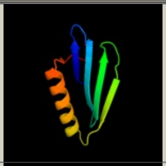
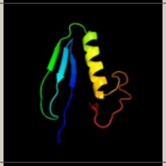
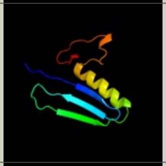
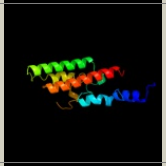
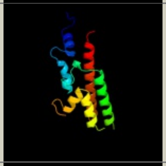
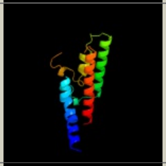
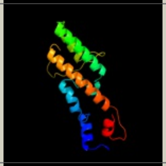
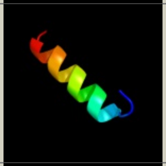
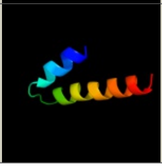
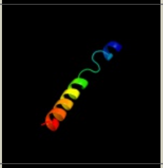
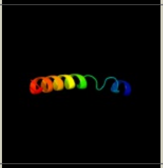
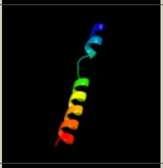
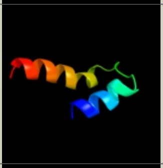
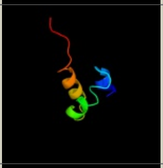
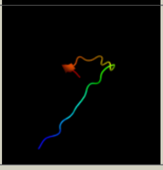
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P78271 |
| Date | Thu Jan 5 12:33:11 GMT 2012 |
| Unique Job ID | f5fa2af14e75ab84 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2ra8A_ | Alignment |  | 99.7 | 45 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein q64v53_bacfr;<br>**PDBTitle:** crystal structure of the q64v53_bacfr protein from bacteroides2 fragilis. northeast structural genomics consortium target bfr43 |
| 2 | c2eocA_ | Alignment |  | 99.6 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 3;<br>**PDBTitle:** solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3 |
| 3 | d2cr9a1 | Alignment |  | 99.4 | 17 | **Fold:**WGR domain-like<br>**Superfamily:**WGR domain-like<br>**Family:**WGR domain |
| 4 | d1efya1 | Alignment |  | 99.4 | 13 | **Fold:**Domain of poly(ADP-ribose) polymerase<br>**Superfamily:**Domain of poly(ADP-ribose) polymerase<br>**Family:**Domain of poly(ADP-ribose) polymerase |
| 5 | d2rd6a1 | Alignment |  | 99.3 | 15 | **Fold:**Domain of poly(ADP-ribose) polymerase<br>**Superfamily:**Domain of poly(ADP-ribose) polymerase<br>**Family:**Domain of poly(ADP-ribose) polymerase |
| 6 | d1gs0a1 | Alignment |  | 99.2 | 12 | **Fold:**Domain of poly(ADP-ribose) polymerase<br>**Superfamily:**Domain of poly(ADP-ribose) polymerase<br>**Family:**Domain of poly(ADP-ribose) polymerase |
| 7 | c3c4hA_ | Alignment |  | 99.1 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase 3;<br>**PDBTitle:** human poly(adp-ribose) polymerase 3, catalytic fragment in complex2 with an inhibitor dr2313 |
| 8 | c1gs0B_ | Alignment |  | 99.0 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**poly (adp-ribose) polymerase-2;<br>**PDBTitle:** crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2 |
| 9 | c2paxA_ | Alignment |  | 99.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase;<br>**PDBTitle:** the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide |
| 10 | c2l9vA_ | Alignment |  | 22.1 | 11 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a;<br>**PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state |
| 11 | c1nohB_ | Alignment |  | 19.4 | 18 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**head morphogenesis protein;<br>**PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c1zp9A_ | Alignment |  | 14.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rio1 kinase;<br>**PDBTitle:** crystal structure of full-legnth a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions. |
| 13 | c1oxzA_ | Alignment |  | 13.7 | 10 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1;<br>**PDBTitle:** crystal structure of the human gga1 gat domain |
| 14 | d1oxza_ | Alignment |  | 13.7 | 10 | **Fold:**Spectrin repeat-like<br>**Superfamily:**GAT-like domain<br>**Family:**GAT domain |
| 15 | c1nafA_ | Alignment |  | 12.7 | 10 | **PDB header:**signaling protein, membrane protein<br>**Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1;<br>**PDBTitle:** crystal structure of the human gga1 gat domain |
| 16 | c3mtuE_ | Alignment |  | 11.5 | 27 | **PDB header:**contractile protein<br>**Chain:** E: **PDB Molecule:**head morphogenesis protein, tropomyosin alpha-1 chain;<br>**PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle |
| 17 | d1vdla_ | Alignment |  | 11.2 | 15 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 18 | c3bsuF_ | Alignment |  | 10.3 | 14 | **PDB header:**hydrolase/rna/dna<br>**Chain:** F: **PDB Molecule:**ribonuclease h1;<br>**PDBTitle:** hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna |
| 19 | d1dp7p_ | Alignment |  | 10.0 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**P4 origin-binding domain-like |
| 20 | d1vbka2 | Alignment |  | 9.0 | 24 | **Fold:**THUMP domain<br>**Superfamily:**THUMP domain-like<br>**Family:**THUMP domain |
| 21 | c2zfhA_ | Alignment | not modelled | 8.9 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**cuta;<br>**PDBTitle:** crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution |
| 22 | d1kr4a_ | Alignment | not modelled | 8.9 | 35 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 23 | c3godA_ | Alignment | not modelled | 8.7 | 12 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**cas1;<br>**PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense |
| 24 | d1p1la_ | Alignment | not modelled | 8.5 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 25 | d1uzca_ | Alignment | not modelled | 8.2 | 14 | **Fold:**Another 3-helical bundle<br>**Superfamily:**FF domain<br>**Family:**FF domain |
| 26 | d1naqa_ | Alignment | not modelled | 8.1 | 25 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 27 | d1qkia1 | Alignment | not modelled | 8.1 | 28 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 28 | d1ugja_ | Alignment | not modelled | 7.9 | 21 | **Fold:**PRC-barrel domain<br>**Superfamily:**PRC-barrel domain<br>**Family:**RIKEN cDNA 2310057j16 protein (KIAA1543) |
| | | | | | | **Fold:**Retroviral matrix proteins |

| | | | | | | |
|---|---|---|---|---|---|---|
| 29 | d2f76x1 | Alignment | not modelled | 7.5 | 12 | **Superfamily:**Retroviral matrix proteins<br>**Family:**Mason-Pfizer monkey virus matrix protein |
| 30 | c1xk8A_ | Alignment | not modelled | 7.5 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta;<br>**PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888 |
| 31 | d2zfha1 | Alignment | not modelled | 7.5 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 32 | c3c4mC_ | Alignment | not modelled | 7.5 | 40 | **PDB header:**membrane protein<br>**Chain:** C: **PDB Molecule:**parathyroid hormone;<br>**PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r) |
| 33 | c3c4mD_ | Alignment | not modelled | 7.5 | 40 | **PDB header:**membrane protein<br>**Chain:** D: **PDB Molecule:**parathyroid hormone;<br>**PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r) |
| 34 | c1zwgA_ | Alignment | not modelled | 7.0 | 40 | **PDB header:**hormone<br>**Chain:** A: **PDB Molecule:**parathyroid hormone;<br>**PDBTitle:** succinyl human parathyroid hormone 4-37, nmr, 10 structures |
| 35 | c2zomC_ | Alignment | not modelled | 7.0 | 25 | **PDB header:**unknown function<br>**Chain:** C: **PDB Molecule:**protein cuta, chloroplast, putative, expressed;<br>**PDBTitle:** crystal structure of cuta1 from oryza sativa |
| 36 | d1ukua_ | Alignment | not modelled | 6.9 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 37 | c1vbkA_ | Alignment | not modelled | 6.9 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ph1313;<br>**PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3 |
| 38 | d1osce_ | Alignment | not modelled | 6.8 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 39 | c2nuhA_ | Alignment | not modelled | 6.8 | 5 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**periplasmic divalent cation tolerance protein;<br>**PDBTitle:** crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa |
| 40 | c2bnlE_ | Alignment | not modelled | 6.5 | 18 | **PDB header:**stress-response<br>**Chain:** E: **PDB Molecule:**modulator protein rsbr;<br>**PDBTitle:** the structure of the n-terminal domain of rsbr |
| 41 | c3ejbC_ | Alignment | not modelled | 6.4 | 23 | **PDB header:**oxidoreductase/lipid transport<br>**Chain:** C: **PDB Molecule:**acyl carrier protein;<br>**PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein |
| 42 | c3do6B_ | Alignment | not modelled | 6.4 | 32 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**formate--tetrahydrofolate ligase;<br>**PDBTitle:** crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution |
| 43 | d1vhfa_ | Alignment | not modelled | 6.3 | 35 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 44 | d1nzaa_ | Alignment | not modelled | 6.3 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Divalent ion tolerance proteins CutA (CutA1) |
| 45 | c3ahpA_ | Alignment | not modelled | 6.2 | 20 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**cuta1;<br>**PDBTitle:** crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1 |
| 46 | c2r0qF_ | Alignment | not modelled | 5.7 | 28 | **PDB header:**recombination/dna<br>**Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3;<br>**PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex |
| 47 | d1eg7a_ | Alignment | not modelled | 5.6 | 32 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 48 | c2diuA_ | Alignment | not modelled | 5.4 | 26 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**kiaa0430 protein;<br>**PDBTitle:** solution structure of the rrm domain of kiaa0430 protein |
| 49 | c2xskA_ | Alignment | not modelled | 5.3 | 55 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**csgc;<br>**PDBTitle:** e. coli curli protein csgc - secys |