Phyre²

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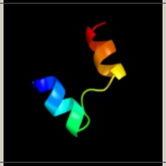
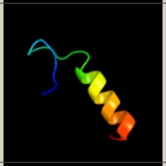
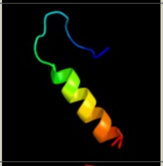
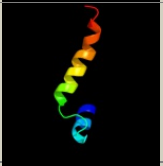
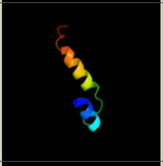
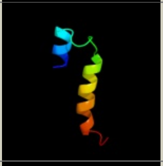
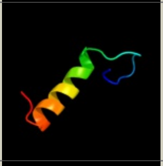
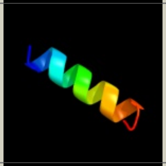
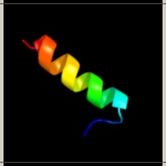
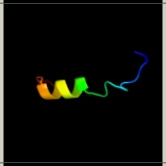
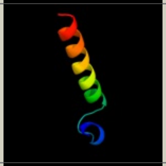
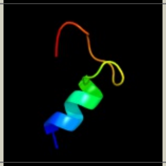
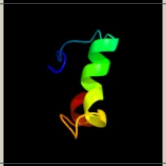
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jrkG_	Alignment		29.8	17	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
2	c2jobA_	Alignment		23.7	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
3	d1tz7a1	Alignment		23.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
4	d1eswa_	Alignment		21.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
5	d1joga_	Alignment		20.1	6	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
6	c1wwpA_	Alignment		17.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
7	d1wtya_	Alignment		15.2	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
8	d2gykb1	Alignment		13.3	9	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
9	d1x1na1	Alignment		10.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	d1e8oa_	Alignment		9.6	20	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
11	d1f6va_	Alignment		7.4	20	**Fold:**C-terminal domain of B transposition protein **Superfamily:**C-terminal domain of B transposition protein **Family:**C-terminal domain of B transposition protein

12	d2oa4a1	Alignment		6.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
13	c1dpuA_	Alignment		6.3	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
14	d1dpua_	Alignment		6.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
15	d1fsha_	Alignment		6.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
16	c3dkbA_	Alignment		5.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** crystal structure of a20, 2.5 angstrom
17	d2p12a1	Alignment		5.9	3	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
18	d1jvaa2	Alignment		5.9	16	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
19	c2jrtA_	Alignment		5.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
20	d2gsca1	Alignment		5.8	6	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
21	d1q88a_	Alignment	not modelled	5.6	40	**Fold:**39 kda initiator binding protein, IBP39, C-terminal domains **Superfamily:**39 kda initiator binding protein, IBP39, C-terminal domains **Family:**39 kda initiator binding protein, IBP39, C-terminal domains
22	c3ml6D_	Alignment	not modelled	5.5	15	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2 **PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2
23	d1jkva_	Alignment	not modelled	5.5	5	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
24	d2axte1	Alignment	not modelled	5.3	7	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits