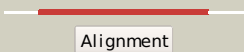
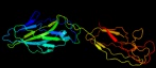
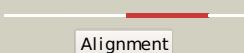


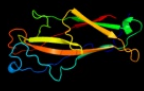







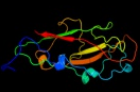
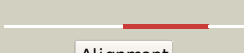
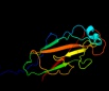





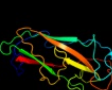

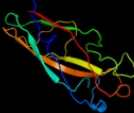
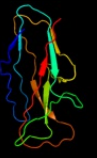
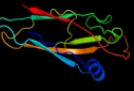
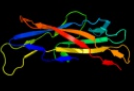

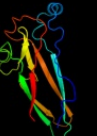
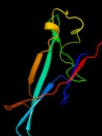
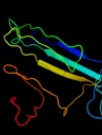


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1klfP_</a>	 Alignment		99.9	14	<b>PDB header:</b> chaperone/adhesin complex <b>Chain:</b> P: <b>PDB Molecule:</b> fimh protein; <b>PDBTitle:</b> fimh adhesin-fimc chaperone complex with d-mannose
2	<a href="#">c2w07B_</a>	 Alignment		99.9	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> minor pilin subunit papf; <b>PDBTitle:</b> structural determinants of polymerization reactivity of the2 p pilus adaptor subunit papf
3	<a href="#">c3bfwA_</a>	 Alignment		99.8	14	<b>PDB header:</b> structural protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein fimg; <b>PDBTitle:</b> crystal structure of truncated fimg (fimgt) in complex with the donor2 strand peptide of fimf (dsf)
4	<a href="#">c3jwnK_</a>	 Alignment		99.8	19	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> K: <b>PDB Molecule:</b> protein fimf; <b>PDBTitle:</b> complex of fimc, fimf, fimg and fimh
5	<a href="#">c3jwnL_</a>	 Alignment		99.8	19	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> L: <b>PDB Molecule:</b> protein fimf; <b>PDBTitle:</b> complex of fimc, fimf, fimg and fimh
6	<a href="#">c3jwnE_</a>	 Alignment		99.8	19	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> E: <b>PDB Molecule:</b> protein fimf; <b>PDBTitle:</b> complex of fimc, fimf, fimg and fimh
7	<a href="#">c2jmrA_</a>	 Alignment		99.8	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fimf; <b>PDBTitle:</b> nmr structure of the e. coli type 1 pilus subunit fimf
8	<a href="#">d2j2zb1</a>	 Alignment		99.8	14	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
9	<a href="#">c3jwnF_</a>	 Alignment		99.8	18	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> F: <b>PDB Molecule:</b> protein fimf; <b>PDBTitle:</b> complex of fimc, fimf, fimg and fimh
10	<a href="#">d1pdkb_</a>	 Alignment		99.8	17	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
11	<a href="#">c2jtyA_</a>	 Alignment		99.7	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> type-1 fimbrial protein, a chain; <b>PDBTitle:</b> self-complemented variant of fima, the main subunit of type 1 pilus

12	<a href="#">d2uy6b1</a>	Alignment		99.7	16	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
13	<a href="#">d1n12a_</a>	Alignment		99.7	21	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
14	<a href="#">d1ze3h1</a>	Alignment		99.7	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
15	<a href="#">c3bwuF_</a>	Alignment		99.6	18	<b>PDB header:</b> chaperone, structural, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> protein fimf; <b>PDBTitle:</b> crystal structure of the ternary complex of fimd (n-terminal domain,2 fimdn) with fimc and the n-terminally truncated pilus subunit fimf3 (fimft)
16	<a href="#">d2bsca1</a>	Alignment		90.9	13	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> F17c-type adhesin
17	<a href="#">d1oioa_</a>	Alignment		88.2	10	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> F17c-type adhesin
18	<a href="#">c2wmpB_</a>	Alignment		72.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> papg protein; <b>PDBTitle:</b> structure of the e. coli chaperone papd in complex with the pilin2 domain of the paggi adhesin
19	<a href="#">d1p5vb_</a>	Alignment		48.9	12	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
20	<a href="#">c2wd6B_</a>	Alignment		31.6	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> agglutinin receptor; <b>PDBTitle:</b> crystal structure of the variable domain of the2 streptococcus gordonii surface protein ssfb
21	<a href="#">d1jmma_</a>	Alignment	not modelled	10.9	10	<b>Fold:</b> Supersandwich <b>Superfamily:</b> V-region of surface antigen I/II (SA I/II, PAC) <b>Family:</b> V-region of surface antigen I/II (SA I/II, PAC)
22	<a href="#">c3fb1A_</a>	Alignment	not modelled	9.6	55	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of orf132 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
23	<a href="#">c3osvC_</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
24	<a href="#">c2voyG_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus