
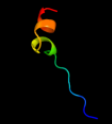

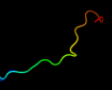

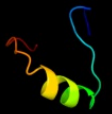






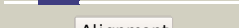
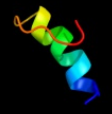
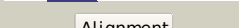

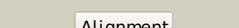

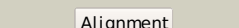
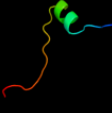
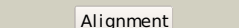
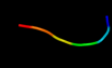


Phyre2

| | |
|---------------|-----------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | P64542 |
| Date | Thu Jan 5 12:09:19 GMT 2012 |
| Unique Job ID | 2ecfe4e849cc4a95 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1kf6c_ |  Alignment |  | 20.4 | 20 | Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD) |
| 2 | d1bvp12 |  Alignment |  | 12.7 | 14 | Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein |
| 3 | c2de0X_ |  Alignment |  | 11.2 | 40 | PDB header: transferase Chain: X: PDB Molecule: alpha-(1,6)-fucosyltransferase; PDBTitle: crystal structure of human alpha 1,6-fucosyltransferase, fut8 |
| 4 | d1ahsa_ |  Alignment |  | 9.8 | 6 | Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein |
| 5 | c3kwpA_ |  Alignment |  | 9.6 | 7 | PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis |
| 6 | d1wj2a_ |  Alignment |  | 9.4 | 67 | Fold: WRKY DNA-binding domain Superfamily: WRKY DNA-binding domain Family: WRKY DNA-binding domain |
| 7 | c2pq4B_ |  Alignment |  | 9.2 | 29 | PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide |
| 8 | d1h3ga1 |  Alignment |  | 9.0 | 29 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes |
| 9 | c2fpeB_ |  Alignment |  | 8.5 | 15 | PDB header: signaling protein Chain: B: PDB Molecule: c-jun-amino-terminal kinase interacting protein PDBTitle: conserved dimerization of the ib1 src-homology 3 domain |
| 10 | c2zomC_ |  Alignment |  | 6.9 | 28 | PDB header: unknown function Chain: C: PDB Molecule: protein cuta, chloroplast, putative, expressed; PDBTitle: crystal structure of cuta1 from oryza sativa |
| 11 | c2aydA_ |  Alignment |  | 6.8 | 67 | PDB header: transcription Chain: A: PDB Molecule: wrky transcription factor 1; PDBTitle: crystal structure of the c-terminal wrky domain of atwrky1,2 an sa-induced and partially npr1-dependent transcription3 factor |

12 [dls4da_](#)

Alignment



5.9

11 **Fold:** Tetrapyrrole methylase
Superfamily: Tetrapyrrole methylase
Family: Tetrapyrrole methylase

13 [c3m3wA](#)

Alignment



5.5

25

PDB header:endocytosis
Chain: A: **PDB Molecule:**protein kinase c and casein kinase ii substrate protein 3;
PDBTitle: crystal strcuture of mouse pacsin3 bar domain mutant