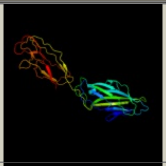
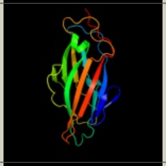
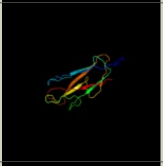
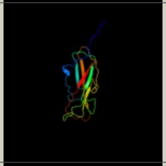
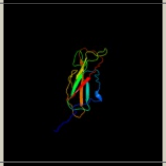
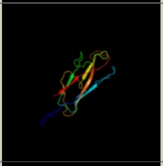
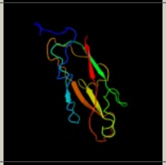
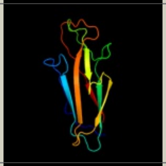
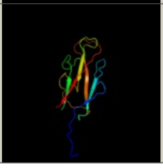
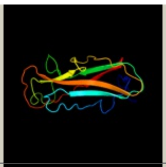
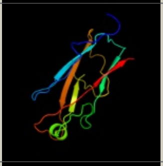
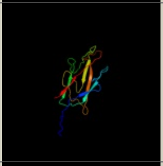
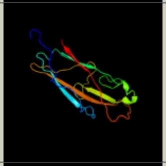
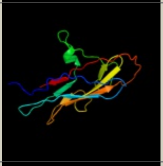
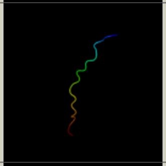
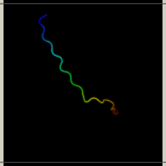
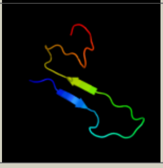
Email	l.a.kelley@imperial.ac.uk
Description	P08191
Date	Thu Jan 5 11:00:48 GMT 2012
Unique Job ID	f8c87cc71054d4c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1klfP_	Alignment		100.0	100	**PDB header:**chaperone/adhesin complex **Chain:** P: **PDB Molecule:**fimh protein; **PDBTitle:** fimh adhesin-fimc chaperone complex with d-mannose
2	d1ze3h1	Alignment		100.0	100	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
3	d1uwfa1	Alignment		99.9	100	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
4	c3bwuF_	Alignment		99.9	24	**PDB header:**chaperone, structural, membrane protein **Chain:** F: **PDB Molecule:**protein fimf; **PDBTitle:** crystal structure of the ternary complex of fimd (n-terminal domain,2 fimdn) with fimc and the n-terminally truncated pilus subunit fimf3 (fimft)
5	c3jwnK_	Alignment		99.9	23	**PDB header:**protein binding/cell adhesion **Chain:** K: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
6	c3jwnL_	Alignment		99.9	23	**PDB header:**protein binding/cell adhesion **Chain:** L: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
7	c3jwnF_	Alignment		99.9	23	**PDB header:**protein binding/cell adhesion **Chain:** F: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
8	c3jwnE_	Alignment		99.9	23	**PDB header:**protein binding/cell adhesion **Chain:** E: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh
9	c2jmrA_	Alignment		99.9	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf
10	c3bfwA_	Alignment		99.9	20	**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)
11	d2j2zb1	Alignment		99.8	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits

12	c2jtyA_	Alignment		99.8	24	**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
13	d1pdkb_	Alignment		99.8	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
14	d2uy6b1	Alignment		99.8	13	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
15	c2w07B_	Alignment		99.7	20	**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
16	d1n12a_	Alignment		99.4	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
17	c2wmpB_	Alignment		91.2	18	**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
18	d2jnaa1	Alignment		32.8	27	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
19	d2noca1	Alignment		13.9	17	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
20	d2oz4a1	Alignment		6.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
21	c3o0rC_	Alignment	not modelled	6.3	20	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
22	c2l18A_	Alignment	not modelled	6.0	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state