Phyre^2

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Description	P0AFC3
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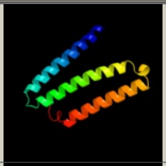
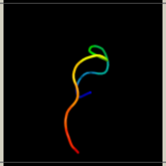
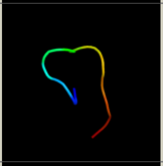
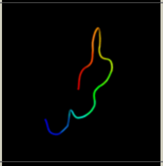
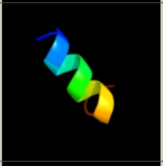
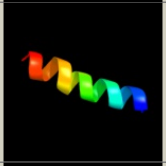
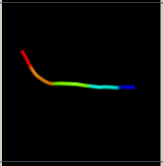
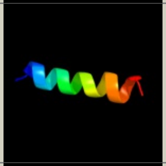
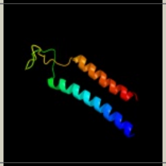
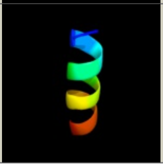
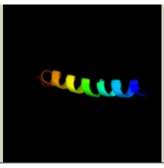
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoA_	Alignment		100.0	98	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase subunit a; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c2k21A_	Alignment		32.0	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
3	d1jwya1	Alignment		25.8	15	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
4	d3bz7a1	Alignment		25.5	15	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
5	d1dtdb_	Alignment		20.2	38	**Fold:**Carboxypeptidase inhibitor **Superfamily:**Carboxypeptidase inhibitor **Family:**Carboxypeptidase inhibitor
6	c3fy6A_	Alignment		16.9	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass3
7	c1zrtD_	Alignment		14.2	21	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
8	c2fynH_	Alignment		11.2	37	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
9	d2csha2	Alignment		10.9	40	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
10	d1k32a1	Alignment		9.2	38	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
11	d2adra2	Alignment		8.6	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2

12	c1t0jC_	Alignment		6.5	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
13	c2yiuE_	Alignment		6.2	42	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
14	c3mk7F_	Alignment		6.1	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
15	c1vytF_	Alignment		5.6	17	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid

16	c1p84D_	Alignment		5.2	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex