
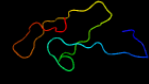

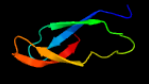

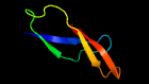

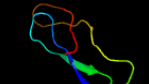

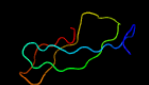





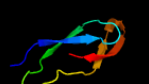



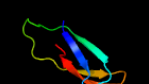


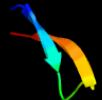



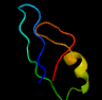
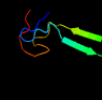

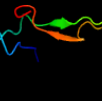



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0634B_rpmG_731715_731882
 Date Fri Jul 26 01:50:20 BST 2019
 Unique Job ID 0e2f19390b9fabe4

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3bbo3_ |  Alignment |  | 99.9 | 55 | PDB header: ribosome Chain: 3; PDB Molecule: ribosomal protein I33; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome |
| 2 | c5o60c_ |  Alignment |  | 99.9 | 90 | PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein I2; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis |
| 3 | c6hma1_ |  Alignment |  | 99.9 | 57 | PDB header: ribosome Chain: 1; PDB Molecule: 50s ribosomal protein I33; PDBTitle: improved model derived from cryo-em map of staphylococcus aureus large2 ribosomal subunit |
| 4 | c3d5d6_ |  Alignment |  | 99.8 | 57 | PDB header: ribosome Chain: 6; PDB Molecule: 50s ribosomal protein I33; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of the second 70s ribosome. the entire3 crystal structure contains two 70s ribosomes as described in remark4 400. |
| 5 | d2gyc11 |  Alignment |  | 99.6 | 37 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p |
| 6 | d2zjr11 |  Alignment |  | 99.6 | 36 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p |
| 7 | c2b9n6_ |  Alignment |  | 99.5 | 36 | PDB header: ribosome Chain: 6; PDB Molecule: 50s ribosomal protein I33; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400. |
| 8 | c5xym1_ |  Alignment |  | 99.2 | 45 | PDB header: ribosome Chain: 1; PDB Molecule: 50s ribosomal protein I33 2; PDBTitle: large subunit of mycobacterium smegmatis |
| 9 | c2ftcP_ |  Alignment |  | 99.2 | 21 | PDB header: ribosome Chain: P; PDB Molecule: mitochondrial ribosomal protein I33 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 10 | c1vw4X_ |  Alignment |  | 98.6 | 11 | PDB header: ribosome Chain: X; PDB Molecule: 54s ribosomal protein I39, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit |
| 11 | c3j21j_ |  Alignment |  | 95.9 | 38 | PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein I14p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |

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|----|--------------------------|-----------|---|------|----|--|
| 12 | d1vqo31 | Alignment |  | 95.7 | 38 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L44e |
| 13 | c4a19C_ | Alignment |  | 95.5 | 31 | PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein l36a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2. |
| 14 | c2zkr4_ | Alignment |  | 95.5 | 50 | PDB header: ribosomal protein/rna Chain: 4: PDB Molecule: 60s ribosomal protein l44e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 15 | c3zf7t_ | Alignment |  | 91.1 | 31 | PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 16 | d2cona1 | Alignment |  | 83.1 | 31 | Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like |
| 17 | c6g5iy_ | Alignment |  | 67.4 | 28 | PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r |
| 18 | c2lccqA_ | Alignment |  | 51.7 | 32 | PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii |
| 19 | c4c2mQ_ | Alignment |  | 31.5 | 15 | PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase i subunit rpa135; PDBTitle: structure of rna polymerase i at 2.8 a resolution |
| 20 | c2vl6C_ | Alignment |  | 30.3 | 25 | PDB header: dna binding protein Chain: C: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: structural analysis of the sulfobolus solfataricus mcm2 protein n-terminal domain |
| 21 | c4pogC_ | Alignment | not modelled | 26.6 | 26 | PDB header: replication, dna binding protein/dna Chain: C: PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure |
| 22 | c5us3A_ | Alignment | not modelled | 26.1 | 50 | PDB header: de novo protein Chain: A: PDB Molecule: heterogeneous-backbone variant of the sp1-3 zinc finger: n- PDBTitle: heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger |
| 23 | d2fy9a1 | Alignment | not modelled | 24.8 | 42 | Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like |
| 24 | c6o3pA_ | Alignment | not modelled | 24.8 | 50 | PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions |
| 25 | c3f9vA_ | Alignment | not modelled | 22.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase |
| 26 | d2cu8a1 | Alignment | not modelled | 21.4 | 33 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain |
| 27 | c1k82D_ | Alignment | not modelled | 21.2 | 35 | PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna |
| 28 | c3w0fA_ | Alignment | not modelled | 21.0 | 75 | PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c2w61A | Alignment | not modelled | 21.0 | 73 | PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei13) PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pogo transposable element with znf domain; PDBTitle: solution structure of the zinc finger domain of human2 kiaa0461 |
| 29 | c2e72A | Alignment | not modelled | 20.8 | 40 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like |
| 30 | d2gmg1 | Alignment | not modelled | 20.1 | 39 | PDB header: hydrolase Chain: A; PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna |
| 31 | c1nnjA | Alignment | not modelled | 19.3 | 31 | PDB header: metal binding protein Chain: B; PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form |
| 32 | c2hr5B | Alignment | not modelled | 19.2 | 43 | PDB header: hydrolase/dna Chain: A; PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2 |
| 33 | c2f5qA | Alignment | not modelled | 19.0 | 27 | PDB header: ribosome Chain: R; PDB Molecule: 40s ribosomal protein s17; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a |
| 34 | c6g4wr | Alignment | not modelled | 15.4 | 29 | Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain |
| 35 | d1twfi2 | Alignment | not modelled | 15.4 | 29 | Fold: SRCR-like Superfamily: SRCR-like Family: Hepsin, N-terminal domain |
| 36 | d1z8ga2 | Alignment | not modelled | 15.2 | 23 | PDB header: oxidoreductase Chain: B; PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin |
| 37 | c1yuzB | Alignment | not modelled | 14.8 | 52 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 38 | d1r2za3 | Alignment | not modelled | 14.6 | 43 | Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit |
| 39 | d1qf8a | Alignment | not modelled | 14.6 | 31 | PDB header: hydrolase Chain: B; PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution |
| 40 | c2gb5B | Alignment | not modelled | 13.3 | 29 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 41 | d1l1ta3 | Alignment | not modelled | 13.3 | 27 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 42 | d1k82a3 | Alignment | not modelled | 13.2 | 43 | Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like |
| 43 | d2ey4e1 | Alignment | not modelled | 13.1 | 36 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 44 | d1tdza3 | Alignment | not modelled | 13.1 | 31 | Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like |
| 45 | d2apob1 | Alignment | not modelled | 12.9 | 45 | PDB header: transferase Chain: M; PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure |
| 46 | c5cm2M | Alignment | not modelled | 12.8 | 43 | PDB header: metal-binding protein Chain: A; PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein |
| 47 | c2kdxA | Alignment | not modelled | 12.7 | 24 | PDB header: viral protein Chain: A; PDB Molecule: protein a41; PDBTitle: the structure of vaccinia virus a41 |
| 48 | c2vgaA | Alignment | not modelled | 12.7 | 45 | PDB header: hydrolase Chain: B; PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg |
| 49 | c3twkB | Alignment | not modelled | 12.6 | 15 | Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit |
| 50 | d1jwhc | Alignment | not modelled | 12.5 | 31 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain |
| 51 | d1imla1 | Alignment | not modelled | 12.4 | 42 | PDB header: transferase Chain: A; PDB Molecule: protein trm112; PDBTitle: crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex. |
| 52 | c2j6aA | Alignment | not modelled | 12.3 | 36 | PDB header: transferase Chain: B; PDB Molecule: thymidine kinase; PDBTitle: catalytic domain of thymidine kinase from trypanosoma2 brucei with dthd |
| 53 | c5fuvB | Alignment | not modelled | 12.0 | 15 | PDB header: transcription Chain: A; PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation |
| 54 | c4i7hA | Alignment | not modelled | 11.9 | 16 | |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | by perr from2 streptococcus pyogenes |
| 55 | d1yfa1 | Alignment | not modelled | 11.7 | 40 | Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like |
| 56 | c1ee8A | Alignment | not modelled | 11.5 | 27 | PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8 |
| 57 | c2e9hA | Alignment | not modelled | 10.8 | 27 | PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: solution structure of the eif-5 eif-2b domain from human2 eukaryotic translation initiation factor 5 |
| 58 | d1ee8a3 | Alignment | not modelled | 10.7 | 27 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 59 | c3h93A | Alignment | not modelled | 10.5 | 21 | PDB header: transcription regulator Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of pseudomonas aeruginosa dsba |
| 60 | c6qg3P | Alignment | not modelled | 10.4 | 17 | PDB header: translation Chain: P: PDB Molecule: eukaryotic translation initiation factor 2 subunit beta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model b) |
| 61 | d1lta | Alignment | not modelled | 10.3 | 20 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA replication initiator (cdc21/cdc54) N-terminal domain |
| 62 | c2mkdA | Alignment | not modelled | 10.3 | 50 | PDB header: dna binding protein Chain: A: PDB Molecule: zinc finger protein 346; PDBTitle: human jaz zf3 residues 168-227 |
| 63 | c3a46B | Alignment | not modelled | 10.0 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex |
| 64 | c2xigA | Alignment | not modelled | 9.9 | 14 | PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites |
| 65 | c3feuA | Alignment | not modelled | 9.6 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri |
| 66 | c2qq0B | Alignment | not modelled | 9.5 | 15 | PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp |
| 67 | c3zf7o | Alignment | not modelled | 9.3 | 46 | PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 68 | c2kvfA | Alignment | not modelled | 9.3 | 44 | PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein |
| 69 | c4c2mX | Alignment | not modelled | 9.2 | 50 | PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution |
| 70 | c2orvB | Alignment | not modelled | 9.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: human thymidine kinase 1 in complex with tp4a |
| 71 | c5xcoB | Alignment | not modelled | 8.9 | 29 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asf-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide |
| 72 | d1lv3a | Alignment | not modelled | 8.8 | 50 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG |
| 73 | c5y06A | Alignment | not modelled | 8.8 | 40 | PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis |
| 74 | c2zkrz | Alignment | not modelled | 8.7 | 38 | PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 75 | c3cc4Z | Alignment | not modelled | 8.6 | 46 | PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit |
| 76 | c4iloA | Alignment | not modelled | 8.6 | 43 | PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis |
| 77 | c3heyA | Alignment | not modelled | 8.4 | 38 | PDB header: de novo protein Chain: A: PDB Molecule: alpha/beta-peptide based on the gcn4-p1i side chain PDBTitle: cyclic residues in alpha/beta-peptide helix bundles: gcn4-p1i side2 chain sequence on an (alpha-alpha-beta) backbone with cyclic beta-3 residues at positions 1, 4, 10, 19 and 28 |
| 78 | d1x6ea2 | Alignment | not modelled | 8.4 | 22 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 79 | c1c4A | Alignment | not modelled | 8.4 | 50 | PDB header: viral protein Chain: A: PDB Molecule: protein (gag polyprotein); |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 79 | c1qf4A | Alignment | not modelled | 8.4 | 30 | PDBTitle: nucleocapsid protein from mason-pfizer monkey virus (mpmv) PDB header: transferase |
| 80 | c2j87D | Alignment | not modelled | 8.4 | 18 | Chain: D: PDB Molecule: thymidine kinase; PDBTitle: structure of vaccinia virus thymidine kinase in complex2 with dttp: insights for drug design |
| 81 | c3dvwA | Alignment | not modelled | 8.3 | 36 | PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis |
| 82 | d1cta1 | Alignment | not modelled | 8.1 | 42 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain |
| 83 | d1vqoz1 | Alignment | not modelled | 8.0 | 46 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae |
| 84 | c3j39p | Alignment | not modelled | 8.0 | 38 | PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins |
| 85 | d2cota1 | Alignment | not modelled | 7.9 | 22 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 86 | c2avuF | Alignment | not modelled | 7.9 | 28 | PDB header: transcription activator Chain: F: PDB Molecule: flagellar transcriptional activator flhc; PDBTitle: structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription |
| 87 | d2avue1 | Alignment | not modelled | 7.9 | 28 | Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like |
| 88 | d1jj2y | Alignment | not modelled | 7.8 | 38 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae |
| 89 | c3j21i | Alignment | not modelled | 7.8 | 38 | PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 90 | c2qkdA | Alignment | not modelled | 7.8 | 23 | PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains |
| 91 | c4b6ap | Alignment | not modelled | 7.7 | 38 | PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1 |
| 92 | c2qa4Z | Alignment | not modelled | 7.7 | 46 | PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit |
| 93 | d1zr9a1 | Alignment | not modelled | 7.5 | 25 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger |
| 94 | c1zr9A | Alignment | not modelled | 7.5 | 25 | PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 593; PDBTitle: solution structure of a human c2h2-type zinc finger protein |
| 95 | d2k4xa1 | Alignment | not modelled | 7.5 | 50 | Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a |
| 96 | c2opfA | Alignment | not modelled | 7.4 | 28 | PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate |
| 97 | c2znmA | Alignment | not modelled | 7.4 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: oxidoreductase nm dsba3 from neisseria meningitidis |
| 98 | c6bo0A | Alignment | not modelled | 7.4 | 7 | PDB header: oxidoreductase Chain: A: PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchothii |
| 99 | c5ionA | Alignment | not modelled | 7.3 | 31 | PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 13 |