



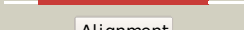

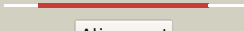









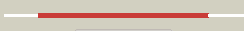
















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2onkc1</a>	 Alignment		100.0	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
2	<a href="#">c2onkC_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease <b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda
3	<a href="#">c3d31D_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease <b>PDBTitle:</b> modbc from methanosarcina acetivorans
4	<a href="#">d3d31c1</a>	 Alignment		100.0	19	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
5	<a href="#">c3fh6F_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malf; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
6	<a href="#">c2r6gF_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malf; <b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter
7	<a href="#">d2r6gf2</a>	 Alignment		100.0	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
8	<a href="#">d3dhwa1</a>	 Alignment		100.0	20	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
9	<a href="#">d2r6gg1</a>	 Alignment		99.9	12	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
10	<a href="#">c2jwaA_</a>	 Alignment		35.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
11	<a href="#">d1ntca_</a>	 Alignment		25.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like

12	<a href="#">c1umqA_</a>	Alignment		23.7	16	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
13	<a href="#">d1umqa_</a>	Alignment		23.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
14	<a href="#">d1fipa_</a>	Alignment		16.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
15	<a href="#">d1etob_</a>	Alignment		15.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
16	<a href="#">c3e7lD_</a>	Alignment		13.0	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
17	<a href="#">d1etxa_</a>	Alignment		12.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">d1g2ha_</a>	Alignment		9.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
19	<a href="#">c2hx6A_</a>	Alignment		8.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease; <b>PDBTitle:</b> solution structure analysis of the phage t42 endoribonuclease regb
20	<a href="#">c2d7dB_</a>	Alignment		7.2	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
21	<a href="#">d2ns0a1</a>	Alignment	not modelled	6.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RHA1 ro06458-like
22	<a href="#">c2lhuA_</a>	Alignment	not modelled	6.0	5	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> mybpc3 protein; <b>PDBTitle:</b> structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain