Phyre^2

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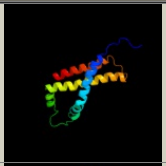
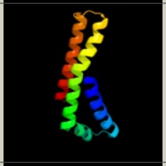
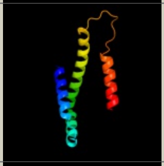
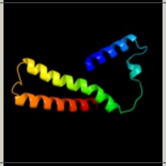
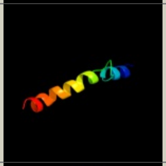
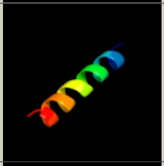
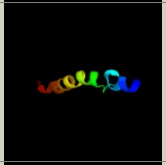
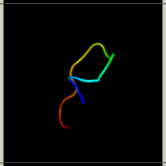
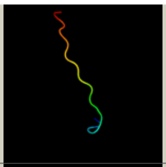
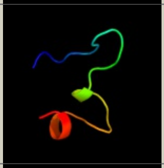
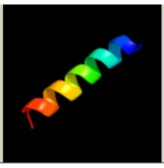
Description	P0A8Q3
Date	Thu Jan 5 11:08:30 GMT 2012
Unique Job ID	b409f80f104edaee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kf6d_	Alignment		100.0	100	**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	d1nekd_	Alignment		96.1	19	**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)
3	d1nekc_	Alignment		96.1	15	**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)
4	d1kf6c_	Alignment		74.3	17	**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)
5	c1yq3C_	Alignment		26.7	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b, large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
6	d1v54m_	Alignment		23.7	16	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
7	c3kdpH_	Alignment		18.5	35	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
8	c3kdpG_	Alignment		18.5	35	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
9	c2y69Z_	Alignment		16.6	16	**PDB header:**electron transport **Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
10	d1kwia_	Alignment		10.9	21	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cathelicidin motif
11	c2jo1A_	Alignment		7.6	21	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles

12	d2bh1a2	Alignment		7.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
13	c3ez3A_	Alignment		6.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**farnesyl pyrophosphate synthase, putative; **PDBTitle:** crystal structure of plasmodium vivax geranylgeranylpyrophosphate2 synthase pvx_092040 with zoledronate and ipp bound
14	c3db3A_	Alignment		6.2	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
15	c3lsnA_	Alignment		5.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**geranyltranstransferase; **PDBTitle:** crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium

16	c2jp3A_	Alignment		5.4	26	**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