Phyre^2

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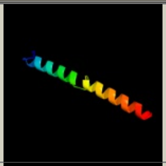
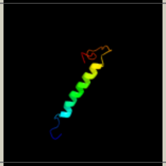
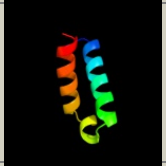
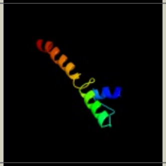
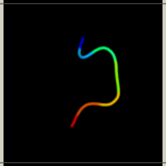
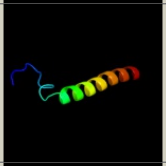
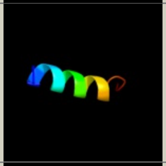
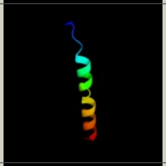
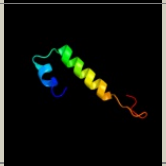
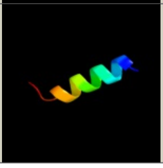
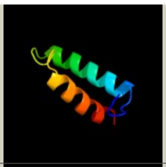
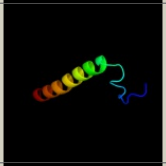
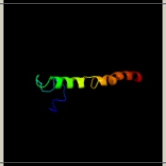
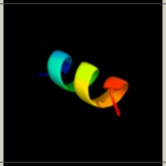
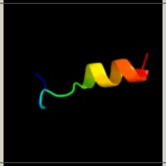
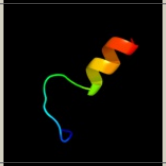
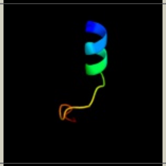
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hg5D_	Alignment		22.5	14	**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
2	d1jb0l_	Alignment		20.1	27	**Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL
3	d2i53a1	Alignment		14.4	16	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
4	d1f6ga_	Alignment		12.8	15	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
5	c1s6xA_	Alignment		12.2	43	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kvap channel; **PDBTitle:** solution structure of vstx
6	d1v54j_	Alignment		11.6	30	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIa **Family:**Mitochondrial cytochrome c oxidase subunit VIIa
7	c3oa1B_	Alignment		10.6	39	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**phosphoprotein; **PDBTitle:** crystal structure of phosphoprotein/protein p/protein m1 residues 69-2 297 from rabies virus reveals degradation to c-terminal domain only
8	d1flca1	Alignment		10.4	43	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Hemagglutinin domain of haemagglutinin-esterase-fusion glycoprotein HEF1
9	d2bs2c1	Alignment		10.3	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Fumarate reductase respiratory complex cytochrome b subunit, FrdC
10	d1v74b_	Alignment		9.9	22	**Fold:**Four-helical up-and-down bundle **Superfamily:**Colicin D immunity protein **Family:**Colicin D immunity protein
11	d1vyia_	Alignment		9.4	39	**Fold:**Phosphoprotein M1, C-terminal domain **Superfamily:**Phosphoprotein M1, C-terminal domain **Family:**Phosphoprotein M1, C-terminal domain

12	d2ivxa1	Alignment		9.4	15	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
13	c2y69W_	Alignment		9.1	30	**PDB header:**electron transport **Chain:** W: **PDB Molecule:**cytochrome c oxidase polypeptide 7a1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
14	c2kb1A_	Alignment		8.9	17	**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
15	c3kfoA_	Alignment		8.8	67	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup133; **PDBTitle:** crystal structure of the c-terminal domain from the nuclear pore2 complex component nup133 from saccharomyces cerevisiae
16	d1qhba_	Alignment		8.7	21	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
17	d1up8a_	Alignment		8.5	21	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
18	d1qi9a_	Alignment		8.5	21	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
19	d1iyea_	Alignment		7.7	29	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
20	d2hkja2	Alignment		7.4	71	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
21	c1uf2K_	Alignment	not modelled	7.0	57	**PDB header:**virus **Chain:** K: **PDB Molecule:**structural protein p7; **PDBTitle:** the atomic structure of rice dwarf virus (rdv)
22	c2xtzB_	Alignment	not modelled	5.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein alpha-1 subunit; **PDBTitle:** crystal structure of the g alpha protein atgpa1 from2 arabidopsis thaliana
23	c1y4eA_	Alignment	not modelled	5.3	67	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
24	c1zcbA_	Alignment	not modelled	5.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**g alpha i/13; **PDBTitle:** crystal structure of g alpha 13 in complex with gdp