Phyre^2

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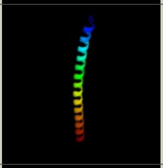
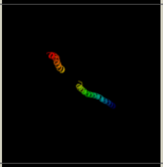
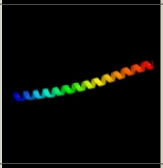
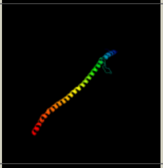
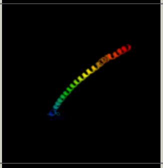
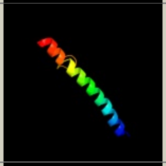
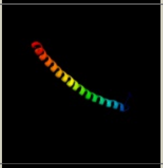
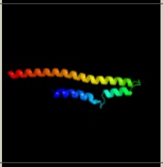
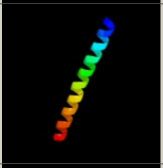
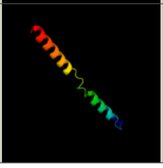
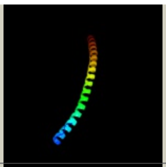
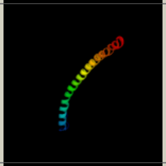
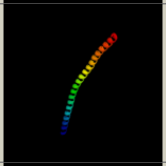
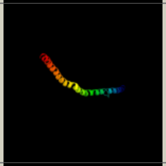
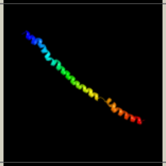
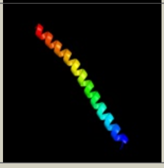
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gk4A_	Alignment		89.0	13	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
2	c1x8yA_	Alignment		84.0	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
3	d1ucua_	Alignment		80.9	11	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
4	c3movB_	Alignment		78.0	9	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
5	c1ei3E_	Alignment		77.7	12	**PDB header:** **PDB COMPND:**
6	c1ik9B_	Alignment		73.2	11	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
7	c2pnvA_	Alignment		69.8	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
8	c1ei3C_	Alignment		63.0	13	**PDB header:** **PDB COMPND:**
9	c2d4yA_	Alignment		61.7	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
10	c2zdiA_	Alignment		55.6	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**prefoldin subunit beta; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
11	d1fxka_	Alignment		52.8	15	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin

12	c1sfcD_	Alignment		52.4	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein (snap-25b); **PDBTitle:** neuronal synaptic fusion complex
13	c1deqO_	Alignment		48.8	12	**PDB header:** **PDB COMPND:**
14	c1l4aD_	Alignment		47.5	10	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**s-snap25 fusion protein; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
15	c3ojaA_	Alignment		45.0	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
16	c3ghgD_	Alignment		44.2	11	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
17	c2gr7C_	Alignment		43.4	18	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
18	d2gr7a1	Alignment		43.4	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
19	c3ghgK_	Alignment		43.0	9	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
20	c3swyB_	Alignment		42.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
21	c1deqF_	Alignment	not modelled	42.3	8	**PDB header:** **PDB COMPND:**
22	c1kzzA_	Alignment	not modelled	37.0	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** downstream regulator tank binds to the cd40 recognition2 site on traf3
23	c2npsD_	Alignment	not modelled	36.3	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**syntaxin-6; **PDBTitle:** crystal structure of the early endosomal snare complex
24	c2zdiC_	Alignment	not modelled	30.9	11	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
25	c1flIA_	Alignment	not modelled	29.4	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** molecular basis for cd40 signaling mediated by traf3
26	c3k8vB_	Alignment	not modelled	27.3	12	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
27	c1m1jA_	Alignment	not modelled	26.7	9	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
28	c1zxaB_	Alignment	not modelled	24.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia

29	c1r48A_	Alignment	not modelled	22.4	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
30	c3b5nL_	Alignment	not modelled	22.2	17	**PDB header:**membrane protein **Chain:** L: **PDB Molecule:**protein transport protein sec9; **PDBTitle:** structure of the yeast plasma membrane snare complex
31	c2j69D_	Alignment	not modelled	22.2	7	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
32	c2ayuA_	Alignment	not modelled	21.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein; **PDBTitle:** the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
33	d2ayua1	Alignment	not modelled	21.9	13	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
34	c1aq5C_	Alignment	not modelled	20.8	24	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
35	d2j0na1	Alignment	not modelled	20.4	13	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
36	c2nrjA_	Alignment	not modelled	20.4	12	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hbl b protein; **PDBTitle:** crystal structure of hemolysin binding component from2 bacillus cereus
37	c1ca9D_	Alignment	not modelled	19.0	3	**PDB header:**tnf signaling **Chain:** D: **PDB Molecule:**protein (tnf receptor associated factor 2); **PDBTitle:** structure of tnf receptor associated factor 2 in complex2 with a peptide from tnf-r2
38	d1fxkc_	Alignment	not modelled	18.3	5	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
39	c1gl2D_	Alignment	not modelled	17.3	8	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**syntaxin 8; **PDBTitle:** crystal structure of an endosomal snare core complex
40	c2zvfG_	Alignment	not modelled	16.8	7	**PDB header:**ligase **Chain:** G: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
41	c2fxmB_	Alignment	not modelled	16.3	13	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
42	d1z0pa1	Alignment	not modelled	15.6	16	**Fold:**Long alpha-hairpin **Superfamily:**SPy1572-like **Family:**SPy1572-like
43	c3bvhE_	Alignment	not modelled	14.7	15	**PDB header:**blood clotting **Chain:** E: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
44	c2oqqB_	Alignment	not modelled	14.4	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
45	c3ci9B_	Alignment	not modelled	14.2	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
46	d1ivsa1	Alignment	not modelled	14.2	13	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
47	c2z5hB_	Alignment	not modelled	13.8	20	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin **PDBTitle:** crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
48	c1l8dB_	Alignment	not modelled	11.4	12	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
49	c1htmB_	Alignment	not modelled	11.3	7	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion
50	c2oszA_	Alignment	not modelled	11.1	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
51	d1owaa_	Alignment	not modelled	11.1	7	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
52	c3ibpA_	Alignment	not modelled	10.9	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
53	c3swfA_	Alignment	not modelled	10.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
54	d1wa8b1	Alignment	not modelled	10.5	18	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like

55	c2akfB_	Alignment	not modelled	9.4	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
56	c2akfA_	Alignment	not modelled	9.4	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
57	c2akfC_	Alignment	not modelled	9.4	10	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
58	c3f6hA_	Alignment	not modelled	8.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
59	c2xdjF_	Alignment	not modelled	8.7	13	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
60	c2xzrA_	Alignment	not modelled	7.6	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
61	c3ipkA_	Alignment	not modelled	7.4	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
62	c3bvhC_	Alignment	not modelled	7.4	6	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
63	c3l9oA_	Alignment	not modelled	7.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
64	d1hq1a_	Alignment	not modelled	6.9	22	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
65	c2dq3A_	Alignment	not modelled	6.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
66	c2hpcH_	Alignment	not modelled	6.8	11	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
67	c2d3eD_	Alignment	not modelled	6.8	11	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
68	c3na7A_	Alignment	not modelled	6.7	5	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
69	d2azeb1	Alignment	not modelled	6.7	9	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
70	c3dtpA_	Alignment	not modelled	6.6	13	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
71	c1x59A_	Alignment	not modelled	6.5	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** solution structures of the whep-trs domain of human2 histidyl-trna synthetase
72	c2gtlO_	Alignment	not modelled	6.5	15	**PDB header:**oxygen storage/transport **Chain:** O: **PDB Molecule:**extracellular hemoglobin linker l3 subunit; **PDBTitle:** lumbricus erythrocruorin at 3.5a resolution
73	d1e52a_	Alignment	not modelled	6.5	15	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
74	d1jyoa_	Alignment	not modelled	6.4	18	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
75	c1dlcA_	Alignment	not modelled	6.4	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
76	c2h3sB_	Alignment	not modelled	6.4	25	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-azobenzene-avian pancreatic polypeptide bound to dpc2 micelles
77	c2h4bC_	Alignment	not modelled	6.4	25	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
78	c2h3tB_	Alignment	not modelled	6.4	25	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**pancreatic hormone; **PDBTitle:** trans-(4-aminomethyl)phenylazobenzoic acid-app bound to dpc2 micelles
79	c2h4bD_	Alignment	not modelled	6.4	25	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
80	d1r6fa_	Alignment	not modelled	6.3	15	**Fold:**Virulence-associated V antigen **Superfamily:**Virulence-associated V antigen **Family:**Virulence-associated V antigen

81	c2ym9C_	Alignment	not modelled	6.3	11	**PDB header:**cell invasion **Chain:** C: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** sipd from salmonella typhimurium
82	c2k48A_	Alignment	not modelled	6.2	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
83	c3rrkA_	Alignment	not modelled	6.2	5	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**v-type atpase 116 kda subunit; **PDBTitle:** crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase
84	d1w8oa1	Alignment	not modelled	6.1	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
85	c3g9rF_	Alignment	not modelled	6.1	0	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fusion complex of hiv-1 envelope glycoprotein **PDBTitle:** structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
86	c1jsdB_	Alignment	not modelled	6.1	17	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**haemagglutinin (ha2 chain); **PDBTitle:** crystal structure of swine h9 haemagglutinin
87	d2okua1	Alignment	not modelled	6.0	10	**Fold:**N-cbl like **Superfamily:**PG0775 C-terminal domain-like **Family:**PG0775 C-terminal domain-like
88	c2v71A_	Alignment	not modelled	6.0	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
89	c2hpcF_	Alignment	not modelled	5.9	14	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
90	c1bf5A_	Alignment	not modelled	5.9	8	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
91	c2ykqC_	Alignment	not modelled	5.8	11	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
92	c3bj4B_	Alignment	not modelled	5.8	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily kqt **PDBTitle:** the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
93	c3mtuE_	Alignment	not modelled	5.8	16	**PDB header:**contractile protein **Chain:** E: **PDB Molecule:**head morphogenesis protein, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
94	c2ic6B_	Alignment	not modelled	5.7	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** the coiled-coil domain (residues 1-75) structure of the sin2 nombre virus nucleocapsid protein
95	c1ezjA_	Alignment	not modelled	5.6	13	**PDB header:**viral protein, transferase **Chain:** A: **PDB Molecule:**nucleocapsid phosphoprotein; **PDBTitle:** crystal structure of the multimerization domain of the phosphoprotein2 from sendai virus
96	c2ym0B_	Alignment	not modelled	5.6	12	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** truncated sipd from salmonella typhimurium
97	c1t6zB_	Alignment	not modelled	5.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
98	c1ic2B_	Alignment	not modelled	5.4	18	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**tropomyosin alpha chain, skeletal muscle; **PDBTitle:** deciphering the design of the tropomyosin molecule
99	c3hfeC_	Alignment	not modelled	5.4	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**potassium voltage-gated channel subfamily kqt member 1; **PDBTitle:** a trimeric form of the kv7.1 a domain tail