# Phyre$^2$

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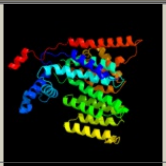
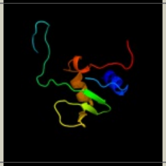
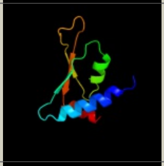
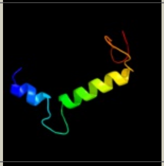
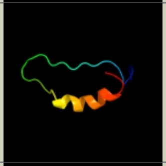
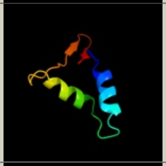
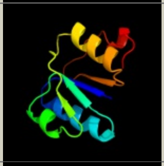
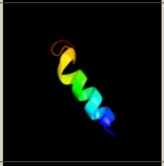
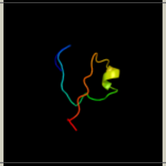
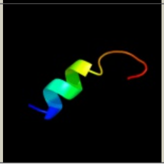
| Description | P76473 |
| Date | Thu Jan 5 12:23:18 GMT 2012 |
| Unique Job ID | 97e9d0b188fbdcfc |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3rceA_ | Alignment |  | 99.8 | 13 | **PDB header:**transferase/peptide<br>**Chain:** A: **PDB Molecule:**oligosaccharide transferase to n-glycosylate proteins;<br>**PDBTitle:** bacterial oligosaccharyltransferase pglb |
| 2 | c3ervA_ | Alignment |  | 48.0 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative c39-like peptidase;<br>**PDBTitle:** crystal structure of an putative c39-like peptidase from2 bacillus anthracis |
| 3 | d1q59a_ | Alignment |  | 11.6 | 10 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 4 | c2qmlA_ | Alignment |  | 10.7 | 3 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**bh2621 protein;<br>**PDBTitle:** crystal structure of an uncharacterized protein (bh2621) from bacillus2 halodurans at 1.55 a resolution |
| 5 | d1un2a_ | Alignment |  | 9.5 | 13 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**DsbA-like |
| 6 | c2l42A_ | Alignment |  | 8.9 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**dna-binding protein rap1;<br>**PDBTitle:** the solution structure of rap1 brct domain from saccharomyces2 cerevisiae |
| 7 | c2zmeB_ | Alignment |  | 7.4 | 16 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**vacuolar protein-sorting-associated protein 36;<br>**PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex |
| 8 | d1gsoa2 | Alignment |  | 7.2 | 12 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 9 | d2jm6b1 | Alignment |  | 7.1 | 15 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 10 | c1vjqB_ | Alignment |  | 7.1 | 15 | **PDB header:**structural genomics, de novo protein<br>**Chain:** B: **PDB Molecule:**designed protein;<br>**PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability. |
| 11 | d2i09a2 | Alignment |  | 7.0 | 20 | **Fold:**DeoB insert domain-like<br>**Superfamily:**DeoB insert domain-like<br>**Family:**DeoB insert domain-like |

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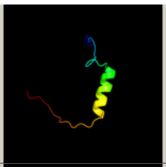
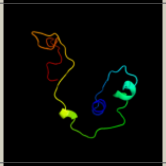
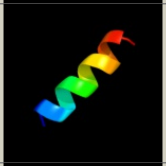
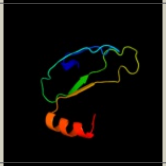
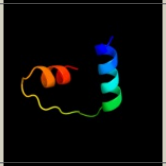
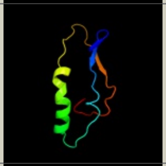
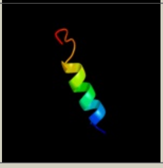
| 12 | c1js8A_ | Alignment |  | 7.0 | 14 | **PDB header:**oxygen storage/transport<br>**Chain:** A: **PDB Molecule:**hemocyanin;<br>**PDBTitle:** structure of a functional unit from octopus hemocyanin |
| 13 | d1hqta_ | Alignment |  | 6.9 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**NAD(P)-linked oxidoreductase<br>**Family:**Aldo-keto reductases (NADP) |
| 14 | c3chtA_ | Alignment |  | 6.6 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**p-aminobenzoate n-oxygenase;<br>**PDBTitle:** crystal structure of di-iron aurf with partially bound ligand |
| 15 | c1qleB_ | Alignment |  | 6.6 | 21 | **PDB header:**oxidoreductase/immune system<br>**Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii;<br>**PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment |
| 16 | c1ar1B_ | Alignment |  | 6.6 | 21 | **PDB header:**complex (oxidoreductase/antibody)<br>**Chain:** B: **PDB Molecule:**cytochrome c oxidase;<br>**PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment |
| 17 | c2dplA_ | Alignment |  | 6.2 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b;<br>**PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3 |
| 18 | d2oqza1 | Alignment |  | 6.1 | 13 | **Fold:**Sortase<br>**Superfamily:**Sortase<br>**Family:**Sortase |
| 19 | c3t6oA_ | Alignment |  | 6.0 | 11 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**sulfate transporter/antisigma-factor antagonist stas;<br>**PDBTitle:** the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus. |
| 20 | c2xa0A_ | Alignment |  | 6.0 | 25 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2;<br>**PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide |
| 21 | c3c67B_ | Alignment | not modelled | 6.0 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**uncharacterized protein ygjk;<br>**PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose |
| 22 | d1wdpa1 | Alignment | not modelled | 5.9 | 48 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 23 | d1b1ya_ | Alignment | not modelled | 5.8 | 48 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 24 | d1o0la_ | Alignment | not modelled | 5.7 | 25 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 25 | d2fcia1 | Alignment | not modelled | 5.7 | 9 | **Fold:**SH2-like<br>**Superfamily:**SH2 domain<br>**Family:**SH2 domain |
| 26 | d1fa2a_ | Alignment | not modelled | 5.6 | 48 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 27 | d2nwua1 | Alignment | not modelled | 5.6 | 29 | **Fold:**RL5-like<br>**Superfamily:**RL5-like<br>**Family:**SSO1042-like |
| 28 | c2yv6A_ | Alignment | not modelled | 5.5 | 20 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**bcl-2 homologous antagonist/killer;<br>**PDBTitle:** crystal structure of human bcl-2 family protein bak |
| 29 | c2o2fA_ | Alignment | not modelled | 5.5 | 25 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2;<br>**PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 |

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| | | | | | | complex with an acyl-sulfonamide-based ligand |
| 30 | c3k8uA_ | Alignment | not modelled | 5.4 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative abc transporter, atp-binding protein<br>**PDBTitle:** crystal structure of the peptidase domain of streptococcus2 coma, a bi-functional abc transporter involved in quorum3 sensing pathway |
| 31 | d1pq1a_ | Alignment | not modelled | 5.2 | 15 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 32 | c2vofA_ | Alignment | not modelled | 5.2 | 13 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**bcl-2-related protein a1;<br>**PDBTitle:** structure of mouse a1 bound to the puma bh3-domain |
| 33 | d1qwza_ | Alignment | not modelled | 5.2 | 13 | **Fold:**Sortase<br>**Superfamily:**Sortase<br>**Family:**Sortase |
| 34 | d1piia1 | Alignment | not modelled | 5.1 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |