Phyre^2

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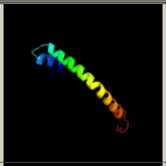
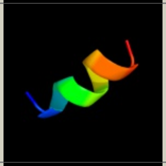
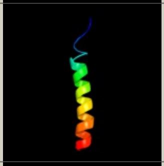
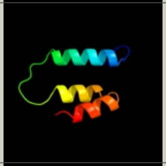
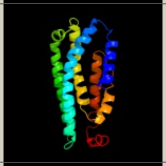
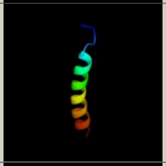
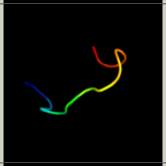
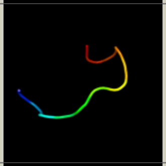
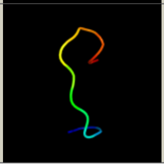
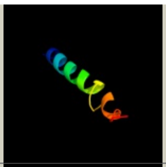
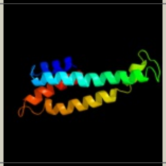
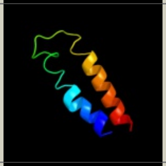
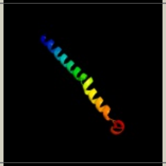
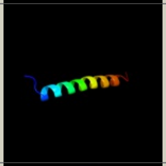
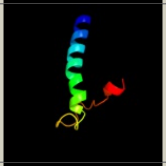
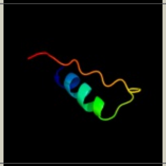
Description	P42910
Date	Thu Jan 5 12:02:07 GMT 2012
Unique Job ID	6be97c196ec9113d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		38.0	18	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	c2l34B_	Alignment		32.0	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
3	c2kdxA_	Alignment		31.0	36	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
4	c2l35B_	Alignment		29.4	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
5	c1ciiA_	Alignment		23.6	18	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
6	c3mkuA_	Alignment		22.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
7	c2l34A_	Alignment		20.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
8	c2eelA_	Alignment		19.3	7	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-a; **PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a
9	d1ibxb_	Alignment		15.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
10	c1ibxB_	Alignment		15.4	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**chimera of igg binding protein g and dna **PDBTitle:** nmr structure of dff40 and dff45 n-terminal domain complex
11	d1d4ba_	Alignment		14.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain

12	c2l35A_	Alignment		14.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dap12-nkg2c_tm; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
13	d1f2ri_	Alignment		12.6	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
14	d1iwga8	Alignment		10.5	7	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
15	d1fftc_	Alignment		9.1	15	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
16	d1v54i_	Alignment		7.2	16	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
17	d1eysh2	Alignment		7.1	13	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
18	c2jo1A_	Alignment		6.8	12	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
19	c2ko6A_	Alignment		6.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yihd; **PDBTitle:** solution structure of protein sf3929 from shigella flexneri2 2a. northeast structural genomics consortium target3 sfr81/ontario center for structural proteomics target4 sf3929
20	d1r7ma1	Alignment		5.7	36	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
21	c3fseB_	Alignment	not modelled	5.4	88	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution