


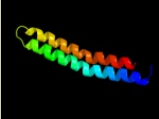





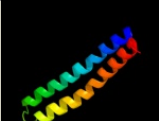



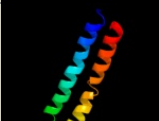










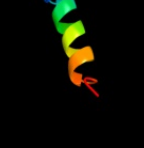
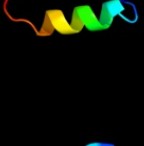
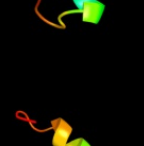



Phyre2

| | |
|---------------|-----------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | P68699 |
| Date | Thu Jan 5 12:11:09 GMT 2012 |
| Unique Job ID | 337fad83694dc3a4 |

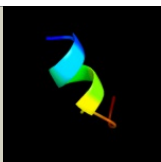
Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1c99a_ |  Alignment |  | 100.0 | 100 | Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C |
| 2 | c1wu0A_ |  Alignment |  | 99.9 | 44 | PDB header: hydrolase Chain: A: PDB Molecule: atp synthase c chain; PDBTitle: solution structure of subunit c of f1fo-atp synthase from2 the thermophilic bacillus ps3 |
| 3 | c2x2vG_ |  Alignment |  | 99.9 | 39 | PDB header: membrane protein Chain: G: PDB Molecule: atp synthase subunit c; PDBTitle: structural basis of a novel proton-coordination type in an2 f1fo-atp synthase rotor ring |
| 4 | c2w5jM_ |  Alignment |  | 99.8 | 31 | PDB header: hydrolase Chain: M: PDB Molecule: atp synthase c chain, chloroplastic; PDBTitle: structure of the c14-rotor ring of the proton translocating2 chloroplast atp synthase |
| 5 | c1yceD_ |  Alignment |  | 99.8 | 24 | PDB header: membrane protein Chain: D: PDB Molecule: subunit c; PDBTitle: structure of the rotor ring of f-type na+-atpase from ilyobacter2 tartaricus |
| 6 | c2wpdP_ |  Alignment |  | 99.6 | 21 | PDB header: hydrolase Chain: P: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: the mg.adp inhibited state of the yeast f1c10 atp synthase |
| 7 | c2xndK_ |  Alignment |  | 99.5 | 23 | PDB header: hydrolase Chain: K: PDB Molecule: atp synthase lipid-binding protein, mitochondrial; PDBTitle: crystal structure of bovine f1-c8 sub-complex of atp2 synthase |
| 8 | c2bl2F_ |  Alignment |  | 98.1 | 13 | PDB header: hydrolase Chain: F: PDB Molecule: v-type sodium atp synthase subunit k; PDBTitle: the membrane rotor of the v-type atpase from enterococcus2 hirae |
| 9 | c2qqpD_ |  Alignment |  | 12.5 | 47 | PDB header: virus Chain: D: PDB Molecule: small capsid protein; PDBTitle: crystal structure of authentic providence virus |
| 10 | d1cf2o1 |  Alignment |  | 11.1 | 30 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 11 | c2voyD_ |  Alignment |  | 7.9 | 50 | PDB header: hydrolase Chain: D: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus |

| | | | | | | |
|----|-------------------------|-----------|--|-----|----|---|
| 12 | d1b7go1 | Alignment |  | 7.7 | 30 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 13 | c1cf2Q_ | Alignment |  | 7.4 | 30 | PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate dehydrogenase); PDBTitle: three-dimensional structure of d-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus |
| 14 | d1r0ka2 | Alignment |  | 6.2 | 32 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 15 | c2czcD_ | Alignment |  | 6.0 | 26 | PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3 |
| 16 | d2bbya_ | Alignment |  | 5.8 | 36 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding domain from rap30 |
| 17 | c1b7gO_ | Alignment |  | 5.4 | 32 | PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase |

18 [c1vjgB_](#)

Alignment



5.2

55

PDB header: structural genomics, de novo protein
Chain: B: **PDB Molecule:** designed protein;
PDBTitle: designed protein based on backbone conformation of 2
procarboxypeptidase-a (1aye) with sidechains chosen for maximal 3
predicted stability.