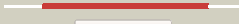



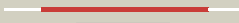






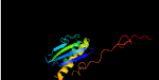



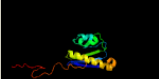

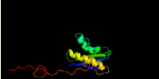




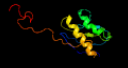

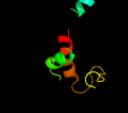




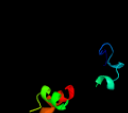
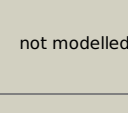


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3442c_(rpsl)_3861675_3862130
 Date Fri Aug 9 18:20:11 BST 2019
 Unique Job ID 7a6f36c6cd42aff

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5o5jl_ |  Alignment |  | 100.0 | 90 | PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s9; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis |
| 2 | d2gy9i1 |  Alignment |  | 100.0 | 50 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components |
| 3 | d2vqei1 |  Alignment |  | 100.0 | 52 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components |
| 4 | c3bbnl_ |  Alignment |  | 100.0 | 53 | PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome. |
| 5 | c3j6vl_ |  Alignment |  | 100.0 | 31 | PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome |
| 6 | c2xzml_ |  Alignment |  | 100.0 | 28 | PDB header: ribosome Chain: I: PDB Molecule: rps16e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 7 | c2zkqi_ |  Alignment |  | 100.0 | 33 | PDB header: ribosomal protein/rna Chain: I: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 8 | c3zeyK_ |  Alignment |  | 100.0 | 27 | PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 9 | c5xyiQ_ |  Alignment |  | 100.0 | 30 | PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 10 | c3j20K_ |  Alignment |  | 100.0 | 35 | PDB header: ribosome Chain: K: PDB Molecule: 30s ribosomal protein s9p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 11 | c1s1hl_ |  Alignment |  | 100.0 | 34 | PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s16; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i. |

| | | | | | | |
|----|------------------------|-----------|---|-------|----|--|
| 12 | c3iz6l | Alignment |  | 100.0 | 32 | PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s16 (s9p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 13 | c5ujaA | Alignment |  | 79.1 | 22 | PDB header: protein transport Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1)2 bound to leukotriene c4 |
| 14 | c5uj9A | Alignment |  | 78.7 | 22 | PDB header: transport protein Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1) |
| 15 | c6bhuA | Alignment |  | 73.9 | 22 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1) |
| 16 | c3g5uB | Alignment |  | 68.0 | 26 | PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding |
| 17 | c4ry2A | Alignment |  | 67.8 | 29 | PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1 |
| 18 | c5mkkA | Alignment |  | 67.1 | 23 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap |
| 19 | c5mkkB | Alignment |  | 66.5 | 18 | PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap |
| 20 | c4f4cA | Alignment |  | 65.0 | 28 | PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter |
| 21 | c3u5eh | Alignment | not modelled | 62.4 | 20 | PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a |
| 22 | c3j3bh | Alignment | not modelled | 60.9 | 29 | PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9; PDBTitle: structure of the human 60s ribosomal proteins |
| 23 | c6c0vA | Alignment | not modelled | 59.7 | 28 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance protein 1; PDBTitle: molecular structure of human p-glycoprotein in the atp-bound, outward-2 facing conformation |
| 24 | c5tsiA | Alignment | not modelled | 58.2 | 21 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of the cystic fibrosis transmembrane conductance regulator2 (cftr) from zebrafish |
| 25 | c1s3bB | Alignment | not modelled | 57.2 | 41 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b; PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan |
| 26 | c3wmeA | Alignment | not modelled | 53.7 | 26 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette, sub-family b, member 1; PDBTitle: crystal structure of an inward-facing eukaryotic abc multidrug2 transporter |
| 27 | c4aa3A | Alignment | not modelled | 52.6 | 30 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter,2 abcb10 (plate form) |
| | | | | | | PDB header: hydrolase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | c5ochH | Alignment | not modelled | 49.4 | 29 | Chain: H: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state |
| 29 | d1d5ta1 | Alignment | not modelled | 49.2 | 20 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 30 | c5ttkB | Alignment | not modelled | 48.8 | 36 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida |
| 31 | c2v6oA | Alignment | not modelled | 48.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr) |
| 32 | c1v0jB | Alignment | not modelled | 48.5 | 33 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis |
| 33 | d1wdda1 | Alignment | not modelled | 47.1 | 28 | Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain |
| 34 | c3j39h | Alignment | not modelled | 46.3 | 29 | PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein I9; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins |
| 35 | c6c3oE | Alignment | not modelled | 46.1 | 17 | PDB header: transport protein Chain: E: PDB Molecule: atp-binding cassette sub-family c member 8; PDBTitle: cryo-em structure of human katp bound to atp and adp in quatrefoil2 form |
| 36 | c3zf7k | Alignment | not modelled | 45.0 | 32 | PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein I10, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 37 | c6j0zC | Alignment | not modelled | 44.4 | 32 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpk |
| 38 | c5l22B | Alignment | not modelled | 43.4 | 26 | PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtD t1ss abc transporter |
| 39 | c2rrlA | Alignment | not modelled | 42.7 | 20 | PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik |
| 40 | d1rbla1 | Alignment | not modelled | 42.0 | 30 | Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain |
| 41 | c1ltxR | Alignment | not modelled | 40.9 | 20 | PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid |
| 42 | c3cp8C | Alignment | not modelled | 40.1 | 27 | PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum |
| 43 | c3cp2A | Alignment | not modelled | 39.0 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli |
| 44 | c2yl4A | Alignment | not modelled | 39.0 | 29 | PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10 |
| 45 | c5u1dB | Alignment | not modelled | 38.0 | 26 | PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter |
| 46 | c4i58A | Alignment | not modelled | 37.8 | 38 | PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a |
| 47 | c6on2A | Alignment | not modelled | 37.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate |
| 48 | c3qf4A | Alignment | not modelled | 37.2 | 26 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation |
| 49 | c5ykfH | Alignment | not modelled | 36.5 | 20 | PDB header: membrane protein Chain: H: PDB Molecule: atp-binding cassette sub-family c member 8 isoform x2; PDBTitle: structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a) |
| 50 | c4a1eU | Alignment | not modelled | 36.1 | 35 | PDB header: ribosome Chain: U: PDB Molecule: rpl35; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rRNA, 5.8s rRNA3 and proteins of molecule 1 |
| 51 | c3jskN | Alignment | not modelled | 35.9 | 21 | PDB header: biosynthetic protein Chain: N: PDB Molecule: cybbp37 protein; PDBTitle: thiazole synthase from neurospora crassa |
| 52 | c2hydB | Alignment | not modelled | 35.6 | 21 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866 |
| 53 | d2bcgg1 | Alignment | not modelled | 35.2 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain |

| | | | | | | Family:GDI-like N domain |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c3k7tB | Alignment | not modelled | 34.1 | 40 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-hydroxy-l-nicotine oxidase; PDBTitle: crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121 |
| 55 | d1hyua1 | Alignment | not modelled | 33.0 | 23 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 56 | c5do7A | Alignment | not modelled | 32.7 | 23 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8 |
| 57 | c2uzzD | Alignment | not modelled | 32.5 | 24 | PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox) |
| 58 | c5wgyA | Alignment | not modelled | 32.3 | 29 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex |
| 59 | c4cnjD | Alignment | not modelled | 32.0 | 30 | PDB header: oxidoreductase Chain: D: PDB Molecule: l-amino acid oxidase; PDBTitle: l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins |
| 60 | c5u71A | Alignment | not modelled | 31.9 | 24 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr) |
| 61 | c2zxiC | Alignment | not modelled | 31.7 | 38 | PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: structure of aquifex aeolicus gida in the form ii crystal |
| 62 | c6bznA | Alignment | not modelled | 31.4 | 23 | PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm |
| 63 | c4y4nE | Alignment | not modelled | 31.0 | 31 | PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus |
| 64 | d1gesa1 | Alignment | not modelled | 30.9 | 36 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 65 | c3rhaA | Alignment | not modelled | 29.1 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus |
| 66 | c5wuaF | Alignment | not modelled | 28.8 | 14 | PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel |
| 67 | c4yshA | Alignment | not modelled | 27.6 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus |
| 68 | c4ia6B | Alignment | not modelled | 26.8 | 32 | PDB header: immune system Chain: B: PDB Molecule: myosin-crossreactive antigen; PDBTitle: hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah) |
| 69 | c2olnA | Alignment | not modelled | 26.7 | 43 | PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution |
| 70 | c1ryiB | Alignment | not modelled | 26.0 | 33 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate |
| 71 | c3g05B | Alignment | not modelled | 26.0 | 32 | PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg |
| 72 | c2qaeA | Alignment | not modelled | 25.6 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase |
| 73 | c6c87A | Alignment | not modelled | 25.2 | 21 | PDB header: protein transport Chain: A: PDB Molecule: rab gdp dissociation inhibitor alpha; PDBTitle: crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri |
| 74 | c1f8sA | Alignment | not modelled | 25.1 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate. |
| 75 | d1rrea | Alignment | not modelled | 25.1 | 22 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: ATP-dependent protease Lon (La), catalytic domain |
| 76 | c2nvkX | Alignment | not modelled | 24.4 | 32 | PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster |
| 77 | d1h6va1 | Alignment | not modelled | 23.7 | 32 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 78 | c5ez7A | Alignment | not modelled | 23.1 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | pa4991 from2 pseudomonas aeruginosa PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: dihydroliipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum |
| 79 | c1dxlC_ | Alignment | not modelled | 23.0 | 32 | |
| 80 | c3ihgA_ | Alignment | not modelled | 21.7 | 20 | PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone |
| 81 | c6bwtD_ | Alignment | not modelled | 21.6 | 27 | PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase; PDBTitle: 2.45 angstrom resolution crystal structure thioredoxin reductase from2 francisella tularensis. |
| 82 | c5ochF_ | Alignment | not modelled | 21.6 | 32 | PDB header: hydrolase Chain: F: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state |
| 83 | c3dmeB_ | Alignment | not modelled | 21.5 | 38 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141 |
| 84 | d2hzaa1 | Alignment | not modelled | 21.0 | 22 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 85 | d2i0za1 | Alignment | not modelled | 20.3 | 32 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like |
| 86 | c3m6aC_ | Alignment | not modelled | 20.3 | 24 | PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain |
| 87 | d2gf3a1 | Alignment | not modelled | 20.2 | 24 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 88 | d1chua2 | Alignment | not modelled | 20.0 | 26 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 89 | c5e7sG_ | Alignment | not modelled | 19.9 | 19 | PDB header: hydrolase Chain: G: PDB Molecule: lon protease; PDBTitle: hexameric structure of a lon protease domain in active state |
| 90 | d2gmha1 | Alignment | not modelled | 19.9 | 33 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 91 | d1seza1 | Alignment | not modelled | 19.8 | 37 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 92 | c2cfyB_ | Alignment | not modelled | 19.8 | 35 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1 |
| 93 | c3nyeA_ | Alignment | not modelled | 19.7 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine |
| 94 | d1dxa1 | Alignment | not modelled | 19.5 | 32 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 95 | c3uteB_ | Alignment | not modelled | 19.4 | 35 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex |
| 96 | c1z47B_ | Alignment | not modelled | 19.3 | 29 | PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius |
| 97 | c2e1mA_ | Alignment | not modelled | 19.3 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6 |
| 98 | c4b1bB_ | Alignment | not modelled | 18.8 | 36 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom |
| 99 | d3lada1 | Alignment | not modelled | 18.8 | 30 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |