Phyre2

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Description	P16429
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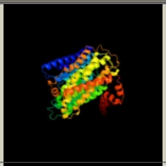
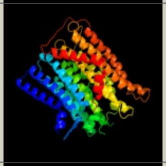
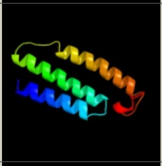
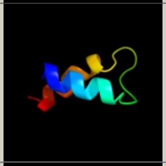
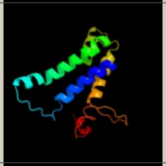
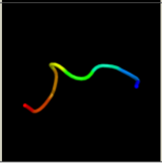
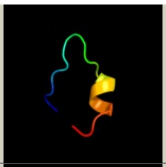
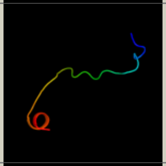
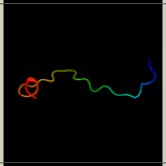
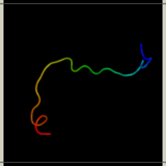
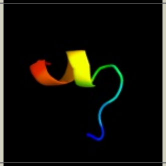
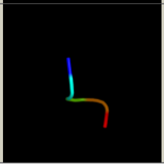
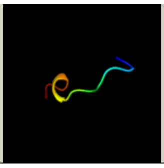
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoM_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c3rkoN_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	c3rkoK_	Alignment		33.2	16	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
5	c2l3iA_	Alignment		24.2	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
6	d1s1qa_	Alignment		24.0	19	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
7	d1a6qa1	Alignment		19.3	12	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
8	d1o8bb1	Alignment		14.4	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
9	c3na2C_	Alignment		10.5	25	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
10	d1j4na_	Alignment		9.3	16	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
11	d3d37a2	Alignment		8.3	38	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like

12	d2yrka1	Alignment		6.9	26	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
13	d2c1ha1	Alignment		6.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
14	d1l6sa_	Alignment		6.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
15	d1gzga_	Alignment		6.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
16	d2q09a1	Alignment		5.7	36	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
17	c2z84A_	Alignment		5.4	80	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ufm1-specific protease 1; **PDBTitle:** insights from crystal and solution structures of mouse ufsp1

18	d2imra1	Alignment		5.4	38	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**DR0824-like