

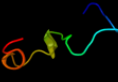

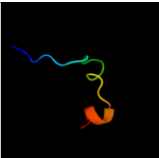


Phyre2

| | |
|---------------|-----------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | P32693 |
| Date | Thu Jan 5 11:50:15 GMT 2012 |
| Unique Job ID | 7244f029c76c16e7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|-------------------------|--|---|------------|--------|---|
| 1 | c2zxeG_ |  Alignment |  | 21.1 | 38 | PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state |
| 2 | c3n23E_ |  Alignment |  | 15.2 | 32 | PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump |
| 3 | d3vuba_ |  Alignment |  | 12.8 | 24 | Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB |
| 4 | c3jrZA_ |  Alignment |  | 9.9 | 50 | PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdvfi-formii-ph5.6 |
| 5 | c2jo1A_ |  Alignment |  | 9.0 | 45 | PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles |
| 6 | c2jp3A_ |  Alignment |  | 8.5 | 29 | PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles |
| 7 | c2l3yA_ |  Alignment |  | 7.3 | 42 | PDB header: transcription Chain: A: PDB Molecule: interleukin-6; PDBTitle: solution structure of mouse il-6 |
| 8 | d2qv8a2 |  Alignment |  | 7.0 | 23 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 9 | d1aila_ |  Alignment |  | 6.1 | 63 | Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: N-terminal, RNA-binding domain of nonstructural protein NS1 |

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|----|-------------------------|-----------|--|-----|----|--|
| 10 | c3lfkC_ | Alignment |  | 5.8 | 50 | PDB header: unknown function Chain: C: PDB Molecule: marr like protein, tv90766549; PDB Title: a reported archaeal mechanosensitive channel is a structural2 homolog of marr-like transcriptional regulators |
|----|-------------------------|-----------|--|-----|----|--|