Phyre2

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Description	P36647
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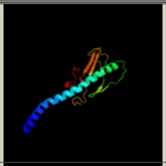
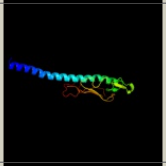
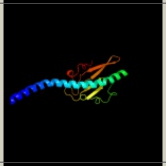
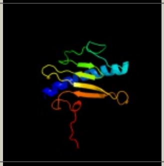
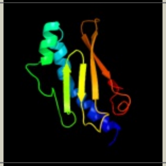
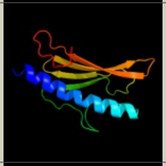
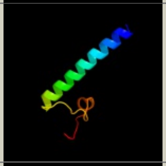
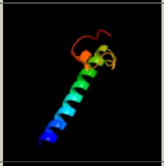
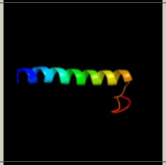
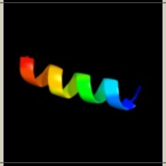
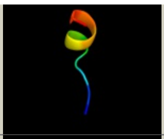
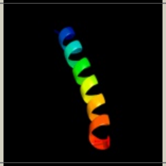
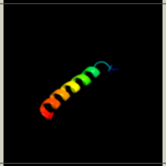
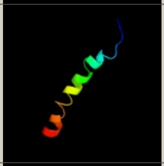
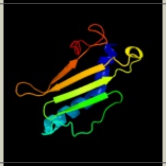
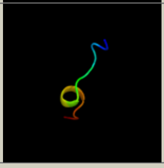
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sokB_	Alignment		99.9	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
2	d1oqwa_	Alignment		99.9	27	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
3	d2pila_	Alignment		99.9	30	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
4	d1qvea_	Alignment		99.0	21	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
5	c3jyzA_	Alignment		99.0	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**type iv pilin structural subunit; **PDBTitle:** crystal structure of pseudomonas aeruginosa (strain:2 pa110594) typeiv pilin in space group p41212
6	d1x6za1	Alignment		98.6	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
7	c3fu1B_	Alignment		93.9	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**general secretion pathway protein g; **PDBTitle:** crystal structure of the major pseudopilin from the type 2 secretion2 system of vibrio cholerae
8	d1t92a_	Alignment		93.7	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pseudopilin
9	c2kepA_	Alignment		91.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general secretion pathway protein g; **PDBTitle:** solution structure of xcpt, the main component of the type 22 secretion system of pseudomonas aeruginosa
10	c1bttA_	Alignment		41.7	31	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
11	c1btsA_	Alignment		41.0	33	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3

12	c4a18U_	Alignment		39.6	64	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**rpl13; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
13	c3u5eL_	Alignment		38.5	55	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
14	d3ehbb2	Alignment		36.4	31	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
15	d1v54b2	Alignment		29.5	20	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
16	d1fftb2	Alignment		28.9	13	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
17	c3sojA_	Alignment		28.3	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pile; **PDBTitle:** francisella tularensis pilin pile
18	c2kxeA_	Alignment		14.7	71	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii small subunit; **PDBTitle:** n-terminal domain of the dp1 subunit of an archaeal d-family dna2 polymerase
19	c1afoB_	Alignment		14.7	13	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
20	d1r89a1	Alignment		14.2	62	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
21	c2wsfG_	Alignment	not modelled	13.9	25	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** improved model of plant photosystem i
22	c1xmeB_	Alignment	not modelled	13.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
23	c1qleB_	Alignment	not modelled	13.2	25	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
24	c1ar1B_	Alignment	not modelled	13.2	25	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
25	d3dtub2	Alignment	not modelled	12.8	25	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
26	c2kadB_	Alignment	not modelled	11.8	47	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
27	c2kadC_	Alignment	not modelled	11.8	47	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
						PDB header:membrane protein

28	c2kadD_	Alignment	not modelled	11.8	47	**Chain:** D: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
29	c2kadA_	Alignment	not modelled	11.8	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
30	d1m56d_	Alignment	not modelled	11.2	21	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
31	d1r3jc_	Alignment	not modelled	10.6	9	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
32	c2o01G_	Alignment	not modelled	10.2	25	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
33	c2ljcA_	Alignment	not modelled	10.0	47	**PDB header:**transport protein/inhibitor **Chain:** A: **PDB Molecule:**m2 protein, bm2 protein chimera; **PDBTitle:** structure of the influenza am2-bm2 chimeric channel bound to2 rimantadine
34	d1oqva_	Alignment	not modelled	9.7	15	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**TcpA-like pilin
35	d1tcra2	Alignment	not modelled	9.4	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
36	c2kb1A_	Alignment	not modelled	8.1	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
37	c2wscK_	Alignment	not modelled	7.0	50	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit psak, **PDBTitle:** improved model of plant photosystem i
38	d1az3a_	Alignment	not modelled	6.9	38	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
39	c2vvyC_	Alignment	not modelled	6.6	14	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein b15; **PDBTitle:** structure of vaccinia virus protein b14
40	c1mp6A_	Alignment	not modelled	6.6	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
41	c1nyjB_	Alignment	not modelled	6.6	47	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
42	c2kqtA_	Alignment	not modelled	6.6	47	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
43	c2kqtC_	Alignment	not modelled	6.6	47	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
44	c1nyjC_	Alignment	not modelled	6.6	47	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
45	c2kqtB_	Alignment	not modelled	6.6	47	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
46	c1nyjD_	Alignment	not modelled	6.6	47	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
47	c1nyjA_	Alignment	not modelled	6.6	47	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
48	c2kqtD_	Alignment	not modelled	6.6	47	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
49	c2j7aC_	Alignment	not modelled	6.4	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
50	c2dcoA_	Alignment	not modelled	6.4	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**s1p4 first extracellular loop peptidomimetic; **PDBTitle:** s1p4 first extracellular loop peptidomimetic
51	d2a9ha1	Alignment	not modelled	6.3	10	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
52	c3lw5K_	Alignment	not modelled	6.1	26	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak; **PDBTitle:** improved model of plant photosystem i

53	c3f5dA_	Alignment	not modelled	6.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
54	c1spfA_	Alignment	not modelled	5.8	25	**PDB header:**lipoprotein(surface film) **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated polypeptide c; **PDBTitle:** the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
55	c1tiiC_	Alignment	not modelled	5.7	50	**PDB header:**enterotoxin **Chain:** C: **PDB Molecule:**heat labile enterotoxin type iib; **PDBTitle:** escherichia coli heat labile enterotoxin type iib
56	d1xmeb2	Alignment	not modelled	5.5	50	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
57	c1b22A_	Alignment	not modelled	5.4	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
58	d1b22a_	Alignment	not modelled	5.4	20	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
59	d2ab0a1	Alignment	not modelled	5.3	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI