







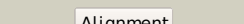

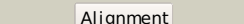

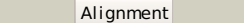

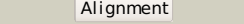

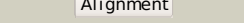
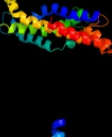
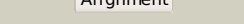

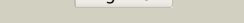


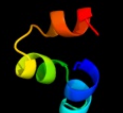
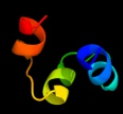




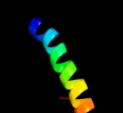



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2r6gF_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malf; <b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter
2	<a href="#">d2r6gf2</a>	 Alignment		100.0	19	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
3	<a href="#">c3fh6F_</a>	 Alignment		100.0	20	<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
4	<a href="#">c2onkC_</a>	 Alignment		100.0	30	<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
5	<a href="#">d2onkc1</a>	 Alignment		100.0	30	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
6	<a href="#">c3d31D_</a>	 Alignment		100.0	33	<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
7	<a href="#">d3d31c1</a>	 Alignment		100.0	33	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
8	<a href="#">d2r6gg1</a>	 Alignment		100.0	24	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
9	<a href="#">d3dhwa1</a>	 Alignment		99.9	13	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
10	<a href="#">c2jwaA_</a>	 Alignment		47.5	21	<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="#">c1umqA_</a>	 Alignment		36.5	23	<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

12	<a href="#">d1umqa_</a>	Alignment		36.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
13	<a href="#">d1fipa_</a>	Alignment		29.4	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
14	<a href="#">d1ntca_</a>	Alignment		29.1	25	<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		25.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
16	<a href="#">d1etxa_</a>	Alignment		18.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
17	<a href="#">d1g2ha_</a>	Alignment		17.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">c3e7ID_</a>	Alignment		17.3	22	<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
19	<a href="#">c2hx6A_</a>	Alignment		9.7	12	<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="#">c2cw1A_</a>	Alignment		9.3	47	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn4m; <b>PDBTitle:</b> solution structure of the de novo-designed lambda cro fold2 protein
21	<a href="#">c2rddB_</a>	Alignment	not modelled	8.4	7	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> upf0092 membrane protein yajc; <b>PDBTitle:</b> x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
22	<a href="#">c2d7dB_</a>	Alignment	not modelled	8.2	23	<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
23	<a href="#">c1p7bB_</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> integral membrane channel and cytosolic domains; <b>PDBTitle:</b> crystal structure of an inward rectifier potassium channel
24	<a href="#">c2k21A_</a>	Alignment	not modelled	5.6	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e <b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c