







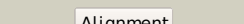

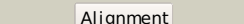

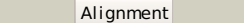

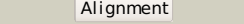

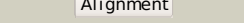

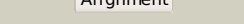

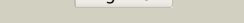


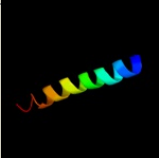

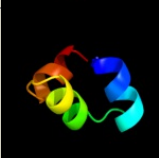
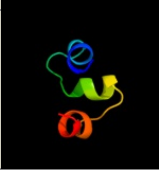


Detailed template information

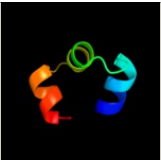
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2r6gg1</a>	 Alignment		100.0	96	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
2	<a href="#">c3fh6F_</a>	 Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> 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
3	<a href="#">c2r6gF_</a>	 Alignment		100.0	21	<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
4	<a href="#">d2r6gf2</a>	 Alignment		100.0	21	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
5	<a href="#">d2onkc1</a>	 Alignment		100.0	22	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
6	<a href="#">c2onkC_</a>	 Alignment		100.0	22	<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
7	<a href="#">c3d31D_</a>	 Alignment		100.0	23	<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
8	<a href="#">d3d31c1</a>	 Alignment		100.0	23	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
9	<a href="#">d3dhwa1</a>	 Alignment		99.8	17	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
10	<a href="#">d2r6gf1</a>	 Alignment		88.0	14	<b>Fold:</b> MalF N-terminal region-like <b>Superfamily:</b> MalF N-terminal region-like <b>Family:</b> MalF N-terminal region-like
11	<a href="#">d1l7va_</a>	 Alignment		33.6	11	<b>Fold:</b> ABC transporter involved in vitamin B12 uptake, BtuC <b>Superfamily:</b> ABC transporter involved in vitamin B12 uptake, BtuC <b>Family:</b> ABC transporter involved in vitamin B12 uptake, BtuC

12	<a href="#">c2hx6A_</a>	Alignment		26.8	18	<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
13	<a href="#">c3ipdB_</a>	Alignment		10.0	4	<b>PDB header:</b> exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> syntaxin-1a; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
14	<a href="#">c1umqA_</a>	Alignment		9.7	19	<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
15	<a href="#">d1umqa_</a>	Alignment		9.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
16	<a href="#">d1ntca_</a>	Alignment		7.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like

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[d1etob\\_](#)

Alignment



7.7

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**Fold:** DNA/RNA-binding 3-helical bundle  
**Superfamily:** Homeodomain-like  
**Family:** FIS-like