Phyre2

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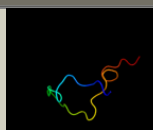
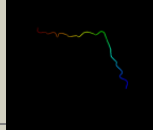
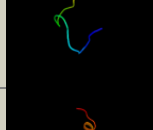
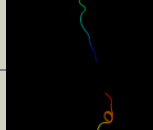
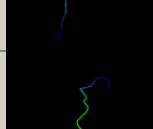
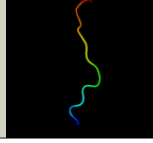
| Description | P75917 |
| Date | Thu Jan 5 12:16:01 GMT 2012 |
| Unique Job ID | 49753e2b121b702c |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2jtyA_ | Alignment |  | 94.6 | 39 | **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 |
| 2 | c3jwnE_ | Alignment |  | 90.4 | 20 | **PDB header:**protein binding/cell adhesion **Chain:** E: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 3 | c3jwnK_ | Alignment |  | 90.4 | 20 | **PDB header:**protein binding/cell adhesion **Chain:** K: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 4 | c2jmrA_ | Alignment |  | 89.8 | 20 | **PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf |
| 5 | c3jwnL_ | Alignment |  | 89.0 | 20 | **PDB header:**protein binding/cell adhesion **Chain:** L: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 6 | c3jwnF_ | Alignment |  | 88.7 | 20 | **PDB header:**protein binding/cell adhesion **Chain:** F: **PDB Molecule:**protein fimf; **PDBTitle:** complex of fimc, fimf, fimg and fimh |
| 7 | d2j2zb1 | Alignment |  | 85.4 | 26 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits |
| 8 | d2uy6b1 | Alignment |  | 83.4 | 22 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits |
| 9 | d1cvra1 | Alignment |  | 41.2 | 18 | **Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain |
| 10 | c2w07B_ | Alignment |  | 31.7 | 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 |
| 11 | c1hleB_ | Alignment |  | 31.5 | 29 | **PDB header:**hydrolase inhibitor(serine proteinase) **Chain:** B: **PDB Molecule:**horse leukocyte elastase inhibitor; **PDBTitle:** crystal structure of cleaved equine leucocyte elastase2 inhibitor determined at 1.95 angstroms resolution |

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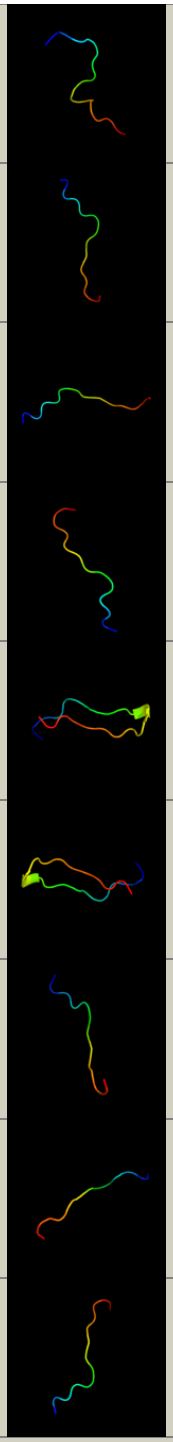
| 12 | d1pdkb_ | Alignment |  | 30.9 | 24 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Pilus subunits |
| 13 | c1jjoE_ | Alignment | | 28.7 | 36 | **PDB header:**signaling protein<br>**Chain:** E: **PDB Molecule:**neuroserpin;<br>**PDBTitle:** crystal structure of mouse neuroserpin (cleaved form) |
| 14 | c2h4qB_ | Alignment | | 28.0 | 29 | **PDB header:**hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**heterochromatin-associated protein ment;<br>**PDBTitle:** crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation |
| 15 | c9paiB_ | Alignment | | 26.5 | 46 | **PDB header:**hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**protein (plasminogen activator inhibitor-1) residues 365-<br>**PDBTitle:** cleaved substrate variant of plasminogen activator inhibitor-1 |
| 16 | d1i8na_ | Alignment | | 25.7 | 32 | **Fold:**Hairpin loop containing domain-like<br>**Superfamily:**Hairpin loop containing domain-like<br>**Family:**Anti-platelet protein |
| 17 | c1i8nA_ | Alignment | | 25.7 | 32 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**anti-platelet protein;<br>**PDBTitle:** crystal structure of leech anti-platelet protein |
| 18 | c2rivB_ | Alignment | | 22.1 | 38 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**thyroxine-binding globulin;<br>**PDBTitle:** crystal structure of the reactive loop cleaved human thyroxine binding2 globulin |
| 19 | c7apiB_ | Alignment | | 20.7 | 31 | **PDB header:**proteinase inhibitor<br>**Chain:** B: **PDB Molecule:**alpha 1-antitrypsin;<br>**PDBTitle:** the s variant of human alpha1-antitrypsin, structure and implications2 for function and metabolism |
| 20 | c3f02C_ | Alignment | | 20.7 | 36 | **PDB header:**hydrolase inhibitor<br>**Chain:** C: **PDB Molecule:**neuroserpin;<br>**PDBTitle:** cleaved human neuroserpin |
| 21 | c1mtpB_ | Alignment | not modelled | 16.2 | 46 | **PDB header:**structural genomics<br>**Chain:** B: **PDB Molecule:**serine proteinase inhibitor (serpin), chain b;<br>**PDBTitle:** the x-ray crystal structure of a serpin from a thermophilic2 prokaryote |
| 22 | c3cooB_ | Alignment | not modelled | 14.1 | 26 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**spondin-1;<br>**PDBTitle:** the crystal structure of reelin-n domain of f-spondin |
| 23 | c3i4oA_ | Alignment | not modelled | 13.3 | 19 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor if-1;<br>**PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis |
| 24 | c2zouB_ | Alignment | not modelled | 11.9 | 26 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**spondin-1;<br>**PDBTitle:** crystal struture of human f-spondin reeler domain (fragment 2) |
| 25 | d1exta2 | Alignment | not modelled | 8.2 | 36 | **Fold:**TNF receptor-like<br>**Superfamily:**TNF receptor-like<br>**Family:**TNF receptor-like |
| 26 | c2j98A_ | Alignment | not modelled | 7.5 | 22 | **PDB header:**rna-binding protein<br>**Chain:** A: **PDB Molecule:**replicase polyprotein 1ab;<br>**PDBTitle:** human coronavirus 229e non structural protein 9 cys69ala2 mutant (nsp9) |
| 27 | d1qz8a_ | Alignment | not modelled | 7.5 | 40 | **Fold:**Replicase NSP9<br>**Superfamily:**Replicase NSP9<br>**Family:**Replicase NSP9 |
| 28 | c1uw7A_ | Alignment | not modelled | 7.4 | 40 | **PDB header:**replicase protein<br>**Chain:** A: **PDB Molecule:**nsp9;<br>**PDBTitle:** nsp9 protein from sars-coronavirus. |

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| 29 | d1gtka2 | Alignment | not modelled | 6.9 | 13 | **Fold:**dsRBD-like<br>**Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain<br>**Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain |
| 30 | c1ow1A_ | Alignment | not modelled | 6.7 | 37 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**smart/hdac1 associated repressor protein;<br>**PDBTitle:** crystal structure of the spoc domain of the human2 transcriptional corepressor, sharp. |
| 31 | d1ow1a_ | Alignment | not modelled | 6.7 | 37 | **Fold:**SPOC domain-like<br>**Superfamily:**SPOC domain-like<br>**Family:**SPOC domain |
| 32 | c2d3jA_ | Alignment | not modelled | 6.7 | 9 | **PDB header:**signaling protein inhibitor<br>**Chain:** A: **PDB Molecule:**wnt inhibitory factor-1;<br>**PDBTitle:** nmr structure of the wif domain from human wif-1 |
| 33 | d1n26a1 | Alignment | not modelled | 6.6 | 22 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Immunoglobulin<br>**Family:**I set domains |
| 34 | d2ij0c1 | Alignment | not modelled | 6.2 | 24 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Immunoglobulin<br>**Family:**V set domains (antibody variable domain-like) |
| 35 | c2kc2A_ | Alignment | not modelled | 5.8 | 27 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**talin-1;<br>**PDBTitle:** nmr structure of the f1 domain (residues 86-202) of the2 talin |
| 36 | c3m6wA_ | Alignment | not modelled | 5.7 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rrna methylase;<br>**PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine |
| 37 | c2frxD_ | Alignment | not modelled | 5.6 | 20 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**hypothetical protein yebu;<br>**PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli |
| 38 | d1ikpa1 | Alignment | not modelled | 5.5 | 17 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Exotoxin A, N-terminal domain |
| 39 | c2dllA_ | Alignment | not modelled | 5.3 | 10 | **PDB header:**cytokine<br>**Chain:** A: **PDB Molecule:**interferon regulatory factor 4;<br>**PDBTitle:** solution structure of the irf domain of human interferon2 regulator factors 4 |
| 40 | d1pdaa2 | Alignment | not modelled | 5.2 | 17 | **Fold:**dsRBD-like<br>**Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain<br>**Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain |
| 41 | d3c2ah1 | Alignment | not modelled | 5.1 | 20 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Immunoglobulin<br>**Family:**V set domains (antibody variable domain-like) |