# Phyre$^2$

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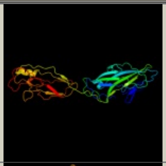
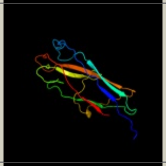
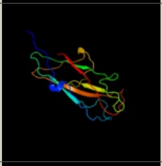
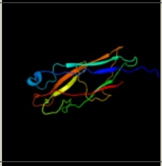
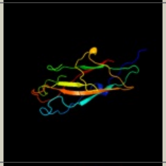
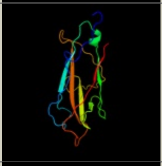
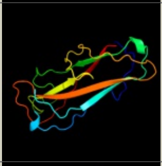
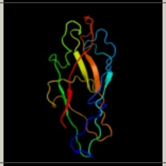
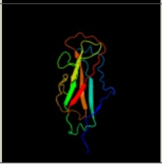
| Description | P76656 |
| Date | Thu Jan 5 12:25:15 GMT 2012 |
| Unique Job ID | e53bd89305e17d96 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1klfP_ | Alignment |  | 100.0 | 13 | **PDB header:**chaperone/adhesin complex<br>**Chain:** P: **PDB Molecule:**fimh protein;<br>**PDBTitle:** fimh adhesin-fimc chaperone complex with d-mannose |
| 2 | c3bfwA_ | Alignment |  | 99.9 | 14 | **PDB header:**structural protein/structural protein<br>**Chain:** A: **PDB Molecule:**protein fimg;<br>**PDBTitle:** crystal structure of truncated fimg (fimgt) in complex with the donor2 strand peptide of fimf (dsf) |
| 3 | c3jwnK_ | Alignment |  | 99.8 | 18 | **PDB header:**protein binding/cell adhesion<br>**Chain:** K: **PDB Molecule:**protein fimf;<br>**PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 4 | c3jwnL_ | Alignment |  | 99.8 | 18 | **PDB header:**protein binding/cell adhesion<br>**Chain:** L: **PDB Molecule:**protein fimf;<br>**PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 5 | c3jwnE_ | Alignment |  | 99.8 | 18 | **PDB header:**protein binding/cell adhesion<br>**Chain:** E: **PDB Molecule:**protein fimf;<br>**PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 6 | c3jwnF_ | Alignment |  | 99.8 | 18 | **PDB header:**protein binding/cell adhesion<br>**Chain:** F: **PDB Molecule:**protein fimf;<br>**PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 7 | d1ze3h1 | Alignment |  | 99.8 | 12 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 8 | c2w07B_ | Alignment |  | 99.8 | 18 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**minor pilin subunit papf;<br>**PDBTitle:** structural determinants of polymerization reactivity of the2 p pilus adaptor subunit papf |
| 9 | c2jtyA_ | Alignment |  | 99.8 | 18 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**type-1 fimbrial protein, a chain;<br>**PDBTitle:** self-complemented variant of fima, the main subunit of type 1 pilus |
| 10 | c2jmrA_ | Alignment |  | 99.8 | 18 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**fimf;<br>**PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf |
| 11 | d2j2zb1 | Alignment |  | 99.8 | 11 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |

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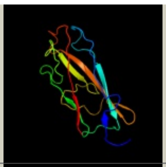
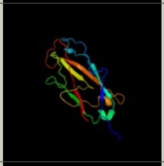
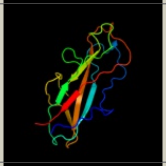
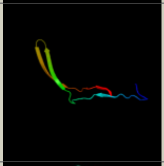
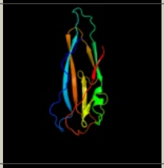
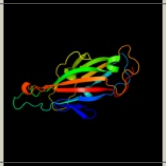
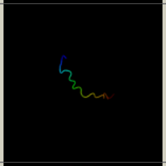
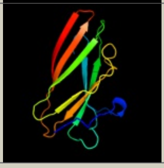
|---|---|---|---|---|---|---|
| 12 | d1pdkb_ | Alignment |  | 99.8 | 19 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 13 | d2uy6b1 | Alignment |  | 99.8 | 16 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 14 | c3bwuF_ | Alignment |  | 99.8 | 16 | **PDB header:**chaperone, structural, membrane protein<br>**Chain:** F: **PDB Molecule:**protein fimf;<br>**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) |
| 15 | d1n12a_ | Alignment |  | 99.6 | 17 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 16 | c1w3gA_ | Alignment |  | 32.0 | 18 | **PDB header:**toxin/lectin<br>**Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus;<br>**PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules. |
| 17 | c2wmpB_ | Alignment |  | 26.1 | 12 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**papg protein;<br>**PDBTitle:** structure of the e. coli chaperone papd in complex with the pilin2 domain of the papgii adhesin |
| 18 | d1uwfa1 | Alignment |  | 22.1 | 15 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 19 | d2jnaa1 | Alignment |  | 11.8 | 18 | **Fold:**Dodecin subunit-like<br>**Superfamily:**YdgH-like<br>**Family:**YdgH-like |
| 20 | d1p4ua_ | Alignment |  | 11.0 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**gamma-adaptin C-terminal appendage domain-like |
| 21 | d1na8a_ | Alignment | not modelled | 9.6 | 10 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**gamma-adaptin C-terminal appendage domain-like |
| 22 | d1gywb_ | Alignment | not modelled | 6.5 | 7 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**gamma-adaptin C-terminal appendage domain-like |
| 23 | c3l48B_ | Alignment | not modelled | 6.2 | 18 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**outer membrane usher protein papc;<br>**PDBTitle:** crystal structure of the c-terminal domain of the papc usher |
| 24 | d1gyva_ | Alignment | not modelled | 6.1 | 5 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**gamma-adaptin C-terminal appendage domain-like |
| 25 | c3ff7B_ | Alignment | not modelled | 6.0 | 33 | **PDB header:**cell adhesion/immunue system<br>**Chain:** B: **PDB Molecule:**epithelial cadherin;<br>**PDBTitle:** structure of nk cell receptor klrg1 bound to e-cadherin |