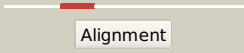

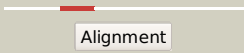



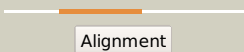
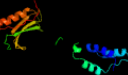
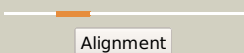

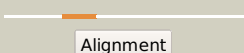


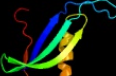




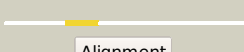

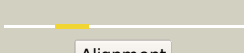

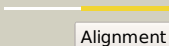

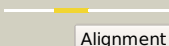
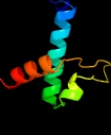
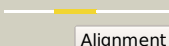

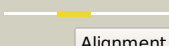

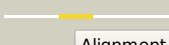

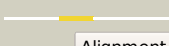


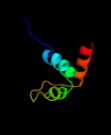







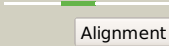
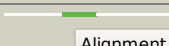


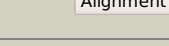


Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3640c_(-)_4078699_4079928 |
| Date | Fri Aug 9 18:20:32 BST 2019 |
| Unique Job ID | 89179578b8a9d639 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1k78a1 |  Alignment |  | 91.0 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 2 | d6paxa1 |  Alignment |  | 90.5 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 3 | c6paxA_ |  Alignment |  | 87.6 | 14 | 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 |
| 4 | c4fcyA_ |  Alignment |  | 87.4 | 18 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome |
| 5 | d1pdnc_ |  Alignment |  | 87.1 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 6 | c1rp3G_ |  Alignment |  | 82.1 | 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 |
| 7 | d1bcoa2 |  Alignment |  | 81.5 | 22 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain |
| 8 | c1au7B_ |  Alignment |  | 81.4 | 21 | PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex |
| 9 | d1e3oc2 |  Alignment |  | 81.2 | 18 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 10 | d1au7a2 |  Alignment |  | 79.7 | 19 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 11 | c1u78A_ |  Alignment |  | 76.0 | 7 | 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 |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c2bw3A_ |  Alignment |  | 72.7 | 17 | PDB header: dna recombination Chain: A: PDB Molecule: transposase; PDBTitle: three-dimensional structure of the hermes dna transposase |
| 13 | c3korD_ |  Alignment |  | 71.6 | 17 | PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 14 | d1jhga_ |  Alignment |  | 71.4 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 15 | c2r0qF_ |  Alignment |  | 70.8 | 26 | PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex |
| 16 | c2k27A_ |  Alignment |  | 70.7 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain |
| 17 | c3l1pA_ |  Alignment |  | 70.4 | 16 | PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex |
| 18 | c2m8eA_ |  Alignment |  | 69.3 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase |
| 19 | c3frwF_ |  Alignment |  | 69.2 | 17 | PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum |
| 20 | c1hf0A_ |  Alignment |  | 66.0 | 19 | 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 |
| 21 | c3hosA_ |  Alignment | not modelled | 62.6 | 14 | 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 |
| 22 | c2gm4B_ |  Alignment | not modelled | 62.5 | 18 | 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 | c3d1nK_ |  Alignment | not modelled | 61.3 | 20 | 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 |
| 24 | c3mzyA_ |  Alignment | not modelled | 59.1 | 14 | 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 |
| 25 | d1trra_ |  Alignment | not modelled | 59.1 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 26 | c1zljE_ |  Alignment | not modelled | 57.2 | 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 |
| 27 | d1xsva_ |  Alignment | not modelled | 56.5 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 28 | c2xsdC_ |  Alignment | not modelled | 55.0 | 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 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | d2bw3a2 | Alignment | not modelled | 50.6 | 16 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Hermes transposase-like |
| 30 | d1hyva | Alignment | not modelled | 48.8 | 21 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain |
| 31 | c2jpcA | Alignment | not modelled | 47.8 | 13 | PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein |
| 32 | c1iufA | Alignment | not modelled | 46.5 | 14 | 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 |
| 33 | d13la1 | Alignment | not modelled | 46.2 | 16 | 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 | c6jqsA | Alignment | not modelled | 45.6 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere |
| 35 | d1fsea | Alignment | not modelled | 44.8 | 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) |
| 36 | c1x3uA | Alignment | not modelled | 42.8 | 19 | 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 |
| 37 | c2rniA | Alignment | not modelled | 41.1 | 10 | PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain |
| 38 | c3izbO | Alignment | not modelled | 40.1 | 12 | 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 |
| 39 | c2krfB | Alignment | not modelled | 40.1 | 10 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a |
| 40 | c3lysC | Alignment | not modelled | 38.1 | 6 | PDB header: recombination Chain: C: PDB Molecule: prophage pi2 protein 01, integrase; PDBTitle: crystal structure of the n-terminal domain of the prophage pi2 protein2 01 (integrase) from lactococcus lactis, northeast structural genomics3 consortium target kr124f |
| 41 | d1yioa1 | Alignment | not modelled | 38.0 | 12 | 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 | d1p4wa | Alignment | not modelled | 36.9 | 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) |
| 43 | d1iufa1 | Alignment | not modelled | 36.8 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding |
| 44 | d2hzaa1 | Alignment | not modelled | 35.0 | 24 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 45 | c6jnyA | Alignment | not modelled | 34.6 | 15 | PDB header: transcription Chain: A: PDB Molecule: antiterminal q protein; PDBTitle: crystal structure of bacteriophage 21 q protein |
| 46 | c2lvsA | Alignment | not modelled | 34.2 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein |
| 47 | c2khqA | Alignment | not modelled | 33.6 | 3 | 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 |
| 48 | c1bcoA | Alignment | not modelled | 33.2 | 22 | PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain |
| 49 | c3sztB | Alignment | not modelled | 30.6 | 11 | 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 |
| 50 | c4go1A | Alignment | not modelled | 30.6 | 23 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lssr; PDBTitle: crystal structure of full length transcription repressor lssr from e.2 coli. |
| 51 | c3cloC | Alignment | not modelled | 30.5 | 18 | 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 |
| 52 | d1a04a1 | Alignment | not modelled | 28.3 | 9 | 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) |
| 53 | d2hzab1 | Alignment | not modelled | 28.1 | 24 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 54 | c2mkA | Alignment | not modelled | 27.1 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c4mq3A | Alignment | not modelled | 27.1 | 7 | PDBTitle: solution structure of n terminal domain of the nub aaa+ atpase PDB header: viral protein |
| 55 | c4mq3A | Alignment | not modelled | 26.6 | 11 | Chain: A; PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of hiv integrase |
| 56 | d1z6ra1 | Alignment | not modelled | 26.2 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain |
| 57 | c3j20Q | Alignment | not modelled | 25.4 | 13 | 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) |
| 58 | c3zeyG | Alignment | not modelled | 24.4 | 11 | PDB header: ribosome Chain: G; PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 59 | c6ez8A | Alignment | not modelled | 23.5 | 21 | PDB header: protein binding Chain: A; PDB Molecule: huntingtin; PDBTitle: human huntingtin-hap40 complex structure |
| 60 | c3iwfA | Alignment | not modelled | 23.1 | 9 | PDB header: transcription regulator Chain: A; PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a |
| 61 | c3q5xA | Alignment | not modelled | 23.1 | 16 | PDB header: cell cycle Chain: A; PDB Molecule: protein cut8; PDBTitle: structure of proteasome tether |
| 62 | c3qyxD | Alignment | not modelled | 22.2 | 16 | 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 |
| 63 | c3u5cN | Alignment | not modelled | 21.5 | 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 |
| 64 | c5mlqA | Alignment | not modelled | 21.4 | 29 | PDB header: ligase Chain: A; PDB Molecule: cdps; PDBTitle: structure of cdps from nocardia brasiliensis |
| 65 | d1smyf2 | Alignment | not modelled | 21.4 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 66 | c5jpmF | Alignment | not modelled | 21.0 | 13 | 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 |
| 67 | c2w48D | Alignment | not modelled | 21.0 | 18 | PDB header: transcription Chain: D; PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae |
| 68 | c3hugA | Alignment | not modelled | 20.5 | 20 | PDB header: transcription/membrane protein Chain: A; PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl |
| 69 | c2keyA | Alignment | not modelled | 20.2 | 10 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c |
| 70 | d2bj7a1 | Alignment | not modelled | 20.2 | 18 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 71 | d1s7oa | Alignment | not modelled | 20.0 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 72 | c5cz1B | Alignment | not modelled | 19.7 | 14 | PDB header: hydrolase Chain: B; PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase |
| 73 | c2kd1A | Alignment | not modelled | 19.3 | 6 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: dna integration/recombination/inversion protein; PDBTitle: solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f |
| 74 | c2derA | Alignment | not modelled | 18.3 | 16 | PDB header: transferase/rna Chain: A; PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state |
| 75 | d1stza1 | Alignment | not modelled | 18.0 | 8 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain |
| 76 | d1yb3a1 | Alignment | not modelled | 17.2 | 13 | Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like |
| 77 | c3geiB | Alignment | not modelled | 17.1 | 9 | PDB header: hydrolase Chain: B; PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp |
| 78 | c2xzmO | Alignment | not modelled | 16.6 | 10 | 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 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 79 | c5wurB | Alignment | not modelled | 16.1 | 16 | PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form |
| 80 | d2fcja1 | Alignment | not modelled | 16.1 | 26 | Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain |
| 81 | c5f64C | Alignment | not modelled | 15.9 | 18 | PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri |
| 82 | c4ky3A | Alignment | not modelled | 15.5 | 13 | PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327 |
| 83 | c3nvbA | Alignment | not modelled | 15.5 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate |
| 84 | c3c3wB | Alignment | not modelled | 15.4 | 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 |
| 85 | d1j0ga | Alignment | not modelled | 15.1 | 31 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like |
| 86 | c5z7iC | Alignment | not modelled | 14.7 | 12 | 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 |
| 87 | c5zx3F | Alignment | not modelled | 14.0 | 14 | 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 |
| 88 | c3leqA | Alignment | not modelled | 13.8 | 21 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cvnb5; PDBTitle: the crystal structure of the roadblock/lc7 domain from streptomyces2 avermitilis to 1.85a |
| 89 | c4kisA | Alignment | not modelled | 13.6 | 3 | PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex |
| 90 | c3nrwA | Alignment | not modelled | 13.6 | 9 | PDB header: recombination Chain: A: PDB Molecule: phage integrase/site-specific recombinase; PDBTitle: crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a |
| 91 | d1v9sa1 | Alignment | not modelled | 13.5 | 18 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 92 | c2oxoA | Alignment | not modelled | 12.8 | 13 | PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase |
| 93 | c3vepA | Alignment | not modelled | 12.7 | 23 | PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda |
| 94 | d1efaa1 | Alignment | not modelled | 12.5 | 28 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 95 | c5uxxC | Alignment | not modelled | 12.5 | 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 |
| 96 | c3klnC | Alignment | not modelled | 12.4 | 9 | PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst |
| 97 | c6gh5M | Alignment | not modelled | 12.3 | 15 | PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex |
| 98 | c5c0xK | Alignment | not modelled | 12.1 | 19 | PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to structured2 rna |
| 99 | d1vi0a1 | Alignment | not modelled | 12.0 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain |