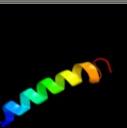
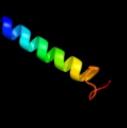
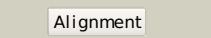
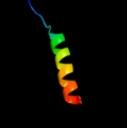
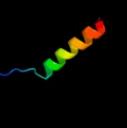
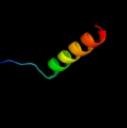
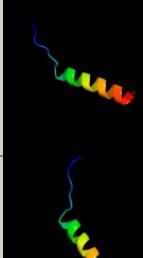
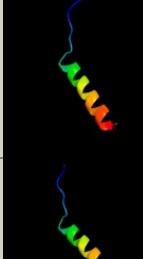
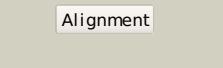
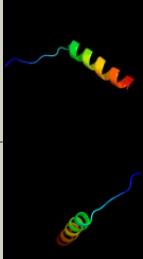
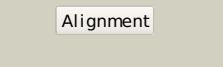
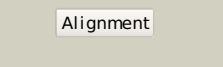
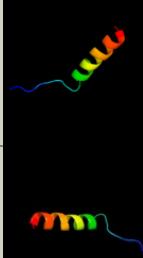
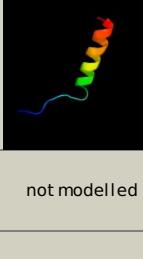
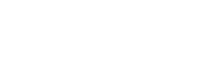


# Phyre<sup>2</sup>

|               |                                |
|---------------|--------------------------------|
| Email         | i.a.kelley@imperial.ac.uk      |
| Description   | P42601                         |
| Date          | Thu Jan 5 12:01:46 GMT<br>2012 |
| Unique Job ID | 3e317dddf4f0c908               |

Detailed template information

| #  | Template | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|----------|---|---|------------|--------|---|
| 1  | c1yewl_  |  Alignment   |    | 11.9       | 13     | <b>PDB header:</b> oxidoreductase, membrane protein<br><b>Chain:</b> I; <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit;<br><b>PDBTitle:</b> crystal structure of particulate methane monooxygenase   |
| 2  | c3rgbA_  |  Alignment   |    | 11.9       | 13     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> methane monooxygenase subunit b2;<br><b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from <i>2 methylococcus capsulatus</i> (bath)   |
| 3  | c1xioA_  |  Alignment   |    | 8.9        | 17     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> anabaena sensory rhodopsin;<br><b>PDBTitle:</b> anabaena sensory rhodopsin  |
| 4  | d1xioa_  |  Alignment   |   | 8.9        | 17     | <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  |
| 5  | d1uaza_  |  Alignment |  | 7.0        | 10     | <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  |
| 6  | d1dxsa_  |  Alignment |  | 6.8        | 21     | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain   |
| 7  | c3prql_  |  Alignment |  | 6.3        | 32     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L; <b>PDB Molecule:</b> photosystem ii reaction center protein l;<br><b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with 2 terbutryl (part 1 of 2). this file contains first monomer of psii3 dimer  |
| 8  | c3bz1L_  |  Alignment |  | 6.3        | 32     | <b>PDB header:</b> electron transport<br><b>Chain:</b> L; <b>PDB Molecule:</b> photosystem ii reaction center protein l;<br><b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer                          |
| 9  | c3prrl_  |  Alignment |  | 6.3        | 32     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L; <b>PDB Molecule:</b> photosystem ii reaction center protein l;<br><b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with 2 terbutryl (part 2 of 2). this file contains second monomer of psii3 dimer |
| 10 | c1s5ll_  |  Alignment |  | 6.3        | 32     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L; <b>PDB Molecule:</b> photosystem ii reaction center l protein;<br><b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center  |
| 11 | c2axtl_  |  Alignment |  | 6.3        | 32     | <b>PDB header:</b> electron transport<br><b>Chain:</b> L; <b>PDB Molecule:</b> photosystem ii reaction center l protein;<br><b>PDBTitle:</b> crystal structure of photosystem ii from <i>thermosynechococcus elongatus</i>  |

|    |                         |   |   |     |    |   |
|----|-------------------------|---|---|-----|----|---|
| 12 | <a href="#">c3arcL_</a> |    |     | 6.3 | 32 | <b>PDB header:</b> electron transport, photosynthesis<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution                    |
| 13 | <a href="#">c1s5IL_</a> |    |    | 6.3 | 32 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein;<br><b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center  |
| 14 | <a href="#">c3bz2L_</a> |    |    | 6.3 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer |
| 15 | <a href="#">c2axtl_</a> |    |    | 6.3 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein;<br><b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus   |
| 16 | <a href="#">d2axt1</a>  |    |    | 6.3 | 32 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Photosystem II reaction center protein L, PsbL<br><b>Family:</b> PsbL-like   |
| 17 | <a href="#">c3kziL_</a> |    |   | 6.3 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii   |
| 18 | <a href="#">c3a0hl_</a> |  |  | 6.2 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex  |
| 19 | <a href="#">c3a0hL_</a> |  |  | 6.2 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex  |
| 20 | <a href="#">c3a0bl_</a> |  |  | 6.2 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex   |
| 21 | <a href="#">c3arcl_</a> |  | not modelled  | 6.2 | 35 | <b>PDB header:</b> electron transport, photosynthesis<br><b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I;<br><b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution                    |
| 22 | <a href="#">d1r3jc_</a> |  | not modelled  | 5.9 | 14 | <b>Fold:</b> Voltage-gated potassium channels<br><b>Superfamily:</b> Voltage-gated potassium channels<br><b>Family:</b> Voltage-gated potassium channels  |