Phyre2

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Description	P09127
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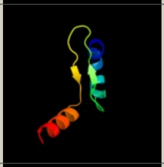
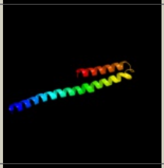
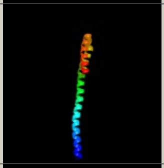
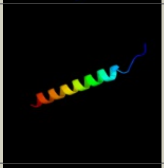
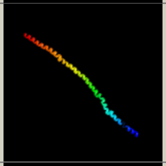
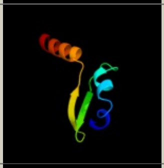
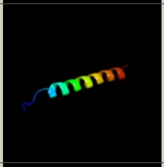
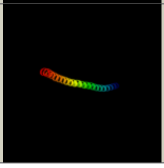
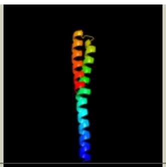
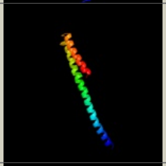
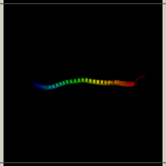
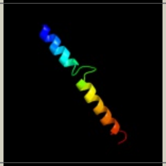
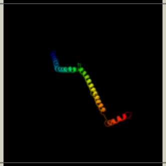
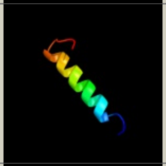
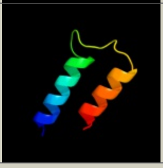
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zbiB_	Alignment		48.8	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin
2	c1deqO_	Alignment		43.4	10	**PDB header:** **PDB COMPND:**
3	d2a6qb1	Alignment		28.4	27	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
4	c2d4xA_	Alignment		27.6	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 3; **PDBTitle:** crystal structure of a 26k fragment of hap3 (flgl)
5	c3k8wA_	Alignment		26.3	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c45
6	c2y69Q_	Alignment		19.9	13	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
7	c3ghgK_	Alignment		19.4	5	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
8	c3g5oA_	Alignment		18.7	20	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
9	d1v54d_	Alignment		18.5	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
10	d2a6qa1	Alignment		17.0	29	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
11	c1gk4A_	Alignment		16.7	17	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)

12	d1io1a_	Alignment		16.6	22	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
13	c3k8vB_	Alignment		15.6	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
14	c1ei3E_	Alignment		15.4	8	**PDB header:** **PDB COMPND:**
15	c3j00Z_	Alignment		15.1	4	**PDB header:**ribosome/ribosomal protein **Chain:** Z: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
16	d1ud0a_	Alignment		13.9	11	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
17	c3ibpA_	Alignment		13.5	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
18	c3pe0B_	Alignment		12.9	12	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the central region of the plakin domain of plectin
19	d3fapb_	Alignment		11.7	21	**Fold:**Four-helical up-and-down bundle **Superfamily:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) **Family:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
20	c3lofF_	Alignment		11.4	17	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock 70 kda protein 1; **PDBTitle:** c-terminal domain of human heat shock 70kda protein 1b.
21	c1ud0B_	Alignment	not modelled	11.0	11	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**70 kda heat-shock-like protein; **PDBTitle:** crystal structure of the c-terminal 10-kda subdomain of hsc70
22	c3mkxC_	Alignment	not modelled	7.2	13	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
23	d2e74a1	Alignment	not modelled	6.5	15	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
24	d1q90b_	Alignment	not modelled	6.4	10	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
25	c1x8yA_	Alignment	not modelled	6.3	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
26	c2rpaA_	Alignment	not modelled	6.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a1; **PDBTitle:** the solution structure of n-terminal domain of microtubule severing2 enzyme
27	c2npuA_	Alignment	not modelled	6.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fkbp12-rapamycin complex-associated protein; **PDBTitle:** the solution structure of the rapamycin-binding domain of2 mtor (frb)
28	c3e1rB_	Alignment	not modelled	5.9	23	**PDB header:**cell cycle/transport protein **Chain:** B: **PDB Molecule:**centrosomal protein of 55 kda; **PDBTitle:** midbody targeting of the escrt machinery by a non-


canonical2 coiled-coil in cep55