
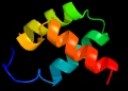
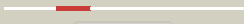




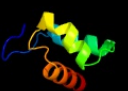





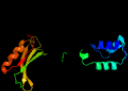



















Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1047_(-)_1169428_1170675 |
| Date | Wed Jul 31 22:05:12 BST 2019 |
| Unique Job ID | 5b50d4fe67b3a011 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | d1k78a1 |  Alignment |  | 92.9 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 2 | d1pdnc_ |  Alignment |  | 92.0 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 3 | d6paxa1 |  Alignment |  | 92.0 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 4 | c6paxA_ |  Alignment |  | 90.7 | 10 | PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions |
| 5 | d1au7a2 |  Alignment |  | 89.0 | 10 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 6 | d1e3oc2 |  Alignment |  | 88.9 | 15 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 7 | c4fcyA_ |  Alignment |  | 88.5 | 19 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transposome |
| 8 | c2m8eA_ |  Alignment |  | 86.2 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase |
| 9 | c1u78A_ |  Alignment |  | 85.7 | 21 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna |
| 10 | c1au7B_ |  Alignment |  | 85.4 | 11 | PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex |
| 11 | c2r0qF_ |  Alignment |  | 82.3 | 16 | PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex |

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|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c2k27A_ | Alignment |  | 80.8 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain |
| 13 | c1hf0A_ | Alignment |  | 80.7 | 15 | PDB header: transcription Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer |
| 14 | d1bcoa2 | Alignment |  | 79.9 | 28 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain |
| 15 | c3d1nK_ | Alignment |  | 79.5 | 18 | PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter |
| 16 | c3zeyG_ | Alignment |  | 78.1 | 14 | PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 17 | c1rp3G_ | Alignment |  | 77.8 | 20 | PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm |
| 18 | c3l1pA_ | Alignment |  | 77.7 | 20 | PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex |
| 19 | c2xzmO_ | Alignment |  | 76.2 | 6 | PDB header: ribosome Chain: O: PDB Molecule: rps13e; 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 |
| 20 | c3u5cN_ | Alignment |  | 76.0 | 6 | PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a |
| 21 | c3izbO_ | Alignment | not modelled | 75.4 | 7 | PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein rps13 (s15p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 22 | c2gm4B_ | Alignment | not modelled | 74.0 | 15 | PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna |
| 23 | c3frwF_ | Alignment | not modelled | 72.6 | 22 | PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trp protein from ruminococcus obeum |
| 24 | c3korD_ | Alignment | not modelled | 70.5 | 21 | PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 25 | c1iufA_ | Alignment | not modelled | 69.2 | 8 | PDB header: dna binding protein Chain: A: PDB Molecule: centromere abp1 protein; PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein |
| 26 | c2xsdC_ | Alignment | not modelled | 68.5 | 15 | PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna |
| 27 | d1jhga_ | Alignment | not modelled | 68.1 | 8 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 28 | c6jnyA_ | Alignment | not modelled | 62.7 | 15 | PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein |

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|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | d1xsva_ | Alignment | not modelled | 62.6 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 30 | d1trra_ | Alignment | not modelled | 61.3 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 31 | c1zljE_ | Alignment | not modelled | 60.7 | 10 | PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain |
| 32 | d1yb3a1 | Alignment | not modelled | 59.5 | 13 | Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like |
| 33 | d1yioa1 | Alignment | not modelled | 57.9 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 34 | c3hosA_ | Alignment | not modelled | 57.4 | 13 | PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg |
| 35 | d1l3la1 | Alignment | not modelled | 56.0 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 36 | c3j20Q_ | Alignment | not modelled | 53.5 | 14 | PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s15p/s13e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 37 | c2jpcA_ | Alignment | not modelled | 50.3 | 10 | PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein |
| 38 | c3mzyA_ | Alignment | not modelled | 49.4 | 13 | PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a |
| 39 | c2rnjA_ | Alignment | not modelled | 49.1 | 8 | PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain |
| 40 | c1x3uA_ | Alignment | not modelled | 47.7 | 10 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot |
| 41 | d1fsea_ | Alignment | not modelled | 47.6 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 42 | c3sztB_ | Alignment | not modelled | 46.5 | 5 | PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone |
| 43 | d1iufa1 | Alignment | not modelled | 46.0 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding |
| 44 | c5xyiN_ | Alignment | not modelled | 45.9 | 11 | PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 45 | c6jqsA_ | Alignment | not modelled | 45.6 | 11 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere |
| 46 | c3cloC_ | Alignment | not modelled | 42.9 | 14 | PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution |
| 47 | c3c3wB_ | Alignment | not modelled | 42.7 | 10 | PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr |
| 48 | c5ipmF_ | Alignment | not modelled | 42.6 | 12 | PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna |
| 49 | c1bcoA_ | Alignment | not modelled | 42.1 | 24 | PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain |
| 50 | d1a04a1 | Alignment | not modelled | 40.7 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 51 | c2lvsA_ | Alignment | not modelled | 40.4 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein |
| 52 | d2bw3a2 | Alignment | not modelled | 38.8 | 16 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Hermes transposase-like |
| 53 | d1p4wa_ | Alignment | not modelled | 38.2 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 54 | c2krfB_ | Alignment | not modelled | 38.2 | 11 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; |

