameric thioferritin in the bacterial domain, characterization2 of the bacterioferritin-related protein from bacteroides fragilis |
| 101 | d1mtyb | Alignment | not modelled | 45.2 | 10 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 102 | c3e6sD | Alignment | not modelled | 44.8 | 10 | PDB header: oxidoreductase Chain: D: PDB Molecule: ferritin; PDBTitle: crystal structure of ferritin soaked with iron from pseudo-nitzschia2 multiseris |
| 103 | c5da5R | Alignment | not modelled | 44.6 | 16 | PDB header: oxidoreductase Chain: R: PDB Molecule: rrru_a0973; PDBTitle: crystal structure of rhodospirillum rubrum rru_a0973 |
| 104 | c3r2rA | Alignment | not modelled | 42.4 | 14 | PDB header: metal binding protein Chain: A: PDB Molecule: bacterioferritin; PDBTitle: 1.65a resolution structure of iron soaked ftna from pseudomonas2 aeruginosa (ph 6.0) |
| 105 | c5n5fC | Alignment | not modelled | 42.3 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: encapsulated ferritin; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 105 | c1h3C_ | Alignment | not modelled | 42.5 | 10 | PDBTitle: crystal structure of haliangium ochraceum encapsulated ferritin |
| 106 | c4am4B_ | Alignment | not modelled | 41.9 | 12 | PDB header: metal binding protein Chain: B: PDB Molecule: bacterioferritin; PDBTitle: bacterioferritin from blastochloris viridis |
| 107 | c2hz8A_ | Alignment | not modelled | 33.1 | 27 | PDB header: de novo protein Chain: A: PDB Molecule: de novo designed diiron protein; PDBTitle: qm/mm structure refined from nmr-structure of a single2 chain diiron protein |
| 108 | d1yuza1 | Alignment | not modelled | 32.8 | 8 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 109 | d1otva_ | Alignment | not modelled | 32.4 | 10 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqqC-like |
| 110 | c5ouwA_ | Alignment | not modelled | 32.2 | 15 | PDB header: metal binding protein Chain: A: PDB Molecule: ferritin; PDBTitle: metal free structure of synftn |
| 111 | c4cmyN_ | Alignment | not modelled | 30.1 | 18 | PDB header: metal transport Chain: N: PDB Molecule: ferritin; PDBTitle: chlorobium tepidum ferritin |
| 112 | c5wljD_ | Alignment | not modelled | 28.2 | 47 | PDB header: de novo protein Chain: D: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1 |
| 113 | c5wljB_ | Alignment | not modelled | 28.2 | 47 | PDB header: de novo protein Chain: B: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1 |
| 114 | c5wljA_ | Alignment | not modelled | 28.2 | 47 | PDB header: de novo protein Chain: A: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1 |
| 115 | c5wljC_ | Alignment | not modelled | 28.2 | 47 | PDB header: de novo protein Chain: C: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1 |
| 116 | c3j20Q_ | Alignment | not modelled | 27.9 | 23 | PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s15p/s13e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 117 | c3fvbB_ | Alignment | not modelled | 26.9 | 11 | PDB header: metal binding protein Chain: B: PDB Molecule: bacterioferritin; PDBTitle: crystal structure of ferritin (bacterioferritin) from brucella2 melitensis |
| 118 | c3ap3A_ | Alignment | not modelled | 26.9 | 33 | PDB header: transferase Chain: A: PDB Molecule: protein-tyrosine sulfotransferase 2; PDBTitle: crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap |
| 119 | d2za7a1 | Alignment | not modelled | 22.6 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 120 | c3qd8M_ | Alignment | not modelled | 21.9 | 11 | PDB header: metal binding protein Chain: M: PDB Molecule: probable bacterioferritin bfrb; PDBTitle: crystal structure of mycobacterium tuberculosis bfrb |