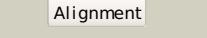
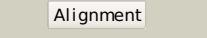
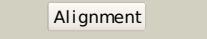
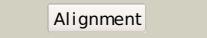


# Phyre<sup>2</sup>

|               |                             |
|---------------|-----------------------------|
| Email         | i.a.kelley@imperial.ac.uk   |
| Description   | Q9JMR5                      |
| Date          | Thu Jan 5 12:37:49 GMT 2012 |
| Unique Job ID | 7f1c1c3caacca747            |

Detailed template information

| #  | Template | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|----------|---|---|------------|--------|--|
| 1  | d1edya_  |  Alignment   |    | 28.0       | 29     | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain   |
| 2  | d1bv8a_  |  Alignment   |    | 27.4       | 29     | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain   |
| 3  | d1ayoa_  |  Alignment   |    | 24.1       | 33     | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain   |
| 4  | d1qhda2  |  Alignment   |    | 19.6       | 48     | <b>Fold:</b> Viral protein domain<br><b>Superfamily:</b> Viral protein domain<br><b>Family:</b> Top domain of virus capsid protein   |
| 5  | c1qgc1_  |  Alignment |  | 19.2       | 28     | <b>PDB header:</b> virus/immune system<br><b>Chain:</b> 1: <b>PDB Molecule:</b> protein (virus capsid protein);<br><b>PDB Fragment:</b> residues 133-156 <b>PDBTitle:</b> structure of the complex of an fab fragment of a neutralizing antibody2 with foot and mouth disease virus          |
| 6  | c2knnA_  |  Alignment |  | 12.7       | 45     | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cycloviolacin-o2;<br><b>PDBTitle:</b> solution structure of the cyclotide cycloviolacin o2 with2 glu6 methylated (cyo2me)  |
| 7  | c2wzr1_  |  Alignment |  | 12.6       | 39     | <b>PDB header:</b> virus<br><b>Chain:</b> 1: <b>PDB Molecule:</b> polyprotein;<br><b>PDBTitle:</b> the structure of foot and mouth disease virus serotype sat1   |
| 8  | d1dt9a3  |  Alignment |  | 10.9       | 47     | <b>Fold:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br><b>Superfamily:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br><b>Family:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 |
| 9  | c2jr7A_  |  Alignment |  | 10.2       | 63     | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> dph3 homolog;<br><b>PDBTitle:</b> solution structure of human desr1  |
| 10 | c2jraB_  |  Alignment |  | 7.9        | 46     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein rpa2121;<br><b>PDBTitle:</b> a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6          |
| 11 | c2kcgA_  |  Alignment |  | 6.8        | 50     | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cycloviolacin-o2;<br><b>PDBTitle:</b> solution structure of cycloviolacin o2   |

