Phyre^2

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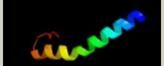
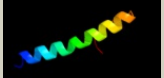
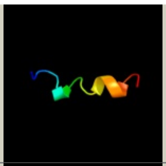
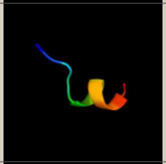
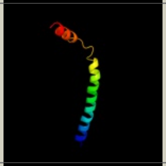
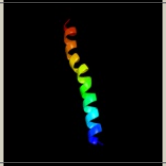
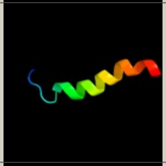
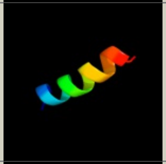
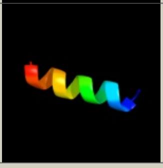
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t92a_	Alignment		99.9	64	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pseudopilin
2	c2kepA_	Alignment		99.9	53	**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
3	c3fu1B_	Alignment		99.9	64	**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
4	d1oqwa_	Alignment		99.7	16	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
5	d2pila_	Alignment		99.7	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
6	c3sokB_	Alignment		99.7	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
7	d1qvea_	Alignment		77.7	12	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
8	d1x6za1	Alignment		68.4	6	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
9	d1pbya4	Alignment		60.2	60	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
10	c1pbyA_	Alignment		53.7	60	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
11	c4a18U_	Alignment		36.8	20	**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

12	c2wsfG_	Alignment		31.6	13	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** improved model of plant photosystem i
13	c3u5eL_	Alignment		31.5	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	d1r3jc_	Alignment		30.1	11	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
15	d1m56d_	Alignment		27.6	29	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
16	d1f6ga_	Alignment		27.2	12	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
17	c2kb1A_	Alignment		23.3	6	**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
18	c3lw5K_	Alignment		23.1	22	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak; **PDBTitle:** improved model of plant photosystem i
19	c1btsA_	Alignment		20.7	25	**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
20	c1bttA_	Alignment		20.7	25	**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
21	d3dtub2	Alignment	not modelled	16.8	30	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
22	d1otsa_	Alignment	not modelled	16.1	20	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
23	c3jyzA_	Alignment	not modelled	15.7	0	**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
24	c2kxeA_	Alignment	not modelled	15.1	27	**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
25	c2o01G_	Alignment	not modelled	14.4	13	**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
26	d1oqva_	Alignment	not modelled	13.7	20	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**TcpA-like pilin
27	c2qksA_	Alignment	not modelled	13.0	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
28	d2a9ha1	Alignment	not modelled	12.7	14	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels

29	c2ljcA_	Alignment	not modelled	12.5	31	**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
30	c2wscK_	Alignment	not modelled	10.8	31	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit psak, **PDBTitle:** improved model of plant photosystem i
31	c1qleB_	Alignment	not modelled	10.0	13	**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
32	c1ar1B_	Alignment	not modelled	10.0	13	**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
33	c2k21A_	Alignment	not modelled	9.7	10	**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
34	c2hg5D_	Alignment	not modelled	9.5	9	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
35	c1afoB_	Alignment	not modelled	8.8	21	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
36	c2j7aC_	Alignment	not modelled	7.7	19	**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
37	c2jo1A_	Alignment	not modelled	7.7	36	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
38	c2kadB_	Alignment	not modelled	7.6	31	**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
39	c2kadC_	Alignment	not modelled	7.6	31	**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
40	c2kadD_	Alignment	not modelled	7.6	31	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
41	c2kadA_	Alignment	not modelled	7.6	31	**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
42	c3ifxB_	Alignment	not modelled	7.5	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-gated potassium channel; **PDBTitle:** crystal structure of the spin-labeled kcsa mutant v48r1
43	d3ehbb2	Alignment	not modelled	7.4	18	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
44	c1m57H_	Alignment	not modelled	7.0	27	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
45	c2jp3A_	Alignment	not modelled	7.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
46	c2jwaA_	Alignment	not modelled	6.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
47	c2qzbB_	Alignment	not modelled	6.7	47	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yfey; **PDBTitle:** crystal structure of the uncharacterized protein yfey from escherichia2 coli
48	c2kqtA_	Alignment	not modelled	6.5	31	**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
49	c1nyjB_	Alignment	not modelled	6.5	31	**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
50	c2kqtC_	Alignment	not modelled	6.5	31	**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
51	c2kqtD_	Alignment	not modelled	6.5	31	**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

52	c1nyjA_	Alignment	not modelled	6.5	31	**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
53	c1mp6A_	Alignment	not modelled	6.5	31	**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
54	c1nyjC_	Alignment	not modelled	6.5	31	**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
55	c1nyjD_	Alignment	not modelled	6.5	31	**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
56	c2kqtB_	Alignment	not modelled	6.5	31	**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
57	c2kncB_	Alignment	not modelled	6.5	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
58	d1az3a_	Alignment	not modelled	6.5	44	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
59	c2gs0B_	Alignment	not modelled	6.4	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** nmr structure of the complex between the ph domain of the2 tfb1 subunit from tfiih and the activation domain of p53
60	c2bnoA_	Alignment	not modelled	5.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
61	c3orgB_	Alignment	not modelled	5.7	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
62	d1ehkb2	Alignment	not modelled	5.7	28	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
63	c3jycA_	Alignment	not modelled	5.7	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**inward-rectifier k+ channel kir2.2; **PDBTitle:** crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
64	c2l2tA_	Alignment	not modelled	5.2	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
65	d1fftb2	Alignment	not modelled	5.0	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region