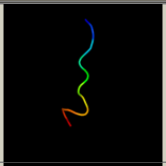
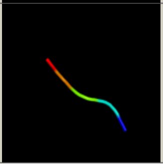
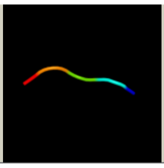
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P37669 |
| Date | Thu Jan 5 11:56:41 GMT 2012 |
| Unique Job ID | 471cbdcea3bccca4 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ujlA_ | Alignment |  | 10.6 | 45 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h<br>**PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker |
| 2 | c2wwbB_ | Alignment |  | 10.4 | 11 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma;<br>**PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome |
| 3 | d1rhzb_ | Alignment |  | 7.5 | 18 | **Fold:**Single transmembrane helix<br>**Superfamily:**Preprotein translocase SecE subunit<br>**Family:**Preprotein translocase SecE subunit |
| 4 | c2adlB_ | Alignment |  | 6.3 | 40 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**ccda;<br>**PDBTitle:** solution structure of the bacterial antitoxin ccda:2 implications for dna and toxin binding |

| | | | | | | |
|---|---|---|---|---|---|---|
| 5 | d2cpga_ | <br>Alignment |  | 6.2 | 20 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |