# Phyre2

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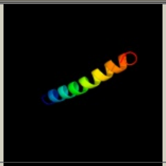
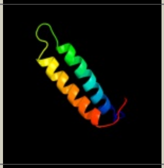
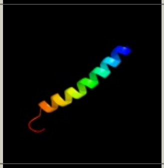
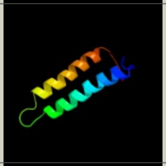
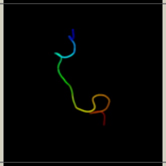
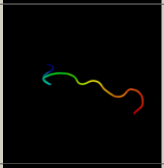
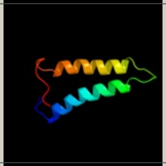
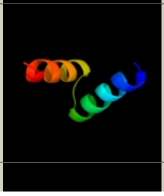
| Email | l.a.kelley@imperial.ac.uk |
| Description | P39267 |
| Date | Thu Jan 5 11:58:39 GMT 2012 |
| Unique Job ID | c5365afec9e12536 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3ku8A_ | Alignment |  | 50.0 | 13 | **PDB header:**toxin/isomerase<br>**Chain:** A: **PDB Molecule:**dna gyrase subunit a;<br>**PDBTitle:** ccdbvfi:gyra14ec |
| 2 | c3jzaB_ | Alignment |  | 49.8 | 25 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**uncharacterized protein drra;<br>**PDBTitle:** crystal structure of human rab1b in complex with the gef domain of2 drra/sidm from legionella pneumophila |
| 3 | d1vmaa1 | Alignment |  | 48.5 | 15 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 4 | d1x75a1 | Alignment |  | 48.2 | 13 | **Fold:**Type II DNA topoisomerase<br>**Superfamily:**Type II DNA topoisomerase<br>**Family:**Type II DNA topoisomerase |
| 5 | c3n6oB_ | Alignment |  | 48.2 | 23 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**guanine nucleotide exchange factor;<br>**PDBTitle:** crystal structure of the gef and p4m domain of drra/sidm from2 legionella pneumophila |
| 6 | d1n9pa_ | Alignment |  | 42.0 | 20 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**Cytoplasmic domain of inward rectifier potassium channel |
| 7 | c3iz6T_ | Alignment |  | 37.7 | 58 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**40s ribosomal protein s21 (s21e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 8 | c2xznZ_ | Alignment |  | 34.5 | 21 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**rps21e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 9 | c3l0mA_ | Alignment |  | 30.0 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**drra;<br>**PDBTitle:** crystal structure of rab1-activation domain and p4m domain of2 sidm/drra from legionella |
| 10 | c3izbT_ | Alignment |  | 29.5 | 57 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**40s ribosomal protein rps21 (s21e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 11 | d1bazb_ | Alignment |  | 28.5 | 19 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |

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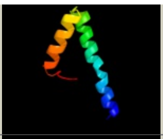
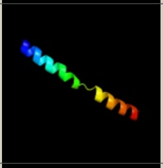
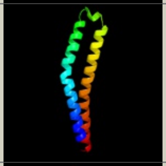
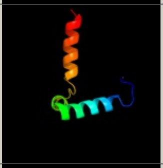
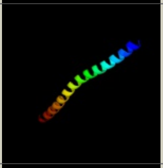
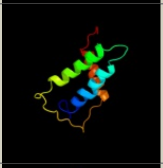
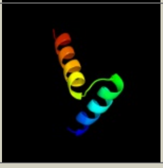
| 12 | d2pgda1 | Alignment |  | 28.1 | 21 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 13 | c1jekA_ | Alignment |  | 27.8 | 15 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**env polyprotein;<br>**PDBTitle:** visna tm core structure |
| 14 | c1z3xA_ | Alignment |  | 27.1 | 11 | **PDB header:**transferase activator<br>**Chain:** A: **PDB Molecule:**putative cytidyltransferase;<br>**PDBTitle:** structure of gun4 from thermosynechococcus elongatus |
| 15 | c3euhB_ | Alignment |  | 25.7 | 13 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**chromosome partition protein mukf;<br>**PDBTitle:** crystal structure of the muke-mukf complex |
| 16 | d1hhsa_ | Alignment |  | 24.9 | 28 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**dsRNA phage RNA-dependent RNA-polymerase |
| 17 | c3p8cD_ | Alignment |  | 24.1 | 12 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**wiskott-aldrich syndrome protein family member 1;<br>**PDBTitle:** structure and control of the actin regulatory wave complex |
| 18 | c3l0iA_ | Alignment |  | 23.1 | 19 | **PDB header:**protein binding/protein transport<br>**Chain:** A: **PDB Molecule:**drra;<br>**PDBTitle:** complex structure of sidm/drra with the wild type rab1 |
| 19 | c2k37A_ | Alignment |  | 23.0 | 28 | **PDB header:**photosynthesis<br>**Chain:** A: **PDB Molecule:**chlorosome protein a;<br>**PDBTitle:** csma |
| 20 | d1myka_ | Alignment |  | 22.6 | 17 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 21 | d1baza_ | Alignment | not modelled | 22.5 | 17 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 22 | c3tbiA_ | Alignment | not modelled | 21.9 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**rna polymerase-associated protein gp33;<br>**PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain |
| 23 | d1bdta_ | Alignment | not modelled | 19.7 | 17 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 24 | c2e4fA_ | Alignment | not modelled | 18.7 | 27 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**g protein-activated inward rectifier potassium channel 2;<br>**PDBTitle:** crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2 |
| 25 | d1i6za_ | Alignment | not modelled | 17.9 | 22 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |
| 26 | d2crna1 | Alignment | not modelled | 16.6 | 11 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 27 | d1gaka_ | Alignment | not modelled | 15.8 | 27 | **Fold:**Fertilization protein<br>**Superfamily:**Fertilization protein<br>**Family:**Fertilization protein |
| 28 | d1u9pa1 | Alignment | not modelled | 15.4 | 13 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 29 | c2xi7B_ | Alignment | not modelled | 14.9 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**rna polymerase l;<br>**PDBTitle:** n-terminal endonuclease domain of la crosse virus l- |

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| | | | | | | protein |
| 30 | c2xi5D_ | Alignment | not modelled | 14.7 | 23 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**rna polymerase l;<br>**PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein |
| 31 | c1wncE_ | Alignment | not modelled | 14.2 | 20 | **PDB header:**viral protein<br>**Chain:** E: **PDB Molecule:**e2 glycoprotein;<br>**PDBTitle:** crystal structure of the sars-cov spike protein fusion core |
| 32 | d1pgja1 | Alignment | not modelled | 13.3 | 13 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 33 | c3hfeC_ | Alignment | not modelled | 12.6 | 25 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**potassium voltage-gated channel subfamily kqt member 1;<br>**PDBTitle:** a trimeric form of the kv7.1 a domain tail |
| 34 | d1z3xa2 | Alignment | not modelled | 12.5 | 11 | **Fold:**GUN4-like<br>**Superfamily:**GUN4-like<br>**Family:**GUN4-like |
| 35 | d2id1a1 | Alignment | not modelled | 12.2 | 18 | **Fold:**Nucleotidyltransferase<br>**Superfamily:**Nucleotidyltransferase<br>**Family:**Iojap/YbeB-like |
| 36 | c2vkzH_ | Alignment | not modelled | 11.8 | 15 | **PDB header:**transferase<br>**Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta;<br>**PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex |
| 37 | d1m50a_ | Alignment | not modelled | 11.5 | 35 | **Fold:**Bacteriochlorophyll A protein<br>**Superfamily:**Bacteriochlorophyll A protein<br>**Family:**Bacteriochlorophyll A protein |
| 38 | c2kz3A_ | Alignment | not modelled | 11.3 | 29 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3;<br>**PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83 |
| 39 | d1mylb_ | Alignment | not modelled | 10.8 | 16 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 40 | c1qgbA_ | Alignment | not modelled | 10.3 | 10 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**protein (fibronectin);<br>**PDBTitle:** solution structure of the n-terminal f1 module pair from2 human fibronectin |
| 41 | c1y6iA_ | Alignment | not modelled | 10.1 | 8 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**mg-chelatase cofactor gun4;<br>**PDBTitle:** synechocystis gun4 |
| 42 | c2ieqC_ | Alignment | not modelled | 9.6 | 17 | **PDB header:**viral protein<br>**Chain:** C: **PDB Molecule:**spike glycoprotein;<br>**PDBTitle:** core structure of s2 from the human coronavirus nl63 spike2 glycoprotein |
| 43 | c2xsbA_ | Alignment | not modelled | 9.5 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase;<br>**PDBTitle:** ogoga pugnac complex |
| 44 | d1iiea_ | Alignment | not modelled | 9.5 | 25 | **Fold:**Class II MHC-associated invariant chain ectoplasmic trimerization domain<br>**Superfamily:**Class II MHC-associated invariant chain ectoplasmic trimerization domain<br>**Family:**Class II MHC-associated invariant chain ectoplasmic trimerization domain |
| 45 | d1y6ia2 | Alignment | not modelled | 8.9 | 8 | **Fold:**GUN4-like<br>**Superfamily:**GUN4-like<br>**Family:**GUN4-like |
| 46 | c3bj4B_ | Alignment | not modelled | 8.8 | 25 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily kqt<br>**PDBTitle:** the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction |
| 47 | c2crnA_ | Alignment | not modelled | 8.8 | 11 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**ubash3a protein;<br>**PDBTitle:** solution structure of the uba domain of human ubash3a2 protein |
| 48 | c2gr7C_ | Alignment | not modelled | 8.7 | 11 | **PDB header:**membrane protein<br>**Chain:** C: **PDB Molecule:**adhesin;<br>**PDBTitle:** hia 992-1098 |
| 49 | d2gr7a1 | Alignment | not modelled | 8.7 | 11 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**YadA C-terminal domain-like |
| 50 | d2cpwa1 | Alignment | not modelled | 8.6 | 4 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 51 | c2kfeA_ | Alignment | not modelled | 8.2 | 14 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**meucin-24;<br>**PDBTitle:** solution structure of meucin-24 |
| 52 | c2kppA_ | Alignment | not modelled | 8.2 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lin0431 protein;<br>**PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112 |
| 53 | d2veaa3 | Alignment | not modelled | 7.6 | 31 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**BphP N-terminal domain-like |
| 54 | d1a8ra_ | Alignment | not modelled | 7.5 | 40 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 55 | c3ejhB | Alignment | not modelled | 7.5 | 11 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**fibronectin; |

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| | | Alignment | not modelled | | 11 | **PDBTitle:** crystal structure of the fibronectin 8-9fni domain pair in complex2 with a type-i collagen peptide |
| 56 | d3cx5h1 | Alignment | not modelled | 7.4 | 50 | **Fold:**Single transmembrane helix<br>**Superfamily:**Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br>**Family:**Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 57 | c3swfA_ | Alignment | not modelled | 7.4 | 11 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1;<br>**PDBTitle:** cnga1 621-690 containing clz domain |
| 58 | c3upsA_ | Alignment | not modelled | 7.4 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**iojap-like protein;<br>**PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis |
| 59 | c2cpwA_ | Alignment | not modelled | 7.2 | 4 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant;<br>**PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna |
| 60 | c2rkzD_ | Alignment | not modelled | 6.9 | 14 | **PDB header:**cell adhesion<br>**Chain:** D: **PDB Molecule:**fibronectin;<br>**PDBTitle:** crystal structure of the second and third fibronectin f12 modules in complex with a fragment of staphylococcus3 aureus fnbpa-1 |
| 61 | d1czan4 | Alignment | not modelled | 6.9 | 100 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**Hexokinase |
| 62 | d1o57a1 | Alignment | not modelled | 6.8 | 29 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**N-terminal domain of Bacillus PurR |
| 63 | c3mmyF_ | Alignment | not modelled | 6.8 | 56 | **PDB header:**nuclear protein<br>**Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98;<br>**PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1 |
| 64 | d1epua_ | Alignment | not modelled | 6.6 | 9 | **Fold:**Sec1/munc18-like (SM) proteins<br>**Superfamily:**Sec1/munc18-like (SM) proteins<br>**Family:**Sec1/munc18-like (SM) proteins |
| 65 | c2dd4H_ | Alignment | not modelled | 6.5 | 16 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**thiocyanate hydrolase beta subunit;<br>**PDBTitle:** thiocyanate hydrolase (scnase) from thiobacillus thioparus2 recombinant apo-enzyme |
| 66 | c2dagA_ | Alignment | not modelled | 6.4 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5;<br>**PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5) |
| 67 | c3iwfA_ | Alignment | not modelled | 6.3 | 9 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcription regulator rpir family;<br>**PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a |
| 68 | d1txka1 | Alignment | not modelled | 6.3 | 33 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**E-set domains of sugar-utilizing enzymes |
| 69 | d2oo3a1 | Alignment | not modelled | 6.1 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**LPG1296-like |
| 70 | d3bqoa1 | Alignment | not modelled | 6.0 | 21 | **Fold:**Telomeric repeat binding factor (TRF) dimerisation domain<br>**Superfamily:**Telomeric repeat binding factor (TRF) dimerisation domain<br>**Family:**Telomeric repeat binding factor (TRF) dimerisation domain |
| 71 | d1whca_ | Alignment | not modelled | 5.9 | 7 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 72 | d1dn1a_ | Alignment | not modelled | 5.7 | 18 | **Fold:**Sec1/munc18-like (SM) proteins<br>**Superfamily:**Sec1/munc18-like (SM) proteins<br>**Family:**Sec1/munc18-like (SM) proteins |
| 73 | d1bg3a4 | Alignment | not modelled | 5.6 | 100 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**Hexokinase |
| 74 | c2y9xC_ | Alignment | not modelled | 5.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**polyphenol oxidase;<br>**PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone |
| 75 | c1aq5C_ | Alignment | not modelled | 5.1 | 19 | **PDB header:**coiled-coil<br>**Chain:** C: **PDB Molecule:**cartilage matrix protein;<br>**PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures |