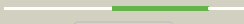
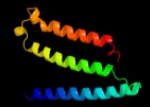
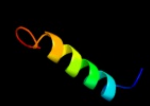


# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | I.a.kelley@imperial.ac.uk   |
| Description   | P18777                      |
| Date          | Thu Jan 5 11:37:08 GMT 2012 |
| Unique Job ID | 803d24247c65fd8e            |

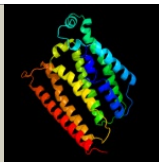
Detailed template information

| # | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                             |
|---|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | <a href="#">c2vpzG_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical membrane spanning protein;<br><b>PDBTitle:</b> polysulfide reductase native structure                                                                    |
| 2 | <a href="#">c2jagA_</a> |  Alignment   |    | 56.0       | 12     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> halorhodopsin;<br><b>PDBTitle:</b> I1-intermediate of halorhodopsin t203v                                                                                           |
| 3 | <a href="#">d1e12a_</a> |  Alignment   |    | 38.8       | 12     | <b>Fold:</b> Family A G protein-coupled receptor-like<br><b>Superfamily:</b> Family A G protein-coupled receptor-like<br><b>Family:</b> Bacteriorhodopsin-like                                                                                   |
| 4 | <a href="#">c2amnA_</a> |  Alignment   |    | 13.6       | 55     | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin;<br><b>PDBTitle:</b> solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken                                 |
| 5 | <a href="#">c3rkoA_</a> |  Alignment |  | 11.1       | 13     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit a;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 6 | <a href="#">c2p9xB_</a> |  Alignment |  | 6.6        | 17     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0832;<br><b>PDBTitle:</b> crystal structure of ph0832 from pyrococcus horikoshii ot3                                    |
| 7 | <a href="#">c2jwaA_</a> |  Alignment |  | 6.4        | 17     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2;<br><b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure                                                         |

8

[c1m56G\\_](#)

Alignment



6.2

8

**PDB header:** oxidoreductase

**Chain:** G: **PDB Molecule:** cytochrome c oxidase;

**PDB Title:** structure of cytochrome c oxidase from rhodobactor2  
sphaeroides (wild type)