Phyre$^2$

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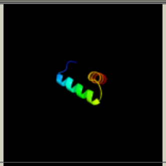
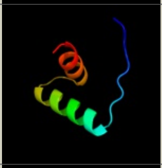
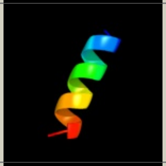
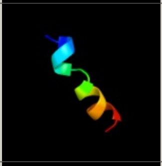
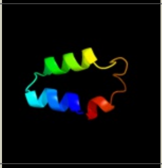
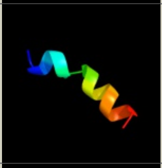
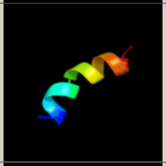
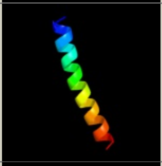
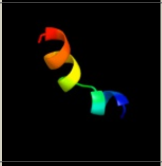
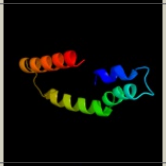
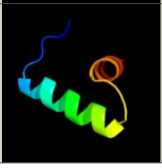
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A8N0 |
| Date | Thu Jan 5 11:08:13 GMT 2012 |
| Unique Job ID | d55e0eeb54e337ff |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3kk4B_ | Alignment |  | 87.0 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein bp1543;<br>**PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i |
| 2 | d2ay0a1 | Alignment |  | 32.6 | 24 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**PutA pre-N-terminal region-like |
| 3 | d2auaa1 | Alignment |  | 22.7 | 40 | **Fold:**ADP-ribosylation<br>**Superfamily:**ADP-ribosylation<br>**Family:**BC2332-like |
| 4 | c3nsnA_ | Alignment |  | 21.0 | 44 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-acetylglucosaminidase;<br>**PDBTitle:** crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin |
| 5 | d1ug3a2 | Alignment |  | 20.2 | 18 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**ARM repeat<br>**Family:**MIF4G domain-like |
| 6 | d1qbaa3 | Alignment |  | 14.4 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-N-acetylhexosaminidase catalytic domain |
| 7 | c1qbaA_ | Alignment |  | 13.8 | 25 | **PDB header:**glycosyl hydrolase<br>**Chain:** A: **PDB Molecule:**chitobiase;<br>**PDBTitle:** bacterial chitobiase, glycosyl hydrolase family 20 |
| 8 | c2pnvA_ | Alignment |  | 12.3 | 22 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium<br>**PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus |
| 9 | c3rcnA_ | Alignment |  | 12.2 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase;<br>**PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens |
| 10 | c2qzcB_ | Alignment |  | 11.5 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**transcriptional activator tena-1;<br>**PDBTitle:** crystal structure of a putative tena-like thiaminase (tena-1, sso2206)2 from sulfolobus solfataricus p2 at 1.50 a resolution |
| 11 | c2rbfB_ | Alignment |  | 10.7 | 25 | **PDB header:**oxidoreductase/dna<br>**Chain:** B: **PDB Molecule:**bifunctional protein puta;<br>**PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2) |

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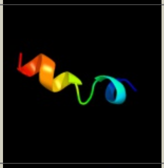
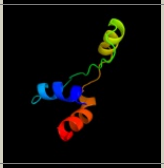
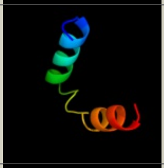
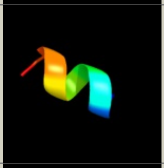
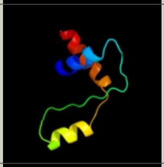
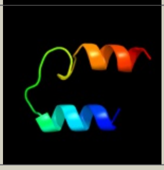
| 12 | c1m04A_ | Alignment |  | 10.6 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase;<br>**PDBTitle:** mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac) |
| 13 | d2ahma1 | Alignment |  | 10.5 | 35 | **Fold:**immunoglobulin/albumin-binding domain-like<br>**Superfamily:**Coronavirus NSP7-like<br>**Family:**Coronavirus NSP7-like |
| 14 | d1ysya1 | Alignment |  | 10.2 | 35 | **Fold:**immunoglobulin/albumin-binding domain-like<br>**Superfamily:**Coronavirus NSP7-like<br>**Family:**Coronavirus NSP7-like |
| 15 | d1jaka1 | Alignment |  | 9.4 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-N-acetylhexosaminidase catalytic domain |
| 16 | c2o59B_ | Alignment |  | 8.4 | 23 | **PDB header:**isomerase/dna<br>**Chain:** B: **PDB Molecule:**dna topoisomerase 3;<br>**PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0 |
| 17 | d2p62a1 | Alignment |  | 8.3 | 31 | **Fold:**PH0156-like<br>**Superfamily:**PH0156-like<br>**Family:**PH0156-like |
| 18 | c2p58A_ | Alignment |  | 7.9 | 44 | **PDB header:**transport protein/chaperone<br>**Chain:** A: **PDB Molecule:**putative type iii secretion protein ysce;<br>**PDBTitle:** structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg |
| 19 | d1i7da_ | Alignment |  | 7.9 | 23 | **Fold:**Prokaryotic type I DNA topoisomerase<br>**Superfamily:**Prokaryotic type I DNA topoisomerase<br>**Family:**Prokaryotic type I DNA topoisomerase |
| 20 | d1v4aa1 | Alignment |  | 7.5 | 21 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Nucleotidyltransferase substrate binding subunit/domain<br>**Family:**Glutamine synthase adenylyltransferase GlnE, domain 2 |
| 21 | d2cpga_ | Alignment | not modelled | 7.2 | 28 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 22 | c3fshC_ | Alignment | not modelled | 7.0 | 39 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**autocrine motility factor receptor, isoform 2;<br>**PDBTitle:** crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78 |
| 23 | c3lmyA_ | Alignment | not modelled | 6.5 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta;<br>**PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine |
| 24 | c3h8kB_ | Alignment | not modelled | 6.4 | 39 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**autocrine motility factor receptor, isoform 2;<br>**PDBTitle:** crystal structure of ube2g2 complxed with the g2br domain of2 gp78 at 1.8-a resolution |
| 25 | d1nowa1 | Alignment | not modelled | 6.2 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-N-acetylhexosaminidase catalytic domain |
| 26 | c1zw3B_ | Alignment | not modelled | 5.7 | 58 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**talin 1;<br>**PDBTitle:** vinculin head (0-258) in complex with the talin rod2 residues 1630-1652 |
| 27 | c1nouA_ | Alignment | not modelled | 5.5 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-hexosaminidase beta chain;<br>**PDBTitle:** native human lysosomal beta-hexosaminidase isoform b |
| 28 | c2ykqC_ | Alignment | not modelled | 5.4 | 21 | **PDB header:**rna-binding protein<br>**Chain:** C: **PDB Molecule:**line-1 orf1p;<br>**PDBTitle:** structure of the human line-1 orf1p trimer |

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| 29 | d1ukfa_ | Alignment | not modelled | 5.4 | 11 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**Avirulence protein Avrpph3 |
| 30 | d1g73a_ | Alignment | not modelled | 5.3 | 37 | **Fold:**Spectrin repeat-like<br>**Superfamily:**Smac/diablo<br>**Family:**Smac/diablo |
| 31 | d1fewa_ | Alignment | not modelled | 5.0 | 37 | **Fold:**Spectrin repeat-like<br>**Superfamily:**Smac/diablo<br>**Family:**Smac/diablo |