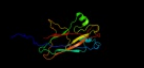
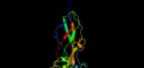
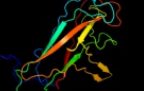
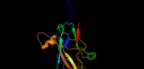
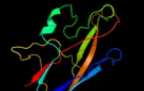
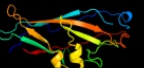
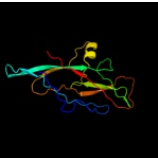
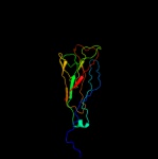
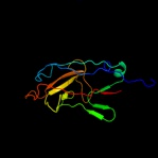
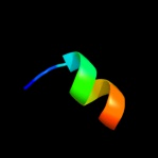
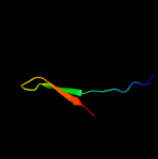
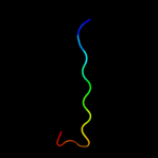


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jwnK_	 Alignment		99.9	16	PDB header: protein binding/cell adhesion Chain: K: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
2	c3jwnL_	 Alignment		99.9	16	PDB header: protein binding/cell adhesion Chain: L: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
3	c3jwnE_	 Alignment		99.9	16	PDB header: protein binding/cell adhesion Chain: E: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
4	c3jwnF_	 Alignment		99.9	16	PDB header: protein binding/cell adhesion Chain: F: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
5	c2jtyA_	 Alignment		99.9	18	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
6	c2jmrA_	 Alignment		99.9	17	PDB header: cell adhesion Chain: A: PDB Molecule: fimf; PDBTitle: nmr structure of the e. coli type 1 pilus subunit fimf
7	d2uy6b1	 Alignment		99.8	11	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
8	d2j2zb1	 Alignment		99.8	15	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
9	d1pdkb_	 Alignment		99.8	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
10	c3bwwF_	 Alignment		99.7	16	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)
11	c3bfwA_	 Alignment		99.7	13	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	d1ze3h1	Alignment		99.6	21	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
13	c1klfp_	Alignment		99.5	21	PDB header: chaperone/adhesin complex Chain: P: PDB Molecule: fimh protein; PDBTitle: fimh adhesin-fimc chaperone complex with d-mannose
14	c2w07B_	Alignment		99.5	13	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
15	d1n12a_	Alignment		99.0	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
16	d1y0ua_	Alignment		26.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
17	c1w3ga_	Alignment		14.5	19	PDB header: toxin/lectin Chain: A: PDB Molecule: hemolytic lectin from laetiporus sulphureus; PDBTitle: hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetylactosamine molecules.
18	c3nqnB_	Alignment		10.7	4	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function. (dr_2006) from2 deinococcus radiodurans at 1.88 a resolution
19	c3rpiA_	Alignment		7.2	58	PDB header: transcription regulator Chain: A: PDB Molecule: curlin genes transcriptional regulator; PDBTitle: structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
20	d3c7ba3	Alignment		6.5	21	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
21	c1bcta_	Alignment	not modelled	6.4	21	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
22	d2v4ja3	Alignment	not modelled	6.2	14	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
23	d3c7bb3	Alignment	not modelled	6.1	16	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
24	d2v4jb3	Alignment	not modelled	5.8	8	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
25	d1aopa4	Alignment	not modelled	5.8	12	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
26	d1z1za1	Alignment	not modelled	5.6	25	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: Lambda phage gpU-like
27	d2akja4	Alignment	not modelled	5.5	12	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like