# Phyre$^2$

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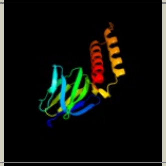
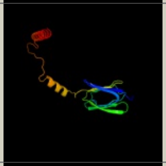
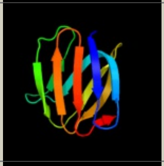
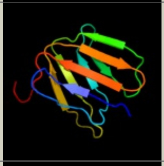
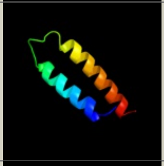
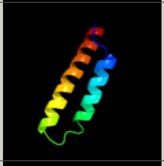
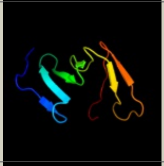
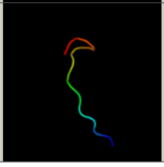
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A6E6 |
| Date | Thu Jan 5 11:02:57 GMT 2012 |
| Unique Job ID | c3b14a7c0fb6a39e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2rq7A_ | Alignment |  | 100.0 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp synthase epsilon chain;<br>**PDBTitle:** solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1 |
| 2 | c2e5yA_ | Alignment |  | 100.0 | 39 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp synthase epsilon chain;<br>**PDBTitle:** epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3 |
| 3 | c1fs0E_ | Alignment |  | 100.0 | 99 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**atp synthase epsilon subunit;<br>**PDBTitle:** complex of gamma/epsilon atp synthase from e.coli |
| 4 | c2qe7H_ | Alignment |  | 100.0 | 39 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**atp synthase subunit epsilon;<br>**PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1 |
| 5 | c2hldH_ | Alignment |  | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**atp synthase delta chain, mitochondrial;<br>**PDBTitle:** crystal structure of yeast mitochondrial f1-atpase |
| 6 | d1aqta2 | Alignment |  | 99.9 | 100 | **Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain<br>**Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal domain<br>**Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain |
| 7 | c1h8eH_ | Alignment |  | 99.9 | 26 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**bovine mitochondrial f1-atpase;<br>**PDBTitle:** (adp.alf4)2(adp.so4) bovine f1-atpase2 (all three catalytic sites occupied) |
| 8 | c2e5tA_ | Alignment |  | 97.9 | 35 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp synthase epsilon chain;<br>**PDBTitle:** c-terminal domain of epsilon subunit of f1f0-atp synthase2 from the thermophilic bacillus ps3 in the presence of atp3 condition |
| 9 | d1aqta1 | Alignment |  | 97.7 | 100 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Epsilon subunit of F1F0-ATP synthase C-terminal domain<br>**Family:**Epsilon subunit of F1F0-ATP synthase C-terminal domain |
| 10 | c3hqxA_ | Alignment |  | 67.6 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0345 protein aciad0356;<br>**PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1 |
| 11 | d1y60a_ | Alignment |  | 25.1 | 33 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Formaldehyde-activating enzyme, FAE |

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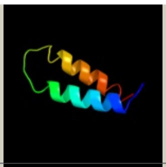
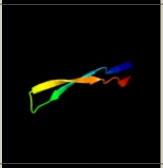
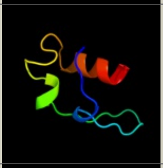
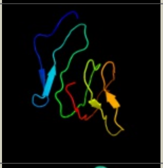
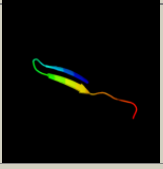
|---|---|---|---|---|---|---|
| 12 | d2jdih1 | Alignment |  | 24.5 | 17 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Epsilon subunit of F1F0-ATP synthase C-terminal domain<br>**Family:**Epsilon subunit of F1F0-ATP synthase C-terminal domain |
| 13 | c2qz7B_ | Alignment |  | 14.9 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein sco6318;<br>**PDBTitle:** the crystal structure of a homologue of telluride resistance protein2 (terd), sco6318 from streptomyces coelicolor a3(2) |
| 14 | d2ck3h1 | Alignment |  | 14.2 | 18 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Epsilon subunit of F1F0-ATP synthase C-terminal domain<br>**Family:**Epsilon subunit of F1F0-ATP synthase C-terminal domain |
| 15 | c2qnuB_ | Alignment |  | 11.1 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein pa0076;<br>**PDBTitle:** crystal structure of pa0076 from pseudomonas aeruginosa pao12 at 2.05 a resolution |
| 16 | d2jera1 | Alignment |  | 10.5 | 14 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Porphyromonas-type peptidylarginine deiminase |
| 17 | d1vkpa_ | Alignment |  | 10.2 | 11 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Porphyromonas-type peptidylarginine deiminase |
| 18 | c3eo6B_ | Alignment |  | 9.8 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**protein of unknown function (duf1255);<br>**PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution |
| 19 | c2jerG_ | Alignment |  | 9.6 | 14 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**agmatine deiminase;<br>**PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction. |
| 20 | c2vhgB_ | Alignment |  | 8.8 | 29 | **PDB header:**dna-binding protein<br>**Chain:** B: **PDB Molecule:**transposase orfa;<br>**PDBTitle:** crystal structure of the ishp608 transposase in complex2 with right end 31-mer dna |
| 21 | c3frnA_ | Alignment | not modelled | 8.6 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**flagellar protein flga;<br>**PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8 |
| 22 | d1vqoe1 | Alignment | not modelled | 8.5 | 11 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 23 | c4a8al_ | Alignment | not modelled | 8.3 | 21 | **PDB header:**hydrolase/hydrolase<br>**Chain:** I: **PDB Molecule:**periplasmic ph-dependent serine endoprotease degq;<br>**PDBTitle:** asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme |
| 24 | c1nh7A_ | Alignment | not modelled | 8.2 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase;<br>**PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis |
| 25 | d2f5ga1 | Alignment | not modelled | 8.2 | 29 | **Fold:**Ferredoxin-like<br>**Superfamily:**Transposase IS200-like<br>**Family:**Transposase IS200-like |
| 26 | d1e3ha5 | Alignment | not modelled | 8.1 | 30 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 27 | c3stjC_ | Alignment | not modelled | 7.8 | 22 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**protease degq;<br>**PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli |
| 28 | d2oyza1 | Alignment | not modelled | 7.8 | 23 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**VPA0057-like |

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|---|---|---|---|---|---|---|
| 29 | d2nn6a2 | Alignment | not modelled | 7.6 | 13 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 30 | d2ewoa1 | Alignment | not modelled | 7.2 | 11 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Porphyromonas-type peptidylarginine deiminase |
| 31 | c3pm9A_ | Alignment | not modelled | 6.8 | 32 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution |
| 32 | d2fyxa1 | Alignment | not modelled | 6.5 | 29 | **Fold:**Ferredoxin-like<br>**Superfamily:**Transposase IS200-like<br>**Family:**Transposase IS200-like |
| 33 | c3brcA_ | Alignment | not modelled | 6.5 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved protein of unknown function;<br>**PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum |
| 34 | c2qngA_ | Alignment | not modelled | 6.3 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein sav2460;<br>**PDBTitle:** crytal structure of unknown function protein sav2460 |
| 35 | d2vjva1 | Alignment | not modelled | 6.2 | 29 | **Fold:**Ferredoxin-like<br>**Superfamily:**Transposase IS200-like<br>**Family:**Transposase IS200-like |
| 36 | d1xkna_ | Alignment | not modelled | 6.2 | 9 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Porphyromonas-type peptidylarginine deiminase |
| 37 | d1kida_ | Alignment | not modelled | 6.1 | 18 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 38 | d2cmua1 | Alignment | not modelled | 5.8 | 9 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Porphyromonas-type peptidylarginine deiminase |
| 39 | c2d3kA_ | Alignment | not modelled | 5.8 | 31 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase;<br>**PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3 |
| 40 | d1sefa_ | Alignment | not modelled | 5.3 | 10 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**YlbA-like |
| 41 | c1sefA_ | Alignment | not modelled | 5.3 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein;<br>**PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis |