# Phyre$^2$

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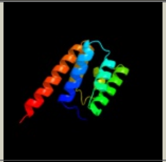
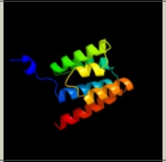
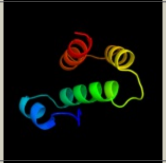
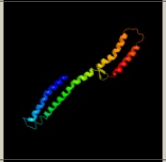
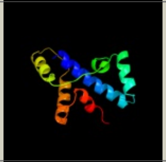
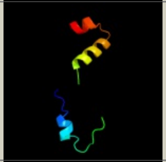
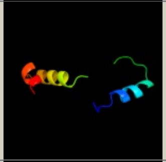
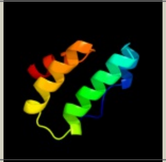
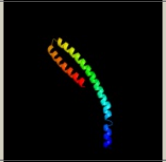
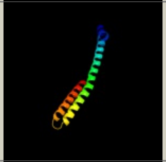
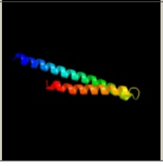
| Email | l.a.kelley@imperial.ac.uk |
| Description | P36646 |
| Date | Thu Jan 5 11:53:26 GMT 2012 |
| Unique Job ID | 52a94c307197f99d |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3c1qA_ | Alignment |  | 99.9 | 26 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**general secretion pathway protein f;<br>**PDBTitle:** the three-dimensional structure of the cytoplasmic domains of epsf2 from the type 2 secretion system of vibrio cholerae |
| 2 | c2whnA_ | Alignment |  | 99.8 | 31 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**pilus assembly protein pilc;<br>**PDBTitle:** n-terminal domain from the pilc type iv pilus biogenesis2 protein |
| 3 | c3i3aC_ | Alignment |  | 54.4 | 13 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-<br>**PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa |
| 4 | c2bbjB_ | Alignment |  | 48.5 | 18 | **PDB header:**metal transport/membrane protein<br>**Chain:** B: **PDB Molecule:**divalent cation transport-related protein;<br>**PDBTitle:** crystal structure of the cora mg2+ transporter |
| 5 | d3cuma1 | Alignment |  | 47.6 | 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 |
| 6 | c3c8mA_ | Alignment |  | 45.1 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium |
| 7 | c2ejwB_ | Alignment |  | 41.4 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8 |
| 8 | d2jf2a1 | Alignment |  | 35.6 | 16 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**UDP N-acetylglucosamine acyltransferase |
| 9 | c2d1lA_ | Alignment |  | 35.1 | 11 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**metastasis suppressor protein 1;<br>**PDBTitle:** structure of f-actin binding domain imd of mim (missing in metastasis) |
| 10 | d1y2oa1 | Alignment |  | 31.7 | 7 | **Fold:**BAR/IMD domain-like<br>**Superfamily:**BAR/IMD domain-like<br>**Family:**IMD domain |
| 11 | c3ok8A_ | Alignment |  | 29.4 | 12 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein<br>**PDBTitle:** i-bar of pinkbar |

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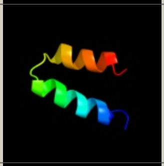
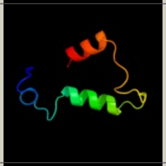
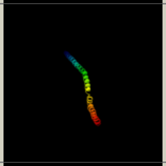
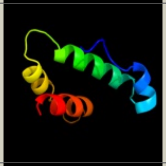
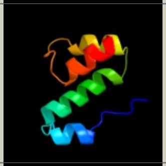
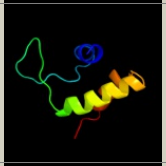
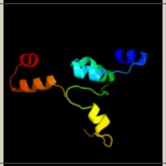
| 12 | c2c5qE_ | Alignment |  | 28.0 | 22 | **PDB header:**structural genomics,unknown function<br>**Chain:** E: **PDB Molecule:**rraa-like protein yer010c;<br>**PDBTitle:** crystal structure of yeast yer010cp |
| 13 | d2ezla_ | Alignment |  | 23.5 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 14 | c3iugA_ | Alignment |  | 19.0 | 17 | **PDB header:**splicing<br>**Chain:** A: **PDB Molecule:**rho/cdc42/rac gtpase-activating protein rics;<br>**PDBTitle:** crystal structure of the rhogap domain of rics |
| 15 | c3ipdB_ | Alignment |  | 18.0 | 12 | **PDB header:**exocytosis<br>**Chain:** B: **PDB Molecule:**syntaxin-1a;<br>**PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21 |
| 16 | d1j2za_ | Alignment |  | 17.7 | 11 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**UDP N-acetylglucosamine acyltransferase |
| 17 | c3r0sA_ | Alignment |  | 17.6 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o-<br>**PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni |
| 18 | c2jmlA_ | Alignment |  | 15.9 | 19 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator;<br>**PDBTitle:** solution structure of the n-terminal domain of cara repressor |
| 19 | c3ingA_ | Alignment |  | 15.3 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution |
| 20 | c3r1fO_ | Alignment |  | 13.5 | 20 | **PDB header:**transcription<br>**Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr;<br>**PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis |
| 21 | c3k4iC_ | Alignment | not modelled | 13.1 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000 |
| 22 | c2pmzN_ | Alignment | not modelled | 13.1 | 10 | **PDB header:**translation, transferase<br>**Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 23 | c3byiA_ | Alignment | not modelled | 12.7 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho gtpase activating protein 15;<br>**PDBTitle:** crystal structure of human rho gtpase activating protein 15 (arhgap15) |
| 24 | c3do5A_ | Alignment | not modelled | 12.3 | 5 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution |
| 25 | c3kuqA_ | Alignment | not modelled | 12.2 | 11 | **PDB header:**hydrolase activator<br>**Chain:** A: **PDB Molecule:**rho gtpase-activating protein 7;<br>**PDBTitle:** crystal structure of the dlc1 rhogap domain |
| 26 | c3neuA_ | Alignment | not modelled | 11.2 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lin1836 protein;<br>**PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262 |
| 27 | d1xa6a1 | Alignment | not modelled | 10.6 | 11 | **Fold:**GTPase activation domain, GAP<br>**Superfamily:**GTPase activation domain, GAP<br>**Family:**BCR-homology GTPase activation domain (BH-domain) |
| 28 | c3gndC_ | Alignment | not modelled | 10.1 | 9 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**aldolase lsrf;<br>**PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| | | | | | | **Fold:**Ribosomal protein L22 |

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| 29 | d1i4ja_ | Alignment | not modelled | 9.0 | 15 | **Superfamily:**Ribosomal protein L22<br>**Family:**Ribosomal protein L22 |
| 30 | d1e8ob_ | Alignment | not modelled | 8.4 | 14 | **Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14<br>**Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14<br>**Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 |
| 31 | d1jnsa_ | Alignment | not modelled | 7.7 | 19 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 32 | c1xa6A_ | Alignment | not modelled | 7.7 | 11 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**beta2-chimaerin;<br>**PDBTitle:** crystal structure of the human beta2-chimaerin |
| 33 | d1wn0a1 | Alignment | not modelled | 7.3 | 19 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Histidine-containing phosphotransfer domain, HPT domain<br>**Family:**Phosphorelay protein-like |
| 34 | c3kc2A_ | Alignment | not modelled | 7.2 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w;<br>**PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae |
| 35 | d2gyqa1 | Alignment | not modelled | 7.1 | 18 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**YciF-like |
| 36 | c1zk6A_ | Alignment | not modelled | 7.1 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**foldase protein prsa;<br>**PDBTitle:** nmr solution structure of b. subtilis prsa ppiase |
| 37 | d1vq3a_ | Alignment | not modelled | 7.0 | 13 | **Fold:**PurS-like<br>**Superfamily:**PurS-like<br>**Family:**PurS subunit of FGAM synthetase |
| 38 | c2zhhA_ | Alignment | not modelled | 6.9 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr;<br>**PDBTitle:** crystal structure of soxr |
| 39 | c3gpkA_ | Alignment | not modelled | 6.5 | 28 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution. |
| 40 | d2gs4a1 | Alignment | not modelled | 6.5 | 20 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**YciF-like |
| 41 | c2ftcM_ | Alignment | not modelled | 6.5 | 19 | **PDB header:**ribosome<br>**Chain:** M: **PDB Molecule:**mitochondrial ribosomal protein l22 isoform a;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 42 | c3ibqA_ | Alignment | not modelled | 6.5 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxal kinase;<br>**PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp |
| 43 | c1sneB_ | Alignment | not modelled | 6.5 | 46 | **PDB header:**de novo protein<br>**Chain:** B: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein;<br>**PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein |
| 44 | c1sneA_ | Alignment | not modelled | 6.5 | 46 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein;<br>**PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein |
| 45 | c2hx1D_ | Alignment | not modelled | 6.5 | 8 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had<br>**PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution |
| 46 | d1914a2 | Alignment | not modelled | 6.4 | 14 | **Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14<br>**Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14<br>**Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 |
| 47 | c1ebuA_ | Alignment | not modelled | 6.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine |
| 48 | d1gtda_ | Alignment | not modelled | 6.0 | 4 | **Fold:**PurS-like<br>**Superfamily:**PurS-like<br>**Family:**PurS subunit of FGAM synthetase |
| 49 | c2eelA_ | Alignment | not modelled | 5.9 | 17 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**cell death activator cide-a;<br>**PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a |
| 50 | c2i7aA_ | Alignment | not modelled | 5.9 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**calpain 13;<br>**PDBTitle:** domain iv of human calpain 13 |
| 51 | c2qjhH_ | Alignment | not modelled | 5.9 | 10 | **PDB header:**lyase<br>**Chain:** H: **PDB Molecule:**putative aldolase mj0400;<br>**PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate |
| 52 | c2zw2B_ | Alignment | not modelled | 5.9 | 8 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178;<br>**PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs) |
| 53 | c2rqsA_ | Alignment | not modelled | 5.8 | 20 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase;<br>**PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin) |

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| 54 | d1hara_ | Alignment | not modelled | 5.7 | 13 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Reverse transcriptase |
| 55 | d1oqwa_ | Alignment | not modelled | 5.5 | 11 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**Pilin |
| 56 | d1d4ba_ | Alignment | not modelled | 5.5 | 21 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**CAD & PB1 domains<br>**Family:**CAD domain |
| 57 | d1eqfa1 | Alignment | not modelled | 5.5 | 6 | **Fold:**Bromodomain-like<br>**Superfamily:**Bromodomain<br>**Family:**Bromodomain |
| 58 | c2kncA_ | Alignment | not modelled | 5.5 | 17 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 59 | d1c9fa_ | Alignment | not modelled | 5.4 | 17 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**CAD & PB1 domains<br>**Family:**CAD domain |
| 60 | c1zzwA_ | Alignment | not modelled | 5.4 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10;<br>**PDBTitle:** crystal structure of catalytic domain of human map kinase2 phosphatase 5 |
| 61 | d2pila_ | Alignment | not modelled | 5.4 | 21 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**Pilin |
| 62 | c3q6aH_ | Alignment | not modelled | 5.4 | 19 | **PDB header:**structure genomics, unknown function<br>**Chain:** H: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116 |
| 63 | d1ibxa_ | Alignment | not modelled | 5.3 | 10 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**CAD & PB1 domains<br>**Family:**CAD domain |
| 64 | d2pv2a1 | Alignment | not modelled | 5.3 | 10 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 65 | c2kgjA_ | Alignment | not modelled | 5.2 | 16 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d;<br>**PDBTitle:** solution structure of parvulin domain of ppid from e.coli |
| 66 | d2cbia1 | Alignment | not modelled | 5.1 | 16 | **Fold:**Hyaluronidase domain-like<br>**Superfamily:**Hyaluronidase post-catalytic domain-like<br>**Family:**Hyaluronidase post-catalytic domain-like |
| 67 | c1zrtD_ | Alignment | not modelled | 5.1 | 4 | **PDB header:**oxidoreductase/metal transport<br>**Chain:** D: **PDB Molecule:**cytochrome c1;<br>**PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound |
| 68 | c3hefB_ | Alignment | not modelled | 5.1 | 12 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**gene 1 protein;<br>**PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit |
| 69 | c3nmeA_ | Alignment | not modelled | 5.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sex4 glucan phosphatase;<br>**PDBTitle:** structure of a plant phosphatase |