# Phyre$^2$

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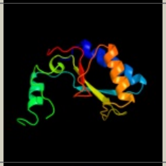
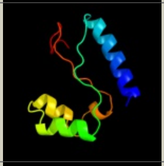
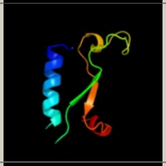
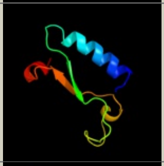
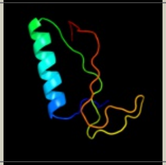
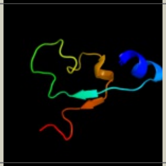
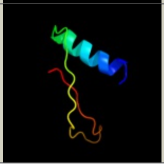
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77790 |
| Date | Thu Jan 5 12:32:53 GMT 2012 |
| Unique Job ID | f73adf9a98f4749d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1r44a_ | Alignment |  | 100.0 | 36 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**VanX-like |
| 2 | d2vo9a1 | Alignment |  | 99.8 | 25 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**VanY-like |
| 3 | c2vo9C_ | Alignment |  | 99.8 | 25 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase;<br>**PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500 |
| 4 | d3d1ma1 | Alignment |  | 95.8 | 19 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**Hedgehog (development protein), N-terminal signaling domain |
| 5 | d1lbua2 | Alignment |  | 95.6 | 20 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**Muramoyl-pentapeptide carboxypeptidase |
| 6 | c1lbuA_ | Alignment |  | 95.5 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase;<br>**PDBTitle:** hydrolase metallo (zn) dd-peptidase |
| 7 | c3m1nB_ | Alignment |  | 94.9 | 19 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**sonic hedgehog protein;<br>**PDBTitle:** crystal structure of human sonic hedgehog n-terminal domain |
| 8 | d2ibge1 | Alignment |  | 93.4 | 18 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**Hedgehog (development protein), N-terminal signaling domain |
| 9 | d1tzpa_ | Alignment |  | 79.7 | 20 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**MepA-like |
| 10 | d1eswa_ | Alignment |  | 33.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 11 | d1nwba_ | Alignment |  | 26.5 | 17 | **Fold:**HesB-like domain<br>**Superfamily:**HesB-like domain<br>**Family:**HesB-like domain |

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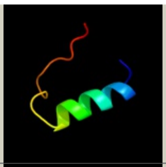
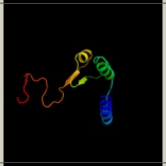
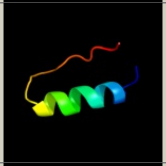
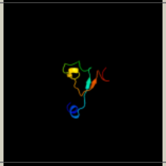
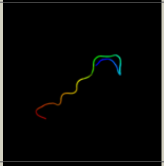
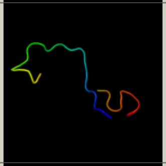
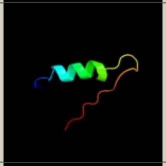
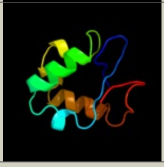
|---|---|---|---|---|---|---|
| 12 | c2k4zA_ | Alignment |  | 26.4 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dsrr;<br>**PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5 |
| 13 | d2j07a2 | Alignment |  | 25.2 | 10 | **Fold:**Cryptochrome/photolyase, N-terminal domain<br>**Superfamily:**Cryptochrome/photolyase, N-terminal domain<br>**Family:**Cryptochrome/photolyase, N-terminal domain |
| 14 | c2apnA_ | Alignment |  | 21.9 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**protein hi1723;<br>**PDBTitle:** hi1723 solution structure |
| 15 | d1x1na1 | Alignment |  | 20.7 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 16 | c3kyzA_ | Alignment |  | 19.8 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein pfes;<br>**PDBTitle:** the crystal structure of the sensor domain of two-component2 sensor pfes from pseudomonas aeruginosa pa01 |
| 17 | d1bhua_ | Alignment |  | 19.3 | 31 | **Fold:**gamma-Crystallin-like<br>**Superfamily:**gamma-Crystallin-like<br>**Family:**Streptomyces metalloproteinase inhibitor, SMPI |
| 18 | d1xpja_ | Alignment |  | 18.9 | 29 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**Hypothetical protein VC0232 |
| 19 | d2d8za1 | Alignment |  | 18.2 | 33 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 20 | c3aq3A_ | Alignment |  | 16.8 | 22 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**6b protein;<br>**PDBTitle:** molecular insights into plant cell proliferation disturbance by2 agrobacterium protein 6b |
| 21 | d2cura2 | Alignment | not modelled | 16.6 | 25 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 22 | c3d2hA_ | Alignment | not modelled | 14.3 | 6 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme;<br>**PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form |
| 23 | d1n8ja_ | Alignment | not modelled | 14.0 | 14 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Glutathione peroxidase-like |
| 24 | c2ipiD_ | Alignment | not modelled | 13.6 | 8 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox);<br>**PDBTitle:** crystal structure of aclacinomycin oxidoreductase |
| 25 | d2nlya1 | Alignment | not modelled | 11.1 | 17 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**Divergent polysaccharide deacetylase |
| 26 | d2qn6b1 | Alignment | not modelled | 9.3 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**eIF-2-alpha, C-terminal domain<br>**Family:**eIF-2-alpha, C-terminal domain |
| 27 | c3fwaA_ | Alignment | not modelled | 9.1 | 6 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**reticuline oxidase;<br>**PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline |
| 28 | d2pp6a1 | Alignment | not modelled | 9.1 | 13 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**gpFII-like |
| 29 | c3kebB_ | Alignment | not modelled | 9.0 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable thiol peroxidase; |

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| | | | | | | **PDBTitle:** thiol peroxidase from chromobacterium violaceum |
| 30 | d1vk9a_ | Alignment | not modelled | 8.3 | 25 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Hypothetical protein TM1506 |
| 31 | d2r4qa1 | Alignment | not modelled | 8.3 | 28 | **Fold:**Phosphotyrosine protein phosphatases I-like<br>**Superfamily:**PTS system IIB component-like<br>**Family:**PTS system, Fructose specific IIB subunit-like |
| 32 | c2ov2O_ | Alignment | not modelled | 8.2 | 27 | **PDB header:**protein binding/transferase<br>**Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4;<br>**PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4) |
| 33 | c3lklB_ | Alignment | not modelled | 8.0 | 16 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas;<br>**PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides |
| 34 | d1np7a2 | Alignment | not modelled | 7.8 | 11 | **Fold:**Cryptochrome/photolyase, N-terminal domain<br>**Superfamily:**Cryptochrome/photolyase, N-terminal domain<br>**Family:**Cryptochrome/photolyase, N-terminal domain |
| 35 | c3o2iB_ | Alignment | not modelled | 7.6 | 31 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba |
| 36 | d1tz7a1 | Alignment | not modelled | 7.5 | 7 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 37 | c1dxyA_ | Alignment | not modelled | 7.4 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase;<br>**PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase |
| 38 | c2h31A_ | Alignment | not modelled | 7.2 | 16 | **PDB header:**ligase, lyase<br>**Chain:** A: **PDB Molecule:**multifunctional protein ade2;<br>**PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis |
| 39 | d2r48a1 | Alignment | not modelled | 7.0 | 28 | **Fold:**Phosphotyrosine protein phosphatases I-like<br>**Superfamily:**PTS system IIB component-like<br>**Family:**PTS system, Fructose specific IIB subunit-like |
| 40 | c2kyrA_ | Alignment | not modelled | 6.7 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1;<br>**PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544 |
| 41 | d1lvaa3 | Alignment | not modelled | 6.5 | 4 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**C-terminal fragment of elongation factor SelB |
| 42 | c1s1iS_ | Alignment | not modelled | 6.2 | 26 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h. |
| 43 | c2zkru_ | Alignment | not modelled | 6.2 | 26 | **PDB header:**ribosomal protein/rna<br>**Chain:** U: **PDB Molecule:**rna expansion segment es41;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 44 | d1j4aa1 | Alignment | not modelled | 6.1 | 25 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Formate/glycerate dehydrogenases, NAD-domain |
| 45 | c1ybaC_ | Alignment | not modelled | 6.1 | 22 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase;<br>**PDBTitle:** the active form of phosphoglycerate dehydrogenase |
| 46 | c3fzeA_ | Alignment | not modelled | 5.7 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**protein ste5;<br>**PDBTitle:** structure of the 'minimal scaffold' (ms) domain of ste52 that cocatalyzes fus3 phosphorylation by ste7 |
| 47 | d1yj5a1 | Alignment | not modelled | 5.7 | 25 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**phosphatase domain of polynucleotide kinase |
| 48 | d1owla2 | Alignment | not modelled | 5.5 | 17 | **Fold:**Cryptochrome/photolyase, N-terminal domain<br>**Superfamily:**Cryptochrome/photolyase, N-terminal domain<br>**Family:**Cryptochrome/photolyase, N-terminal domain |
| 49 | c3izcZ_ | Alignment | not modelled | 5.5 | 26 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 50 | c3lloA_ | Alignment | not modelled | 5.5 | 13 | **PDB header:**motor protein<br>**Chain:** A: **PDB Molecule:**prestin;<br>**PDBTitle:** crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5) |
| 51 | c4a1eT_ | Alignment | not modelled | 5.5 | 21 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**rpl24;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1 |
| 52 | d2naca1 | Alignment | not modelled | 5.5 | 15 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Formate/glycerate dehydrogenases, NAD-domain |
| 53 | c3iz5Z_ | Alignment | not modelled | 5.4 | 21 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| | | | | | | **Fold:**FAD-binding/transporter-associated domain-like |

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| 54 | d2i0ka2 | Alignment | not modelled | 5.4 | 11 | **Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 55 | c3isyA_ | Alignment | not modelled | 5.3 | 21 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor;<br>**PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution |
| 56 | c3d8uA_ | Alignment | not modelled | 5.3 | 14 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**purr transcriptional regulator;<br>**PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633 |
| 57 | c1vkzA_ | Alignment | not modelled | 5.2 | 9 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase;<br>**PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution |
| 58 | d1vqou1 | Alignment | not modelled | 5.2 | 25 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**Ribosomal protein L24e |
| 59 | d1dnpa2 | Alignment | not modelled | 5.1 | 13 | **Fold:**Cryptochrome/photolyase, N-terminal domain<br>**Superfamily:**Cryptochrome/photolyase, N-terminal domain<br>**Family:**Cryptochrome/photolyase, N-terminal domain |