Phyre^2

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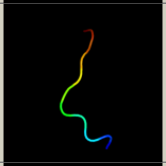
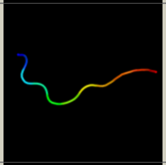
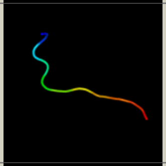
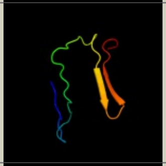
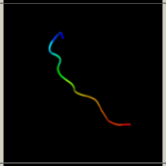
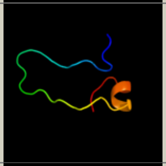
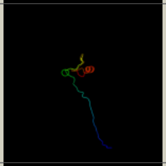
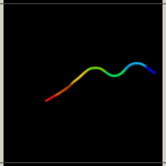
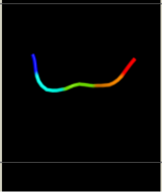
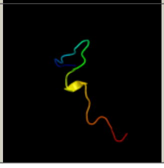
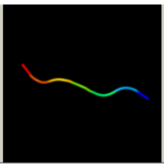
Description	P31121
Date	Thu Jan 5 11:47:08 GMT 2012
Unique Job ID	98424e086c3fa485

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1c4ea_	Alignment		36.9	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Gurmarin-like **Family:**Gurmarin, a sweet taste-suppressing polypeptide
2	d1a0ca_	Alignment		20.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
3	d1a0ea_	Alignment		19.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
4	d1a0da_	Alignment		10.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
5	c2vscD_	Alignment		9.4	10	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**leukocyte surface antigen cd47; **PDBTitle:** structure of the immunoglobulin-superfamily ectodomain of2 human cd47
6	d1an8a1	Alignment		8.4	36	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
7	d1ty0a1	Alignment		7.4	36	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
8	c2c2pA_	Alignment		7.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/u mismatch-specific dna glycosylase; **PDBTitle:** the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
9	d2jnaa1	Alignment		7.0	21	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
10	d1ujpa_	Alignment		6.6	43	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
11	d1l0nk_	Alignment		5.9	60	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)

12	d2fyuk1	Alignment		5.8	80	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
13	c3r24A_	Alignment		5.8	36	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible

14	d1eg3a3	Alignment		5.7	71	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain