





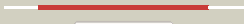
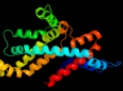


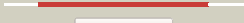









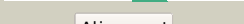







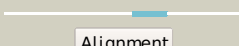

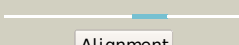

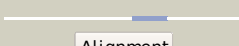

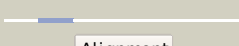





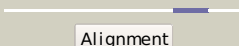

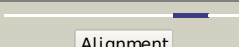
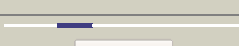

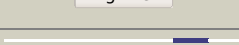
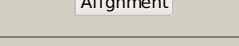
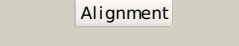



| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3fh6F_ |  Alignment |  | 100.0 | 18 | PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli |
| 2 | d2r6gg1 |  Alignment |  | 100.0 | 21 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 3 | c2onkC_ |  Alignment |  | 100.0 | 19 | PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda |
| 4 | d2onkc1 |  Alignment |  | 100.0 | 19 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 5 | d3d31c1 |  Alignment |  | 100.0 | 20 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 6 | c3d31D_ |  Alignment |  | 100.0 | 20 | PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans |
| 7 | c2r6gF_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter |
| 8 | d2r6gf2 |  Alignment |  | 100.0 | 21 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 9 | d3dhwa1 |  Alignment |  | 99.9 | 15 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 10 | d2r6gf1 |  Alignment |  | 87.7 | 10 | Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like |
| 11 | d1ntca_ |  Alignment |  | 48.8 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |

| | | | | | | | |
|----|-------------------------|---|-----------|---|------|----|--|
| 12 | d1umqa_ |  | Alignment |  | 46.3 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 13 | c1umqA_ |  | Alignment |  | 46.3 | 19 | PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity |
| 14 | d1fipa_ |  | Alignment |  | 37.2 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 15 | d1etob_ |  | Alignment |  | 34.2 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 16 | c3e7ID_ |  | Alignment |  | 30.9 | 26 | PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain |
| 17 | d1etxa_ |  | Alignment |  | 26.0 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 18 | c1bctA_ |  | Alignment |  | 22.7 | 19 | PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution |
| 19 | d1g2ha_ |  | Alignment |  | 18.6 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 20 | c1etfB_ |  | Alignment |  | 15.6 | 40 | PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure |
| 21 | c1etgB_ |  | Alignment | not modelled | 15.6 | 40 | PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures |
| 22 | c2hx6A_ |  | Alignment | not modelled | 13.6 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb |
| 23 | c2x7IP_ |  | Alignment | not modelled | 7.7 | 36 | PDB header: immune system Chain: P: PDB Molecule: hiv rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element |
| 24 | c2jwaA_ |  | Alignment | not modelled | 6.0 | 15 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure |
| 25 | d1cf7a_ |  | Alignment | not modelled | 5.9 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp |
| 26 | c3lphD_ |  | Alignment | not modelled | 5.8 | 33 | PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer |
| 27 | c2qksA_ |  | Alignment | not modelled | 5.6 | 11 | PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera |
| 28 | c2kluA_ |  | Alignment | not modelled | 5.5 | 22 | PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4 |
| | |  | | | | | Fold: ABC transporter transmembrane region |

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|----|-------------------------|-----------|--------------|-----|---|---|
| 29 | d1pf4a2 | Alignment | not modelled | 5.3 | 6 | Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region |
|----|-------------------------|-----------|--------------|-----|---|---|