Phyre^2

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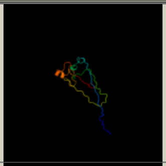
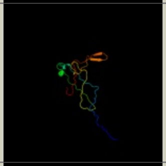
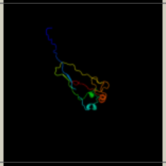
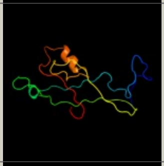
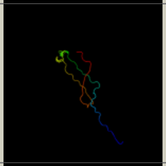
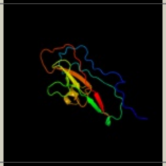
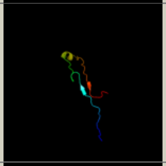
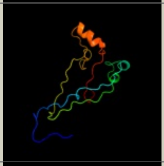
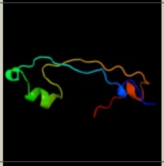
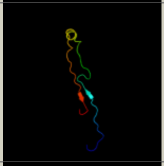
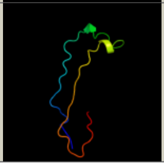
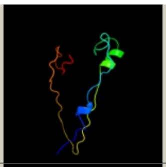
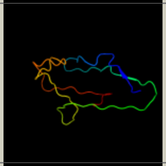
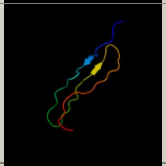
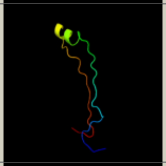
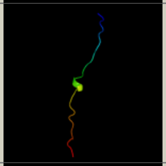
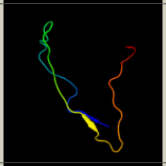
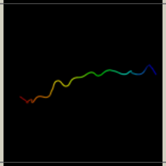
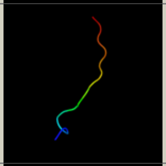
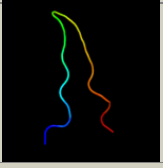
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jwnK_	Alignment		97.4	17	**PDB header:**protein binding/cell adhesion **Chain:** K: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
2	c3jwnL_	Alignment		97.3	17	**PDB header:**protein binding/cell adhesion **Chain:** L: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
3	c3jwnE_	Alignment		97.3	17	**PDB header:**protein binding/cell adhesion **Chain:** E: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
4	c2jtyA_	Alignment		97.2	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**type-1 fimbrial protein, a chain; **PDBTitle:** self-complemented variant of fima, the main subunit of type 1 pilus
5	c3jwnF_	Alignment		97.1	18	**PDB header:**protein binding/cell adhesion **Chain:** F: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
6	c2w07B_	Alignment		96.1	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**minor pilin subunit papf; **PDBTitle:** structural determinants of polymerization reactivity of the2 p pilus adaptor subunit papf
7	d2uy6b1	Alignment		95.0	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
8	c2jmrA_	Alignment		94.5	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf
9	d1n12a_	Alignment		94.0	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
10	d2j2zb1	Alignment		94.0	19	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
11	c3bfwA_	Alignment		92.9	24	**PDB header:**structural protein/structural protein **Chain:** A: **PDB Molecule:**protein fimg; **PDBTitle:** crystal structure of truncated fimg (fimgt) in complex with the donor2 strand peptide of fimf (dsf)

12	c2wmpB_	Alignment		92.5	27	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**papg protein; **PDBTitle:** structure of the e. coli chaperone papd in complex with the pilin2 domain of the papgii adhesin
13	d1ze3h1	Alignment		91.7	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
14	c1klfP_	Alignment		89.7	14	**PDB header:**chaperone/adhesin complex **Chain:** P: **PDB Molecule:**fimh protein; **PDBTitle:** fimh adhesin-fimc chaperone complex with d-mannose
15	d1pdkb_	Alignment		85.7	4	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
16	d2jnaa1	Alignment		13.3	35	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
17	c3qbtH_	Alignment		8.6	9	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp
18	c2kr7A_	Alignment		8.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
19	c2kfwA_	Alignment		7.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
20	c3klqB_	Alignment		7.0	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative pilus anchoring protein; **PDBTitle:** crystal structure of the minor pilin fctb from streptococcus pyogenes2 90/306s
21	c2xzzA_	Alignment	not modelled	6.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase k; **PDBTitle:** crystal structure of the human transglutaminase 1 beta-barrel domain