



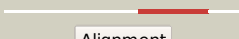


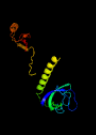



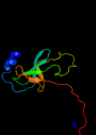

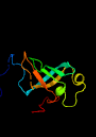


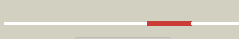
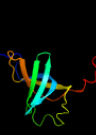

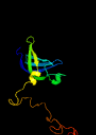




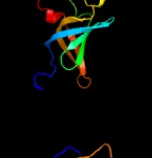
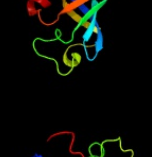
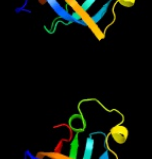

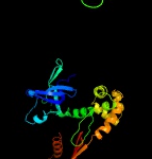

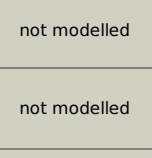


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1630_(rpsA)_1833549_1834994 |
| Date | Fri Aug 2 13:30:22 BST 2019 |
| Unique Job ID | f0c0697c2064d106 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3go5A_ |  Alignment |  | 100.0 | 22 | PDB header: gene regulation Chain: A; PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution |
| 2 | c4q7jD_ |  Alignment |  | 100.0 | 41 | PDB header: translation/transferase Chain: D; PDB Molecule: 30s ribosomal protein s1; PDBTitle: complex structure of viral rna polymerase |
| 3 | c4nnkA_ |  Alignment |  | 100.0 | 100 | PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of mycobacterium tuberculosis by pyrazinamide |
| 4 | c3j81j_ |  Alignment |  | 100.0 | 24 | PDB header: ribosome Chain: J; PDB Molecule: us4; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex |
| 5 | c1kl9A_ |  Alignment |  | 99.9 | 19 | PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 2 subunit 1; PDBTitle: crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha |
| 6 | c5x8r8_ |  Alignment |  | 99.9 | 30 | PDB header: ribosome Chain: 8; PDB Molecule: 30s ribosomal protein s1, chloroplastic; PDBTitle: structure of the 30s small subunit of chloroplast ribosome from2 spinach |
| 7 | c2cqoA_ |  Alignment |  | 99.9 | 28 | PDB header: ribosome Chain: A; PDB Molecule: nucleolar protein of 40 kda; PDBTitle: solution structure of the s1 rna binding domain of human2 hypothetical protein fj11067 |
| 8 | c1q46A_ |  Alignment |  | 99.9 | 24 | PDB header: translation Chain: A; PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia |
| 9 | c2khiA_ |  Alignment |  | 99.9 | 45 | PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1 |
| 10 | c2k4kA_ |  Alignment |  | 99.9 | 27 | PDB header: rna binding protein Chain: A; PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis |
| 11 | c5xq5A_ |  Alignment |  | 99.9 | 38 | PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 5 of the e. coli ribosomal protein s1 |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c2khjA | Alignment |  | 99.9 | 34 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1 |
| 13 | c1q8kA | Alignment |  | 99.9 | 22 | PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2 |
| 14 | c6qh2A | Alignment |  | 99.9 | 41 | PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphrylase at 298k compiled using the3 comand method |
| 15 | c1yz6A | Alignment |  | 99.8 | 29 | PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi |
| 16 | c2oceA | Alignment |  | 99.8 | 38 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 17 | d1q46a2 | Alignment |  | 99.8 | 31 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 18 | c2eqsA | Alignment |  | 99.8 | 40 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8 |
| 19 | c2ahoB | Alignment |  | 99.8 | 17 | PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha-gamma2 heterodimer from sulfobolus solfataricus complexed with gdpnp |
| 20 | c4aimA | Alignment |  | 99.8 | 35 | PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnase e2 recognition peptide |
| 21 | d1go3e1 | Alignment | not modelled | 99.8 | 26 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 22 | c5lm7A | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex |
| 23 | d3bzka4 | Alignment | not modelled | 99.8 | 36 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 24 | d1sroa | Alignment | not modelled | 99.8 | 43 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 25 | c2k52A | Alignment | not modelled | 99.8 | 27 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1198; PDBTitle: structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b |
| 26 | c1hh2P | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima |
| 27 | c2mfIA | Alignment | not modelled | 99.8 | 24 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 2 of e. coli ribosomal protein s1 |
| 28 | c3psiA | Alignment | not modelled | 99.8 | 21 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451) |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | d2ba0a1 | Alignment | not modelled | 99.8 | 23 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 30 | c1l2fA | Alignment | not modelled | 99.8 | 14 | PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain |
| 31 | d1kl9a2 | Alignment | not modelled | 99.8 | 33 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 32 | d1wi5a | Alignment | not modelled | 99.8 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 33 | c6gmhM | Alignment | not modelled | 99.8 | 24 | PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6 |
| 34 | c2mfiA | Alignment | not modelled | 99.7 | 18 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 1 of e. coli ribosomal protein s1 |
| 35 | d2ahob2 | Alignment | not modelled | 99.7 | 25 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 36 | d2z0sa1 | Alignment | not modelled | 99.7 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 37 | c2z0sA | Alignment | not modelled | 99.7 | 15 | PDB header: rna binding protein Chain: A: PDB Molecule: probable exosome complex rna-binding protein 1; PDBTitle: crystal structure of putative exosome complex rna-binding2 protein |
| 38 | d2je6i1 | Alignment | not modelled | 99.7 | 24 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 39 | d1y14b1 | Alignment | not modelled | 99.6 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 40 | d2nn6h1 | Alignment | not modelled | 99.6 | 18 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 41 | c6flqF | Alignment | not modelled | 99.5 | 18 | PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa |
| 42 | c2ba0A | Alignment | not modelled | 99.5 | 19 | PDB header: rna binding protein Chain: A: PDB Molecule: archaeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core |
| 43 | d1hh2p1 | Alignment | not modelled | 99.5 | 22 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 44 | d2nn6i1 | Alignment | not modelled | 99.4 | 20 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 45 | c2je6I | Alignment | not modelled | 99.4 | 20 | PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome |
| 46 | c1go3E | Alignment | not modelled | 99.4 | 26 | PDB header: transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: structure of an archeal homolog of the eukaryotic rna polymerase ii2 rpb4/rpb7 complex |
| 47 | d2c35b1 | Alignment | not modelled | 99.4 | 18 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 48 | c2bh8B | Alignment | not modelled | 99.4 | 24 | PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11 |
| 49 | c2pmzE | Alignment | not modelled | 99.3 | 29 | PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus |
| 50 | c4qiwE | Alignment | not modelled | 99.2 | 29 | PDB header: transcription Chain: E: PDB Molecule: dna-directed rna polymerase, subunit e'; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis |
| 51 | c5x50G | Alignment | not modelled | 99.2 | 21 | PDB header: transferase Chain: G: PDB Molecule: rna polymerase ii subunit; PDBTitle: rna polymerase ii from komagataella pastoris (type-2 crystal) |
| 52 | d1smxa | Alignment | not modelled | 99.2 | 22 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 53 | c2ba1B | Alignment | not modelled | 99.2 | 27 | PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core |
| 54 | c2c35F | Alignment | not modelled | 99.2 | 15 | PDB header: transferase Chain: F: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: subunits rpb4 and rpb7 of human rna polymerase ii PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 55 | c5xguB_ | Alignment | not modelled | 99.2 | 33 | Chain: B: PDB Molecule: ribonuclease r; PDBTitle: escherichia coli. rnase r |
| 56 | c2nn6I_ | Alignment | not modelled | 99.2 | 20 | PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 57 | c2b8kG_ | Alignment | not modelled | 99.1 | 18 | PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: 12-subunit rna polymerase ii |
| 58 | c4toiA_ | Alignment | not modelled | 99.1 | 32 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s2,ribosomal protein s1; PDBTitle: crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1 |
| 59 | c3h0gS_ | Alignment | not modelled | 99.1 | 18 | PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase ii subunit rpb7; PDBTitle: rna polymerase ii from schizosaccharomyces pombe |
| 60 | c4nbqB_ | Alignment | not modelled | 99.0 | 33 | PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii |
| 61 | c2ix1A_ | Alignment | not modelled | 98.9 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant |
| 62 | c1nt9G_ | Alignment | not modelled | 98.8 | 17 | PDB header: transcription, transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii |
| 63 | c4mtnA_ | Alignment | not modelled | 98.8 | 25 | PDB header: transcription regulator Chain: A: PDB Molecule: transcription termination factor nusa; PDBTitle: crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776 |
| 64 | c5c0wj_ | Alignment | not modelled | 98.5 | 31 | PDB header: hydrolase/rna Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates |
| 65 | c2wp8I_ | Alignment | not modelled | 98.5 | 28 | PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease |
| 66 | c2asbA_ | Alignment | not modelled | 98.5 | 31 | PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex |
| 67 | c2ckzB_ | Alignment | not modelled | 98.5 | 11 | PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase iii 25 kd polypeptide; PDBTitle: x-ray structure of rna polymerase iii subcomplex c17-c25. |
| 68 | d2asba1 | Alignment | not modelled | 98.5 | 34 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 69 | c4pmwB_ | Alignment | not modelled | 98.4 | 21 | PDB header: hydrolase/rna Chain: B: PDB Molecule: dis3-like exonuclease 2; PDBTitle: structure of mouse dis3l2 in complex with oligou rna substrate |
| 70 | c4oxpA_ | Alignment | not modelled | 98.3 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease e; PDBTitle: x-ray crystal structure of the s1 and 5'-sensor domains of rnase e2 from caulobacter crescentus |
| 71 | c4ifdH_ | Alignment | not modelled | 98.3 | 24 | PDB header: hydrolase/rna Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna |
| 72 | c4ifdI_ | Alignment | not modelled | 98.2 | 21 | PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna |
| 73 | c2vnuD_ | Alignment | not modelled | 98.2 | 30 | PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44 |
| 74 | c6d6rK_ | Alignment | not modelled | 98.2 | 23 | PDB header: hydrolase Chain: K: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction |
| 75 | d2nn6g1 | Alignment | not modelled | 98.2 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 76 | c6d6rH_ | Alignment | not modelled | 98.1 | 20 | PDB header: hydrolase Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction |
| 77 | c3ayhB_ | Alignment | not modelled | 98.1 | 16 | PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase iii subunit rpc8; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii |
| 78 | c2nn6H_ | Alignment | not modelled | 98.1 | 20 | PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 79 | c4ifdG_ | Alignment | not modelled | 98.0 | 22 | PDB header: hydrolase/rna Chain: G: PDB Molecule: exosome complex component rrp40; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna |
| 80 | c2r7fA_ | Alignment | not modelled | 97.9 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | structural genomics3 target drr63 |
| 81 | c2nn6G_ | Alignment | not modelled | 97.9 | 14 | PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 82 | c2c4rL_ | Alignment | not modelled | 97.8 | 25 | PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e |
| 83 | c1k0rB_ | Alignment | not modelled | 97.8 | 31 | PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa |
| 84 | d2ja9a1 | Alignment | not modelled | 97.7 | 23 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 85 | c2ja9A_ | Alignment | not modelled | 97.7 | 22 | PDB header: rna-binding protein Chain: A: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the n-terminal deletion of yeast exosome2 component rrp40 |
| 86 | c2rf4A_ | Alignment | not modelled | 97.6 | 13 | PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43 |
| 87 | c1e3pA_ | Alignment | not modelled | 97.4 | 39 | PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: tungstate derivative of streptomyces antibioticus pnpase/2 gpsi enzyme |
| 88 | c6j9eF_ | Alignment | not modelled | 97.1 | 18 | PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7 |
| 89 | d2ix0a3 | Alignment | not modelled | 96.7 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 90 | c5aj3f_ | Alignment | not modelled | 96.6 | 25 | PDB header: ribosome Chain: F: PDB Molecule: mitoribosomal protein bs6m, mrps6; PDBTitle: structure of the small subunit of the mammalian mitoribosome |
| 91 | c3i4oA_ | Alignment | not modelled | 95.7 | 31 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis |
| 92 | c4ql5A_ | Alignment | not modelled | 95.5 | 32 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4 |
| 93 | c6c00A_ | Alignment | not modelled | 95.5 | 35 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor 1 from clostridium2 difficile |
| 94 | c3d0fA_ | Alignment | not modelled | 95.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718 |
| 95 | c4ro1B_ | Alignment | not modelled | 95.3 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: dis3-like exonuclease 2; PDBTitle: an 3'-5'-exoribonuclease that specifically recognizes rnas. |
| 96 | d1wfga_ | Alignment | not modelled | 95.1 | 21 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 97 | c6f3hB_ | Alignment | not modelled | 95.0 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: exoribonuclease ii, mitochondrial; PDBTitle: crystal structure of dss1 exoribonuclease active site mutant d477n2 from candida glabrata |
| 98 | d1e3pa2 | Alignment | not modelled | 95.0 | 41 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 99 | d1ah9a_ | Alignment | not modelled | 94.9 | 27 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 100 | c2nchA_ | Alignment | not modelled | 94.7 | 28 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi |
| 101 | d1k3ra1 | Alignment | not modelled | 94.6 | 22 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain |
| 102 | c4c3jG_ | Alignment | not modelled | 94.2 | 16 | PDB header: transcription Chain: G: PDB Molecule: dna-directed rna polymerase i subunit rpa43; PDBTitle: structure of 14-subunit rna polymerase i at 3.35 a resolution,2 crystal form c2-90 |
| 103 | c5oikZ_ | Alignment | not modelled | 93.3 | 17 | PDB header: transcription Chain: Z: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of an rna polymerase ii-dsif transcription elongation2 complex |
| 104 | c4ytiB_ | Alignment | not modelled | 92.5 | 29 | PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5. |
| 105 | d1hr0w_ | Alignment | not modelled | 91.4 | 32 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| | | | | | | PDB header: dna binding protein |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 106 | c3aqqD_ | Alignment | not modelled | 90.7 | 20 | Chain: D; PDB Molecule: calcium-regulated heat stable protein 1; PDBTitle: crystal structure of human crhsp-24 |
| 107 | c4qvzB_ | Alignment | not modelled | 89.9 | 20 | PDB header: translation Chain: B; PDB Molecule: fragile x mental retardation protein 1; PDBTitle: fmrp n-terminal domain |
| 108 | d1h95a_ | Alignment | not modelled | 89.5 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 109 | c5vl1D_ | Alignment | not modelled | 89.1 | 22 | PDB header: ligase Chain: D; PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine |
| 110 | d1jga_ | Alignment | not modelled | 88.8 | 21 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 111 | d1luz_ | Alignment | not modelled | 87.3 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 112 | c2yvtA_ | Alignment | not modelled | 87.0 | 17 | PDB header: rna binding protein Chain: A; PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 113 | c2yvtA_ | Alignment | not modelled | 86.5 | 23 | PDB header: rna binding protein Chain: A; PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 114 | d1e1oa1 | Alignment | not modelled | 85.8 | 20 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 115 | c2lssA_ | Alignment | not modelled | 85.3 | 20 | PDB header: rna binding protein, dna binding protein Chain: A; PDB Molecule: cold shock-like protein; PDBTitle: solution structure of the r. rickettsii cold shock-like protein |
| 116 | c2ytxA_ | Alignment | not modelled | 84.9 | 19 | PDB header: rna binding protein Chain: A; PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 117 | c1e22A_ | Alignment | not modelled | 84.6 | 20 | PDB header: ligase Chain: A; PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp |
| 118 | d1bbua1 | Alignment | not modelled | 84.2 | 22 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 119 | c1h9mB_ | Alignment | not modelled | 81.4 | 23 | PDB header: binding protein Chain: B; PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. peg-grown form with4 molybdate bound |
| 120 | c2bkdN_ | Alignment | not modelled | 80.8 | 16 | PDB header: nuclear protein Chain: N; PDB Molecule: fragile x mental retardation 1 protein; PDBTitle: structure of the n-terminal domain of fragile x mental retardation2 protein |