Phyre²

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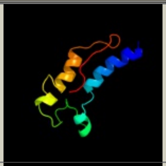
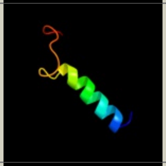
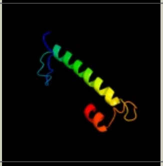
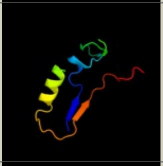
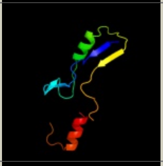
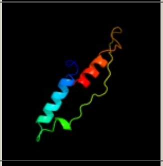
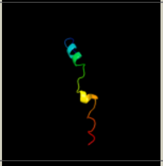
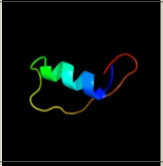
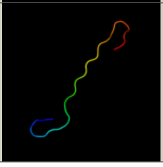
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77656 |
| Date | Thu Jan 5 12:31:23 GMT 2012 |
| Unique Job ID | 3b49cbf9ba08b973 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2kz6A_ | Alignment |  | 98.4 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2 |
| 2 | c3o0rC_ | Alignment |  | 28.1 | 20 | **PDB header:**immune system/oxidoreductase<br>**Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c;<br>**PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment |
| 3 | d1y2oa1 | Alignment |  | 26.3 | 13 | **Fold:**BAR/IMD domain-like<br>**Superfamily:**BAR/IMD domain-like<br>**Family:**IMD domain |
| 4 | d1x4ta1 | Alignment |  | 21.4 | 21 | **Fold:**Long alpha-hairpin<br>**Superfamily:**ISY1 domain-like<br>**Family:**ISY1 N-terminal domain-like |
| 5 | c1fcuA_ | Alignment |  | 21.1 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase;<br>**PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase |
| 6 | d1fcqa_ | Alignment |  | 19.7 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Bee venom hyaluronidase |
| 7 | c3ok8A_ | Alignment |  | 16.5 | 11 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein<br>**PDBTitle:** i-bar of pinkbar |
| 8 | d2fiqa1 | Alignment |  | 15.4 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**GatZ-like |
| 9 | c2clyE_ | Alignment |  | 13.3 | 15 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**atp synthase d chain, mitochondrial;<br>**PDBTitle:** subcomplex of the stator of bovine mitochondrial atp2 synthase |
| 10 | d2gu3a1 | Alignment |  | 12.7 | 10 | **Fold:**Cystatin-like<br>**Superfamily:**Cystatin/monellin<br>**Family:**PepSY-like |
| 11 | c2w56B_ | Alignment |  | 10.2 | 43 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**vc0508;<br>**PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island |

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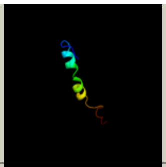
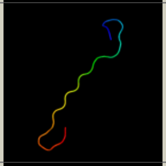
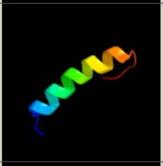
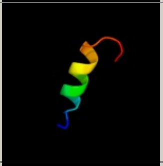
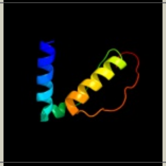
| 12 | d2clyb1 | Alignment |  | 9.3 | 15 | **Fold:**ATP synthase D chain-like<br>**Superfamily:**ATP synthase D chain-like<br>**Family:**ATP synthase D chain-like |
| 13 | c2atmA_ | Alignment |  | 9.1 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase;<br>**PDBTitle:** crystal structure of the recombinant allergen ves v 2 |
| 14 | c2ahmG_ | Alignment |  | 8.4 | 24 | **PDB header:**viral protein, replication<br>**Chain:** G: **PDB Molecule:**replicase polyprotein 1ab, heavy chain;<br>**PDBTitle:** crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer |
| 15 | c2v1lA_ | Alignment |  | 8.1 | 35 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein |
| 16 | d1bgva2 | Alignment |  | 7.6 | 8 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Aminoacid dehydrogenases |
| 17 | d1lrza2 | Alignment |  | 7.4 | 11 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**FemXAB nonribosomal peptidyltransferases |
| 18 | c2odkD_ | Alignment |  | 6.9 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea |
| 19 | d2q22a1 | Alignment |  | 6.7 | 14 | **Fold:**Ava3019-like<br>**Superfamily:**Ava3019-like<br>**Family:**Ava3019-like |
| 20 | d1zaka2 | Alignment |  | 6.7 | 18 | **Fold:**Rubredoxin-like<br>**Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain<br>**Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain |
| 21 | d2ahme1 | Alignment | not modelled | 6.2 | 24 | **Fold:**Coronavirus NSP8-like<br>**Superfamily:**Coronavirus NSP8-like<br>**Family:**Coronavirus NSP8-like |
| 22 | d2pbza2 | Alignment | not modelled | 6.1 | 17 | **Fold:**ATP-grasp<br>**Superfamily:**Glutathione synthetase ATP-binding domain-like<br>**Family:**PurP ATP-binding domain-like |
| 23 | d1zs4a1 | Alignment | not modelled | 5.6 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Bacteriophage CII protein |
| 24 | d2odka1 | Alignment | not modelled | 5.5 | 21 | **Fold:**YefM-like<br>**Superfamily:**YefM-like<br>**Family:**YefM-like |
| 25 | c1p9cA_ | Alignment | not modelled | 5.5 | 32 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4;<br>**PDBTitle:** nmr solution structure of the c-terminal ubiquitin-2 interacting motif of the proteasome subunit s5a |
| 26 | d1k4na_ | Alignment | not modelled | 5.3 | 11 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Hypothetical protein YecM (EC4020) |
| 27 | d1nira1 | Alignment | not modelled | 5.2 | 18 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 28 | d2hq9a1 | Alignment | not modelled | 5.2 | 15 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |

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| 29 | d2fg9a1 | Alignment | not modelled | 5.1 | 13 | **Fold:** Split barrel-like<br>**Superfamily:** FMN-binding split barrel<br>**Family:** PNP-oxidase like |