Phyre^2

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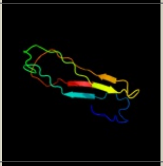
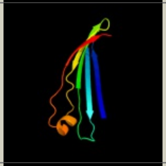
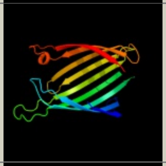
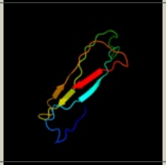
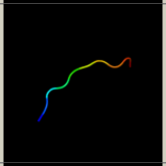
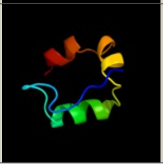
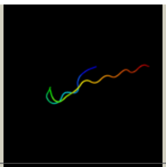
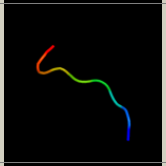
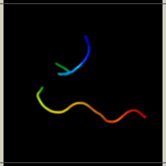
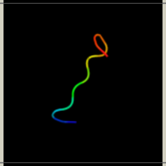
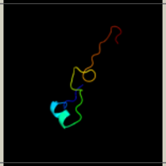
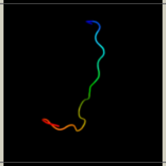
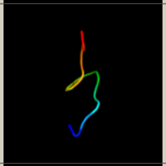
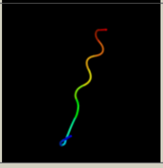
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qd6C_	 Alignment		100.0	100	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
2	c1fw3A_	 Alignment		100.0	99	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
3	c2iwvD_	 Alignment		82.8	15	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
4	c2vveB_	 Alignment		50.8	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike protein p1; **PDBTitle:** crystal structure of the stem and receptor binding domain2 of the spike protein p1 from bacteriophage pm2
5	d2pora_	 Alignment		40.7	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
6	c2w0cL_	 Alignment		29.0	22	**PDB header:**virus **Chain:** L: **PDB Molecule:**protein 2; **PDBTitle:** x-ray structure of the entire lipid-containing2 bacteriophage pm2
7	c2wjqA_	 Alignment		19.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
8	d2fgqx1	 Alignment		17.3	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
9	c2vvdA_	 Alignment		14.7	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike protein p1; **PDBTitle:** crystal structure of the receptor binding domain of the2 spike protein p1 from bacteriophage pm2
10	d1xrsb2	 Alignment		14.2	60	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
11	c2kz3A_	 Alignment		13.6	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83

12	d1wpua1	Alignment		8.8	25	**Fold:**Hut operon positive regulatory protein HutP **Superfamily:**Hut operon positive regulatory protein HutP **Family:**Hut operon positive regulatory protein HutP
13	d1w0na_	Alignment		8.8	33	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
14	d3buxb3	Alignment		8.0	36	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
15	d1aisa1	Alignment		7.1	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
16	d1mp9a1	Alignment		6.7	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
17	c2w56B_	Alignment		6.5	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
18	d1pg5a1	Alignment		6.1	33	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
19	d1uwka_	Alignment		6.0	36	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
20	c3al0B_	Alignment		6.0	36	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
21	c3btpB_	Alignment	not modelled	5.9	67	**PDB header:**dna binding protein, chaperone **Chain:** B: **PDB Molecule:**protein vire1; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
22	d2ogqa1	Alignment	not modelled	5.6	31	**Fold:**Polo-box domain **Superfamily:**Polo-box domain **Family:**Polo-box duplicated region
23	d2zfga1	Alignment	not modelled	5.4	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
24	c2fknC_	Alignment	not modelled	5.4	50	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
25	c1pg5A_	Alignment	not modelled	5.2	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius