Phyre^2

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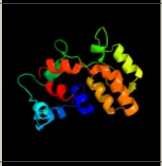
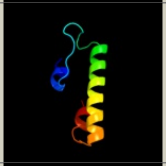
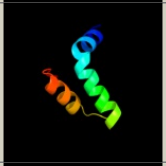
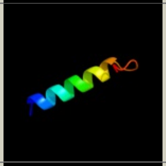
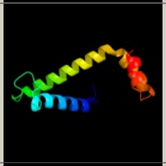
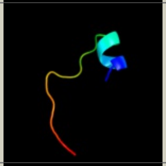
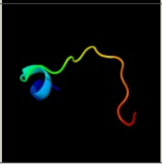
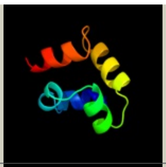
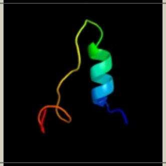
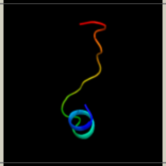
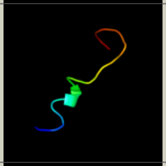
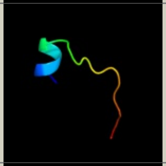
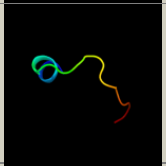
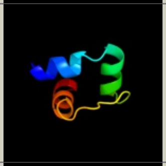
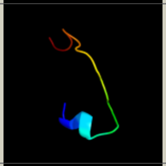
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o9xa1	Alignment		100.0	22	**Fold:**TorD-like **Superfamily:**TorD-like **Family:**TorD-like
2	c2o9xA_	Alignment		99.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**reductase, assembly protein; **PDBTitle:** crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
3	d1n1ca_	Alignment		99.8	19	**Fold:**TorD-like **Superfamily:**TorD-like **Family:**TorD-like
4	d1s9ua_	Alignment		99.8	18	**Fold:**TorD-like **Superfamily:**TorD-like **Family:**TorD-like
5	d2idga1	Alignment		98.5	17	**Fold:**TorD-like **Superfamily:**TorD-like **Family:**TorD-like
6	c2di4B_	Alignment		16.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cell division protein ftsh homolog; **PDBTitle:** crystal structure of the ftsh protease domain
7	d1lvaa3	Alignment		13.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
8	d2ce7a1	Alignment		8.9	14	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
9	d1ghea_	Alignment		8.8	33	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
10	d2g3aa1	Alignment		8.7	28	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
11	d1yx0a1	Alignment		7.8	39	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT

12	c3iwfA_	Alignment		7.4	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
13	d2d6fc2	Alignment		7.0	31	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
14	c2r7hA_	Alignment		6.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative d-alanine n-acetyltransferase of gnat family; **PDBTitle:** crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution
15	c2zw3B_	Alignment		6.5	32	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**gap junction beta-2 protein; **PDBTitle:** structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
16	c2cntD_	Alignment		6.4	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**modification of 30s ribosomal subunit protein s18; **PDBTitle:** rimi - ribosomal s18 n-alpha-protein acetyltransferase in2 complex with coenzymea.
17	c2pswA_	Alignment		5.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase 13; **PDBTitle:** human mak3 homolog in complex with coa
18	d1puza_	Alignment		5.7	10	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
19	c2reeB_	Alignment		5.4	30	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
20	d1ev0a_	Alignment		5.4	57	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
21	d1q8ha_	Alignment	not modelled	5.3	50	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
22	c1q8hA_	Alignment	not modelled	5.3	50	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin