








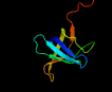







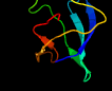

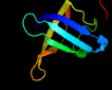

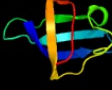


Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0871_(cspB)_967901_968308 |
| Date | Fri Jul 26 01:50:46 BST 2019 |
| Unique Job ID | 8022bbf22df1fd71 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3a0jB_ |  Alignment |  | 99.9 | 40 | PDB header: transcription Chain: B: PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8 |
| 2 | d2es2a1 |  Alignment |  | 99.9 | 45 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 3 | c2k5nA_ |  Alignment |  | 99.9 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein eca15802 from erwinia carotovora, northeast structural genomics consortium3 target ewr156a |
| 4 | d1c9oa_ |  Alignment |  | 99.9 | 45 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 5 | c5o6fA_ |  Alignment |  | 99.9 | 34 | PDB header: dna binding protein Chain: A: PDB Molecule: cold-shock protein; PDBTitle: nmr structure of cold shock protein a from corynebacterium2 pseudotuberculosis |
| 6 | c5xv9A_ |  Alignment |  | 99.9 | 40 | PDB header: rna binding protein Chain: A: PDB Molecule: cold-shock dna-binding domain family protein; PDBTitle: solution structure of cold shock protein from colwellia2 psychrerythraea |
| 7 | c4a4iA_ |  Alignment |  | 99.9 | 34 | PDB header: rna binding protein Chain: A: PDB Molecule: protein lin-28 homolog b; PDBTitle: crystal structure of the human lin28b cold shock domain |
| 8 | d1g6pa_ |  Alignment |  | 99.9 | 48 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 9 | c2kcmA_ |  Alignment |  | 99.9 | 30 | PDB header: nucleic acid binding protein Chain: A: PDB Molecule: cold shock domain family protein; PDBTitle: solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a. |
| 10 | c3aqqD_ |  Alignment |  | 99.8 | 24 | PDB header: dna binding protein Chain: D: PDB Molecule: calcium-regulated heat stable protein 1; PDBTitle: crystal structure of human crhsp-24 |
| 11 | d1mjca_ |  Alignment |  | 99.8 | 45 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3camB_ | Alignment | | 99.8 | 44 | PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis |
| 13 | d1h95a_ | Alignment | | 99.8 | 31 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 14 | c2lssA_ | Alignment | | 99.8 | 44 | 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 |
| 15 | c3trzE_ | Alignment | | 99.8 | 32 | PDB header: rna binding protein/rna Chain: E: PDB Molecule: protein lin-28 homolog a; PDBTitle: mouse lin28a in complex with let-7d microrna pre-element |
| 16 | c2mqhA_ | Alignment | | 99.8 | 39 | PDB header: dna binding protein Chain: A: PDB Molecule: nucleic acid binding protein; PDBTitle: solution structure of the chlamydomonas reinhardtii nab1 cold shock2 domain, csd1 |
| 17 | d1wfga_ | Alignment | | 99.7 | 32 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 18 | c2ytvA_ | Alignment | | 99.7 | 24 | 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) |
| 19 | c2ytxA_ | Alignment | | 99.6 | 25 | 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) |
| 20 | c1x65A_ | Alignment | | 99.5 | 17 | PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 21 | c2ytvA_ | Alignment | not modelled | 99.5 | 25 | 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) |
| 22 | c2bh8B_ | Alignment | not modelled | 99.4 | 48 | PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11 |
| 23 | d2ix0a2 | Alignment | not modelled | 97.2 | 29 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 24 | c2ix1A_ | Alignment | not modelled | 96.7 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant |
| 25 | d1a62a2 | Alignment | not modelled | 94.4 | 28 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 26 | c2a8vA_ | Alignment | not modelled | 92.6 | 31 | PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex |
| 27 | d1smxa_ | Alignment | not modelled | 91.9 | 23 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 28 | d2ix0a1 | Alignment | not modelled | 91.9 | 13 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 29 | c2l0aA_ | Alignment | not modelled | 90.7 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: transcription termination factor rho; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c300A | Alignment | not modelled | 85.7 | 18 | PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima |
| 30 | c1hh2P | Alignment | not modelled | 87.9 | 18 | PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima |
| 31 | c4aimA | Alignment | not modelled | 87.0 | 33 | PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnae2 recognition peptide |
| 32 | d1y14b1 | Alignment | not modelled | 84.9 | 23 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 33 | c1l2fA | Alignment | not modelled | 84.9 | 18 | 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 |
| 34 | c4oxpA | Alignment | not modelled | 83.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease e; PDBTitle: x-ray crystal structure of the s1 and 5'-sensor domains of rnae2 from caulobacter crescentus |
| 35 | c5xguB | Alignment | not modelled | 82.5 | 36 | PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease r; PDBTitle: escherichia coli. rnae r |
| 36 | d1kl9a2 | Alignment | not modelled | 81.8 | 20 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 37 | c1zeqX | Alignment | not modelled | 81.0 | 18 | PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli |
| 38 | c3go5A | Alignment | not modelled | 80.8 | 17 | 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 |
| 39 | d1hh2p1 | Alignment | not modelled | 80.3 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 40 | c2k52A | Alignment | not modelled | 79.6 | 16 | 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 |
| 41 | c5lm7A | Alignment | not modelled | 77.3 | 20 | PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex |
| 42 | d2c35b1 | Alignment | not modelled | 76.2 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 43 | c1xpuB | Alignment | not modelled | 75.1 | 22 | PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomyacin (fpdb) |
| 44 | c2l55A | Alignment | not modelled | 71.0 | 29 | PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans |
| 45 | c6qh2A | Alignment | not modelled | 69.6 | 29 | PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method |
| 46 | d2ba0a1 | Alignment | not modelled | 67.0 | 12 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 47 | c2gu1A | Alignment | not modelled | 66.5 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 48 | c5x50G | Alignment | not modelled | 65.8 | 24 | PDB header: transferase Chain: G: PDB Molecule: rna polymerase ii subunit; PDBTitle: rna polymerase ii from komagataella pastoris (type-2 crystal) |
| 49 | c2c4rL | Alignment | not modelled | 65.7 | 19 | PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnae e |
| 50 | d1wi5a | Alignment | not modelled | 65.0 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 51 | c6flqF | Alignment | not modelled | 62.4 | 20 | 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 |
| 52 | c2b8kG | Alignment | not modelled | 61.6 | 23 | PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: 12-subunit rna polymerase ii |
| 53 | c2vnuD | Alignment | not modelled | 61.5 | 16 | PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44 |
| | | | | | | PDB header: hydrolase/rna |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c4pmwB_ | Alignment | not modelled | 60.4 | 12 | Chain: B; PDB Molecule: dis3-like exonuclease 2; PDBTitle: structure of mouse dis3l2 in complex with oligou rna substrate |
| 55 | c5x8r8_ | Alignment | not modelled | 59.2 | 31 | PDB header: ribosome Chain: 8; PDB Molecule: 30s ribosomal protein s1, chloroplastic; PDBTitle: structure of the 30s small subunit of chloroplast ribosome from2 spinach |
| 56 | c2mf1A_ | Alignment | not modelled | 58.3 | 23 | PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 2 of e. coli ribosomal protein s1 |
| 57 | d1t9ha1 | Alignment | not modelled | 57.6 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 58 | d2z0sa1 | Alignment | not modelled | 56.5 | 13 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 59 | c2c35F_ | Alignment | not modelled | 56.0 | 17 | 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 |
| 60 | c3bpuA_ | Alignment | not modelled | 55.2 | 21 | PDB header: transferase Chain: A; PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant |
| 61 | c5n7gA_ | Alignment | not modelled | 54.8 | 18 | PDB header: signaling protein Chain: A; PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: magi-1 complexed with a synthetic prsk1 peptide |
| 62 | c3tufB_ | Alignment | not modelled | 51.0 | 18 | PDB header: signaling protein Chain: B; PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex. |
| 63 | d1go3e1 | Alignment | not modelled | 50.6 | 26 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 64 | c1ybyB_ | Alignment | not modelled | 50.5 | 16 | PDB header: translation Chain: B; PDB Molecule: translation elongation factor p; PDBTitle: conserved hypothetical protein cth-95 from clostridium thermocellum |
| 65 | c3h0gS_ | Alignment | not modelled | 50.3 | 29 | PDB header: transcription Chain: S; PDB Molecule: dna-directed rna polymerase ii subunit rpb7; PDBTitle: rna polymerase ii from schizosaccharomyces pombe |
| 66 | c2oceA_ | Alignment | not modelled | 50.1 | 26 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 67 | c2eqsA_ | Alignment | not modelled | 49.3 | 26 | 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 |
| 68 | c3sluB_ | Alignment | not modelled | 47.3 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315 |
| 69 | c3nyyA_ | Alignment | not modelled | 45.8 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution |
| 70 | d1q46a2 | Alignment | not modelled | 44.5 | 10 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 71 | d2asba1 | Alignment | not modelled | 44.5 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 72 | d1gpra_ | Alignment | not modelled | 41.4 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 73 | d2gpra_ | Alignment | not modelled | 39.0 | 22 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 74 | c2xnqA_ | Alignment | not modelled | 38.7 | 21 | PDB header: rna binding protein Chain: A; PDB Molecule: nuclear polyadenylated rna-binding protein 3; PDBTitle: structural insights into cis element recognition of non-2 polyadenylated rnas by the nab3-rrm |
| 75 | d2f3ga_ | Alignment | not modelled | 37.7 | 20 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 76 | c2k4kA_ | Alignment | not modelled | 37.1 | 23 | PDB header: rna binding protein Chain: A; PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis |
| 77 | d1glaf_ | Alignment | not modelled | 36.7 | 20 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 78 | d1u0la1 | Alignment | not modelled | 35.0 | 14 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 79 | c2ahoB_ | Alignment | not modelled | 34.9 | 18 | PDB header: translation Chain: B; PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha- |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | gamma2 heterodimer from sulfobolus solfataricus complexed with gdpnp |
| 80 | c2dhxA | Alignment | not modelled | 34.1 | 21 | PDB header: rna binding protein Chain: A: PDB Molecule: poly (adp-ribose) polymerase family, member 10 PDBTitle: solution structure of the rrm domain in the human poly (adp-2 ribose) polymerase family, member 10 variant |
| 81 | d1ueqa | Alignment | not modelled | 34.0 | 17 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain |
| 82 | d1sr3a | Alignment | not modelled | 33.4 | 17 | Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE |
| 83 | c1nt9G | Alignment | not modelled | 32.0 | 22 | PDB header: transcription, transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii |
| 84 | c4wija | Alignment | not modelled | 32.0 | 38 | PDB header: transcription Chain: A: PDB Molecule: splicing factor, proline- and glutamine-rich; PDBTitle: human splicing factor, construct 1 |
| 85 | c4cn0A | Alignment | not modelled | 30.1 | 14 | PDB header: cell cycle Chain: A: PDB Molecule: protein ahnak2; PDBTitle: an intertwined homodimer of the pdz homology domain of ahnak2 |
| 86 | d3bzka4 | Alignment | not modelled | 28.6 | 30 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 87 | c2kjda | Alignment | not modelled | 28.4 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: sodium/hydrogen exchange regulatory cofactor nhe- PDBTitle: solution structure of extended pdz2 domain from nherf1 (150-2 270) |
| 88 | d1j6qa | Alignment | not modelled | 27.4 | 18 | Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE |
| 89 | c1j6qa | Alignment | not modelled | 27.4 | 18 | PDB header: chaperone Chain: A: PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme2 chaperone ccme |
| 90 | d1uwva1 | Alignment | not modelled | 26.5 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain |
| 91 | c3mk4B | Alignment | not modelled | 26.4 | 20 | PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray structure of human pex3 in complex with a pex19 derived peptide |
| 92 | d1m5za | Alignment | not modelled | 26.3 | 19 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain |
| 93 | c1go3E | Alignment | not modelled | 26.1 | 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 |
| 94 | c4pqxC | Alignment | not modelled | 26.0 | 15 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a nigd-like protein (baccac_02139) from2 bacteroides caccae atcc 43185 at 2.39 a resolution |
| 95 | d2nn6h1 | Alignment | not modelled | 25.9 | 15 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 96 | c3ajbB | Alignment | not modelled | 24.6 | 20 | PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: crystal structure of human pex3p in complex with n-terminal pex19p2 peptide |
| 97 | c4mntA | Alignment | not modelled | 24.6 | 12 | 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 |
| 98 | c2cqoA | Alignment | not modelled | 23.2 | 14 | 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 flj11067 |
| 99 | c3a5zD | Alignment | not modelled | 22.8 | 16 | PDB header: ligase Chain: D: PDB Molecule: elongation factor p; PDBTitle: crystal structure of escherichia coli genx in complex with elongation2 factor p |
| 100 | d1tp5a1 | Alignment | not modelled | 22.8 | 19 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain |
| 101 | d1wfla | Alignment | not modelled | 21.7 | 20 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 102 | c1t9hA | Alignment | not modelled | 21.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase. |
| 103 | c3l0oB | Alignment | not modelled | 21.2 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima |
| 104 | c3soeA | Alignment | not modelled | 20.2 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of the human membrane-2 associated guanylate kinase, ww and pdz domain-containing protein 33 (magi3) |