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|----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | c2k1tD | Alignment | not modelled | 38.2 | 11 | PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a PDB header: transcription regulator |
| 55 | c5f64C | Alignment | not modelled | 37.4 | 21 | Chain: C; PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri |
| 56 | c4kisA | Alignment | not modelled | 37.0 | 10 | PDB header: recombination/dna Chain: A; PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex |
| 57 | c3qyxD | Alignment | not modelled | 36.3 | 5 | PDB header: transcription/dna Chain: D; PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment |
| 58 | c3kinC | Alignment | not modelled | 34.0 | 13 | PDB header: transcription Chain: C; PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst |
| 59 | c2mqkA | Alignment | not modelled | 33.2 | 11 | PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase |
| 60 | d2p5ka1 | Alignment | not modelled | 31.9 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain |
| 61 | c2m0nA | Alignment | not modelled | 31.9 | 26 | PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c, seattle structural genomics center for3 infectious disease target myaba.17112.a.a2 |
| 62 | c1e1cA | Alignment | not modelled | 29.1 | 18 | PDB header: isomerase Chain: A; PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant |
| 63 | d1s7oa | Alignment | not modelled | 27.6 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 64 | c5o8yG | Alignment | not modelled | 27.2 | 17 | PDB header: transcription Chain: G; PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator. |
| 65 | c5nwtM | Alignment | not modelled | 27.0 | 11 | PDB header: transferase Chain: M; PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex |
| 66 | c3nf9A | Alignment | not modelled | 26.9 | 28 | PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design |
| 67 | c5u1cD | Alignment | not modelled | 26.7 | 22 | PDB header: viral protein Chain: D; PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome |
| 68 | d1f9na1 | Alignment | not modelled | 26.2 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain |
| 69 | d1pbua | Alignment | not modelled | 25.6 | 15 | Fold: Ferredoxin-like Superfamily: eEF1-gamma domain Family: eEF1-gamma domain |
| 70 | c2vzbzA | Alignment | not modelled | 24.9 | 15 | PDB header: dna-binding protein Chain: A; PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan |
| 71 | c4go1A | Alignment | not modelled | 24.5 | 19 | PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator lsr;rr; PDBTitle: crystal structure of full length transcription repressor lsr from e.2 coli. |
| 72 | c6cy1B | Alignment | not modelled | 24.1 | 13 | PDB header: signaling protein Chain: B; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis |
| 73 | c4if4A | Alignment | not modelled | 24.0 | 8 | PDB header: transcription Chain: A; PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus |
| 74 | d1stza1 | Alignment | not modelled | 23.9 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain |
| 75 | d1b4aa1 | Alignment | not modelled | 23.7 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain |
| 76 | d2fnaa1 | Alignment | not modelled | 23.3 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain |
| 77 | c5z7iC | Alignment | not modelled | 22.1 | 18 | PDB header: dna binding protein/dna Chain: C; PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna |
| 78 | c5zx3F | Alignment | not modelled | 21.5 | 7 | PDB header: transcription Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h |
| 79 | c6ideA | Alignment | not modelled | 21.3 | 21 | PDB header: transcription/dna Chain: A; PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design |

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|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80 | c5hevC | Alignment | not modelled | 20.8 | 10 | PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium |
| 81 | c2khqA | Alignment | not modelled | 20.6 | 7 | PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b |
| 82 | c5cz1B | Alignment | not modelled | 20.4 | 9 | PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase |
| 83 | d1z6ra1 | Alignment | not modelled | 19.8 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain |
| 84 | c2q0oA | Alignment | not modelled | 19.6 | 10 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing |
| 85 | c2bw3A | Alignment | not modelled | 19.2 | 14 | PDB header: dna recombination Chain: A: PDB Molecule: transposase; PDBTitle: three-dimensional structure of the hermes dna transposase |
| 86 | c1h0mD | Alignment | not modelled | 18.7 | 10 | PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna |
| 87 | d2ch5a2 | Alignment | not modelled | 18.6 | 25 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like |
| 88 | c3c65A | Alignment | not modelled | 18.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvrC 5' endonuclease2 domain |
| 89 | c1r6uB | Alignment | not modelled | 18.1 | 13 | PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity |
| 90 | c4lfuA | Alignment | not modelled | 17.3 | 10 | PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2 |
| 91 | c5uxxC | Alignment | not modelled | 17.2 | 6 | PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana |
| 92 | d1g3wa1 | Alignment | not modelled | 17.2 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |
| 93 | c2gqgB | Alignment | not modelled | 16.9 | 17 | PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp) |
| 94 | c2e7xA | Alignment | not modelled | 16.8 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand |
| 95 | d1ku3a | Alignment | not modelled | 15.9 | 5 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 96 | c4yn8A | Alignment | not modelled | 15.9 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system |
| 97 | c2hteB | Alignment | not modelled | 15.9 | 9 | PDB header: transferase Chain: B: PDB Molecule: spermidine synthase; PDBTitle: the crystal structure of spermidine synthase from p. falciparum in2 complex with 5'-methylthioadenosine |
| 98 | c4n1vA | Alignment | not modelled | 15.7 | 11 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu-beta; PDBTitle: structure of dna-binding protein hu from micoplasma spiroplasma2 melliferum |
| 99 | d2isya1 | Alignment | not modelled | 15.6 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |