Phyre^2

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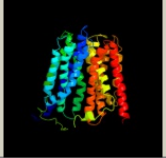
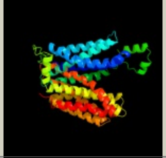
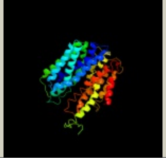
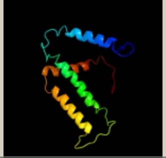
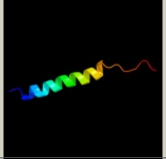
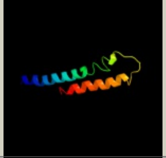
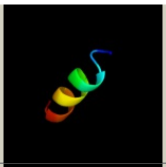
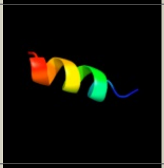
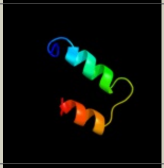
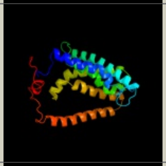
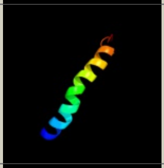
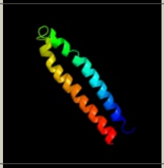
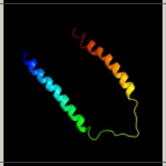
Description	P25744
Date	Thu Jan 5 11:42:32 GMT 2012
Unique Job ID	96711bd6707d7c04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	d1pv7a_	Alignment		100.0	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	c2gfpA_	Alignment		99.9	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
4	c3o7pA_	Alignment		99.9	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		99.9	11	**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	c3mkuA_	Alignment		37.7	9	**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	c3lrcC_	Alignment		28.3	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
8	c3rkoF_	Alignment		22.7	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
9	c2g9pA_	Alignment		20.9	36	**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
10	c2bbjB_	Alignment		16.9	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
11	c2k9pA_	Alignment		13.6	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles

12	c2bbnB_	Alignment		9.9	29	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase; **PDBTitle:** solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
13	c2bbmB_	Alignment		9.9	29	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase; **PDBTitle:** solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
14	d3bl2a1	Alignment		9.2	23	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
15	c3hd6A_	Alignment		8.2	8	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
16	c2k21A_	Alignment		6.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
17	d3b60a2	Alignment		6.6	17	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
18	c3kf9D_	Alignment		6.4	29	**PDB header:**cell cycle/calcium-binding protein **Chain:** D: **PDB Molecule:**myosin light chain kinase 2, skeletal/cardiac muscle; **PDBTitle:** crystal structure of the sdcen/skmlck complex
19	d1pf4a2	Alignment		6.4	9	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
20	c3kf9B_	Alignment		6.2	29	**PDB header:**cell cycle/calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase 2, skeletal/cardiac muscle; **PDBTitle:** crystal structure of the sdcen/skmlck complex
21	c2ksfA_	Alignment	not modelled	6.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c