Phyre^2

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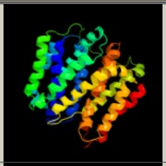
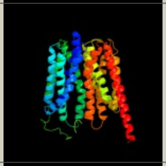
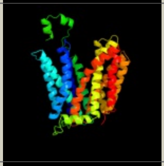
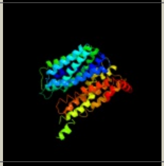
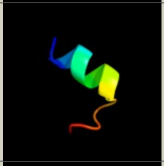
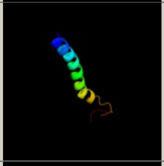
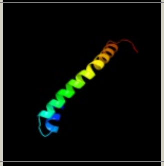
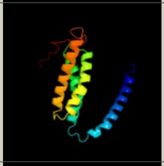
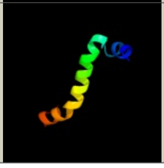
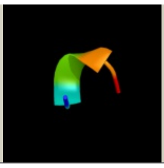
Description	P37597
Date	Thu Jan 5 11:55:44 GMT 2012
Unique Job ID	4d71acc7f1f7384c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gfpA_	Alignment		100.0	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
2	d1pw4a_	Alignment		100.0	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
3	d1pv7a_	Alignment		100.0	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
4	c3o7pA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2xutC_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c2g9pA_	Alignment		22.1	43	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
7	c2kncA_	Alignment		16.7	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
8	c3qnqD_	Alignment		16.5	6	**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
9	c2xq2A_	Alignment		7.5	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
10	d3proc1	Alignment		7.3	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain

11	d1lzia_	Alignment		5.9	80	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like