Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76169
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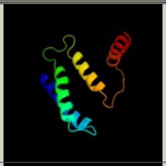
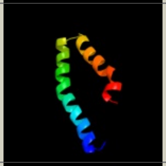
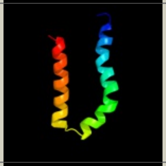
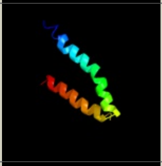
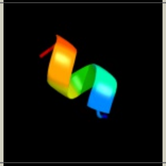
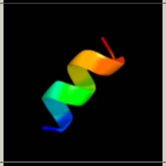
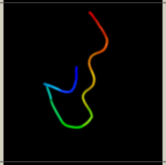
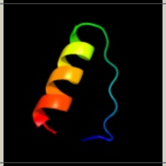
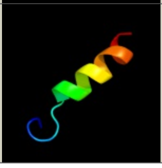
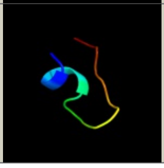
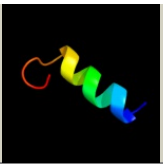
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ba_	Alignment		95.6	25	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
2	d1pv7a_	Alignment		20.1	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	d1pw4a_	Alignment		16.1	15	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
4	c2xutC_	Alignment		12.6	15	**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.
5	c1w8xP_	Alignment		10.3	50	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
6	c3o7pA_	Alignment		10.3	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
7	d2ipqx1	Alignment		8.2	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
8	c3msqC_	Alignment		7.3	38	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**putative ubiquinone biosynthesis protein; **PDBTitle:** crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
9	d1b1ya_	Alignment		6.6	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	c6rlxB_	Alignment		6.5	33	**PDB header:**hormone(muscle relaxant) **Chain:** B: **PDB Molecule:**relaxin, b-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
11	c2kbvA_	Alignment		6.1	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger

12	c2gfpA_	Alignment		6.1	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
13	c3dveB_	Alignment		5.9	63	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-dependent n-type calcium channel subunit alpha-1b; **PDBTitle:** crystal structure of ca2+/cam-cav2.2 iq domain complex
14	c2xfyA_	Alignment		5.7	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-amylase; **PDBTitle:** crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
15	d1wdpa1	Alignment		5.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
16	c3kb4D_	Alignment		5.5	31	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr8543 protein; **PDBTitle:** crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
17	d1fa2a_	Alignment		5.1	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

18	d2fnoa1	Alignment		5.1	28	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain