# Phyre2

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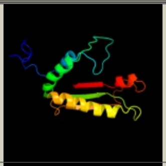
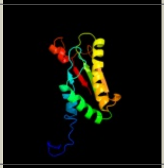
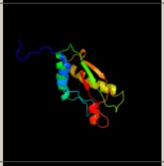
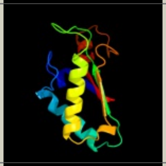
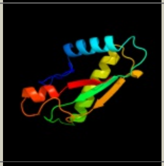
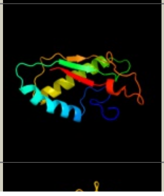
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A912 |
| Date | Thu Jan 5 11:09:08 GMT 2012 |
| Unique Job ID | 2fdbc113e2f538d7 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2l26A_ | Alignment |  | 100.0 | 24 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922;<br>**PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains |
| 2 | d2aizp1 | Alignment |  | 100.0 | 55 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**OmpA-like<br>**Family:**OmpA-like |
| 3 | d2hqsc1 | Alignment |  | 100.0 | 100 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**OmpA-like<br>**Family:**OmpA-like |
| 4 | c2kgwA_ | Alignment |  | 100.0 | 25 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis |
| 5 | c3khnB_ | Alignment |  | 100.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**motb protein, putative;<br>**PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris. |
| 6 | c2k1sA_ | Alignment |  | 100.0 | 24 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad;<br>**PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553. |
| 7 | c3td4D_ | Alignment |  | 100.0 | 25 | **PDB header:**membrane protein,peptide binding protein<br>**Chain:** D: **PDB Molecule:**outer membrane protein omp38;<br>**PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate |
| 8 | c3cyqM_ | Alignment |  | 100.0 | 24 | **PDB header:**membrane protein<br>**Chain:** M: **PDB Molecule:**chemotaxis protein motb;<br>**PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid |
| 9 | c1r1mA_ | Alignment |  | 100.0 | 34 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein class 4;<br>**PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis |
| 10 | d1r1ma_ | Alignment |  | 100.0 | 34 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**OmpA-like<br>**Family:**OmpA-like |
| 11 | c2zvyB_ | Alignment |  | 100.0 | 23 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**chemotaxis protein motb;<br>**PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form ii) |

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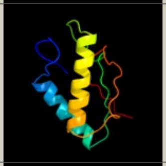
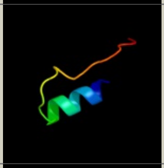
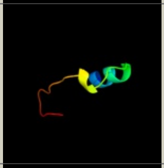
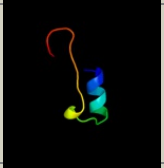
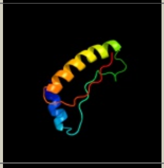
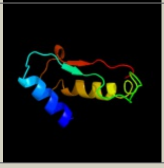
| 12 | c3ldtA_ | Alignment |  | 99.9 | 16 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein;<br>**PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila |
| 13 | c3oonA_ | Alignment |  | 99.9 | 28 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein (tpn50);<br>**PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31 |
| 14 | c2zovA_ | Alignment |  | 99.9 | 26 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**chemotaxis protein motb;<br>**PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i) |
| 15 | c2zf8A_ | Alignment |  | 99.8 | 27 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor;<br>**PDBTitle:** crystal structure of moty |
| 16 | c2r6hC_ | Alignment |  | 48.4 | 38 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f<br>**PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis |
| 17 | d1gvha3 | Alignment |  | 45.4 | 22 | **Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Family:**Flavohemoglobin, C-terminal domain |
| 18 | c1gvhA_ | Alignment |  | 37.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**flavohemoprotein;<br>**PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket |
| 19 | d1tiaa_ | Alignment |  | 36.8 | 27 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Fungal lipases |
| 20 | c3ngmB_ | Alignment |  | 34.8 | 36 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**extracellular lipase;<br>**PDBTitle:** crystal structure of lipase from gibberella zeae |
| 21 | d1tiba_ | Alignment | not modelled | 33.6 | 35 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Fungal lipases |
| 22 | c3g7nA_ | Alignment | not modelled | 32.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lipase;<br>**PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3 |
| 23 | c1tvcA_ | Alignment | not modelled | 24.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**methane monooxygenase component c;<br>**PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath) |
| 24 | d1bwvs_ | Alignment | not modelled | 23.8 | 19 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 25 | c3o0dF_ | Alignment | not modelled | 23.3 | 26 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**triacylglycerol lipase;<br>**PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution |
| 26 | d1uzhc1 | Alignment | not modelled | 22.5 | 16 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 27 | d1bxni_ | Alignment | not modelled | 20.4 | 16 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 28 | d1uwca_ | Alignment | not modelled | 20.1 | 25 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Fungal lipases |
| 29 | d1cqxa3 | Alignment | not modelled | 19.8 | 13 | **Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain |

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| | | | | | | **Family:**Flavohemoglobin, C-terminal domain |
| 30 | d1tvca2 | Alignment | not modelled | 19.7 | 11 | **Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Family:**Aromatic dioxygenase reductase-like |
| 31 | c1cqxB_ | Alignment | not modelled | 19.6 | 15 | **PDB header:**lipid binding protein<br>**Chain:** B: **PDB Molecule:**flavohemoprotein;<br>**PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution |
| 32 | d1krha2 | Alignment | not modelled | 17.5 | 15 | **Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain<br>**Family:**Aromatic dioxygenase reductase-like |
| 33 | c3l7pA_ | Alignment | not modelled | 17.1 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii;<br>**PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans |
| 34 | d1rbli_ | Alignment | not modelled | 16.5 | 17 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 35 | d1xdpa4 | Alignment | not modelled | 16.1 | 9 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 36 | d3tgla_ | Alignment | not modelled | 16.0 | 23 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Fungal lipases |
| 37 | d1gk8i_ | Alignment | not modelled | 15.6 | 16 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 38 | d1svdm1 | Alignment | not modelled | 14.2 | 12 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 39 | d1ir1s_ | Alignment | not modelled | 14.2 | 19 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 40 | d1ej7s_ | Alignment | not modelled | 13.8 | 16 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 41 | d8ruci_ | Alignment | not modelled | 13.8 | 19 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 42 | d2o8ra4 | Alignment | not modelled | 13.3 | 9 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 43 | d4pgaa_ | Alignment | not modelled | 13.2 | 18 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 44 | d2v6ai1 | Alignment | not modelled | 13.1 | 16 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 45 | c2gpjA_ | Alignment | not modelled | 12.7 | 12 | **PDB header:**fad-binding protein<br>**Chain:** A: **PDB Molecule:**siderophore-interacting protein;<br>**PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution |
| 46 | d1uzdc1 | Alignment | not modelled | 12.4 | 13 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 47 | c2ckcA_ | Alignment | not modelled | 12.2 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7;<br>**PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction |
| 48 | d2ckca1 | Alignment | not modelled | 12.2 | 17 | **Fold:**GYF/BRK domain-like<br>**Superfamily:**BRK domain-like<br>**Family:**BRK domain-like |
| 49 | d1wdds_ | Alignment | not modelled | 11.7 | 19 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 50 | d2v0ea1 | Alignment | not modelled | 11.1 | 20 | **Fold:**GYF/BRK domain-like<br>**Superfamily:**BRK domain-like<br>**Family:**BRK domain-like |
| 51 | c2rodB_ | Alignment | not modelled | 10.2 | 17 | **PDB header:**apoptosis<br>**Chain:** B: **PDB Molecule:**noxa;<br>**PDBTitle:** solution structure of mcl-1 complexed with noxaa |
| 52 | c2bgjB_ | Alignment | not modelled | 9.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase;<br>**PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms |
| 53 | d1o7ja_ | Alignment | not modelled | 8.8 | 18 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 54 | c3qbwA_ | Alignment | not modelled | 8.1 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase;<br>**PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate |
| 55 | c3cqyA_ | Alignment | not modelled | 8.1 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase;<br>**PDBTitle:** crystal structure of a functionally unknown protein |

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| | | | | | | (so_1313) from2 shewanella oneidensis mr-1 |
| 56 | c1jrjA_ | Alignment | not modelled | 8.0 | 17 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**exendin-4;<br>**PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol |
| 57 | c2ckaA_ | Alignment | not modelled | 7.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8;<br>**PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction |
| 58 | d2ckaa1 | Alignment | not modelled | 7.9 | 17 | **Fold:**GYF/BRK domain-like<br>**Superfamily:**BRK domain-like<br>**Family:**BRK domain-like |
| 59 | d1agxa_ | Alignment | not modelled | 7.7 | 23 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 60 | c2o8rA_ | Alignment | not modelled | 7.1 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |
| 61 | d1lgya_ | Alignment | not modelled | 7.1 | 22 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Fungal lipases |
| 62 | d1wsaa_ | Alignment | not modelled | 6.8 | 13 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 63 | d2ibge1 | Alignment | not modelled | 6.7 | 13 | **Fold:**Hedgehog/DD-peptidase<br>**Superfamily:**Hedgehog/DD-peptidase<br>**Family:**Hedgehog (development protein), N-terminal signaling domain |
| 64 | c2ogsA_ | Alignment | not modelled | 6.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50;<br>**PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2 |
| 65 | d1uc8a1 | Alignment | not modelled | 6.6 | 26 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**Lysine biosynthesis enzyme LysX, N-terminal domain |
| 66 | d1tkja1 | Alignment | not modelled | 6.5 | 15 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Bacterial dinuclear zinc exopeptidases |
| 67 | c3pe3D_ | Alignment | not modelled | 5.8 | 22 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n-<br>**PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate |
| 68 | c3pa8A_ | Alignment | not modelled | 5.5 | 14 | **PDB header:**toxin/peptide inhibitor<br>**Chain:** A: **PDB Molecule:**toxin b;<br>**PDBTitle:** structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor |
| 69 | c3a9lB_ | Alignment | not modelled | 5.5 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase;<br>**PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase |
| 70 | c2oghA_ | Alignment | not modelled | 5.4 | 18 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1;<br>**PDBTitle:** solution structure of yeast eif1 |
| 71 | c1nauA_ | Alignment | not modelled | 5.3 | 36 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**glucagon;<br>**PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles |