Phyre^2

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Description	P13960
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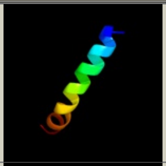
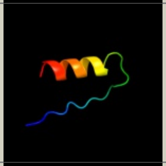
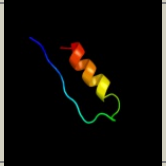
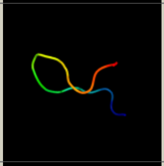
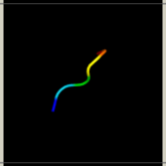
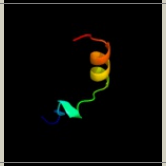
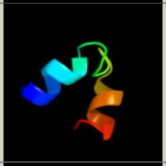
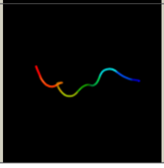
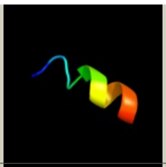
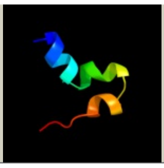
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jp3A_	 Alignment		12.1	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
2	c1tjnA_	 Alignment		11.2	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
3	d1tjna_	 Alignment		11.2	27	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
4	d1i0va_	 Alignment		9.5	33	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Fungal ribonucleases
5	d2drpa2	 Alignment		8.9	83	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
6	c3a9lB_	 Alignment		8.3	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
7	d2crga1	 Alignment		7.5	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
8	c2jo1A_	 Alignment		7.3	23	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
9	c2kaaA_	 Alignment		6.2	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hirsutellin a; **PDBTitle:** solution structure of hirsutellin a from hirsutella2 thompsonii
10	c2oqbA_	 Alignment		6.2	56	**PDB header:**transferase,gene regulation **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
11	d1isua_	 Alignment		5.9	30	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)

12	c3kdpG_	Alignment		5.7	46	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
13	c3kdpH_	Alignment		5.7	46	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump

14	c3m8eA_	Alignment		5.7	50	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** protein structure of type iii plasmid segregation tubr