Phyre^2

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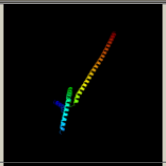
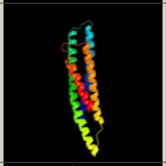
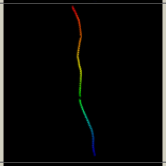
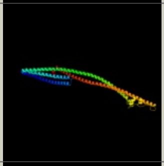
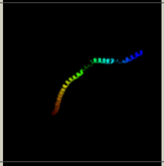
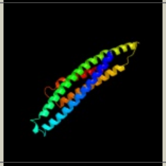
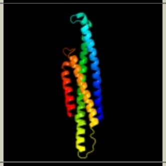
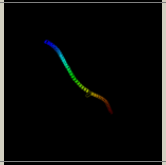
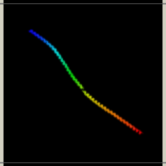
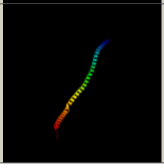
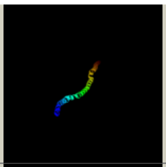
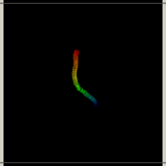
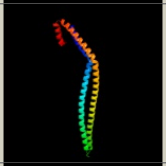
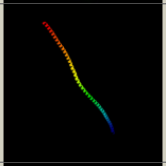
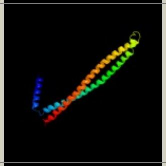
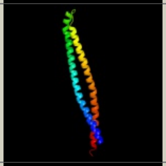
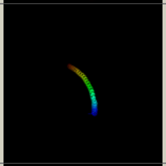
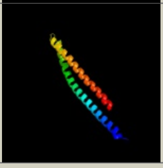
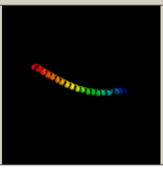
Description	P0AG71
Date	Thu Jan 5 11:28:16 GMT 2012
Unique Job ID	55418f1b0f0beab2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ojaB_	Alignment		97.4	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
2	c1bf5A_	Alignment		96.9	7	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
3	c1c1gA_	Alignment		96.9	8	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
4	c1ciiA_	Alignment		96.8	7	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
5	c1deqF_	Alignment		96.3	7	**PDB header:** **PDB COMPND:**
6	c1bg1A_	Alignment		96.2	6	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
7	c3cwgA_	Alignment		95.7	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
8	c1yvlB_	Alignment		95.4	7	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
9	c2efrB_	Alignment		95.4	9	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
10	c3o0zD_	Alignment		94.5	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i
11	c1ei3E_	Alignment		94.3	10	**PDB header:** **PDB COMPND:**

12	c3ghgK_	Alignment		93.7	12	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
13	c2d3eD_	Alignment		92.9	9	**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
14	c3na7A_	Alignment		92.6	8	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
15	c2v71A_	Alignment		92.5	9	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
16	c1jchC_	Alignment		92.4	3	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
17	c2v66C_	Alignment		92.2	4	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
18	c4a55B_	Alignment		92.0	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
19	c2fxmB_	Alignment		91.2	7	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
20	c2gl2B_	Alignment		90.7	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
21	c1deqO_	Alignment	not modelled	90.5	11	**PDB header:** **PDB COMPND:**
22	c1ei3C_	Alignment	not modelled	89.2	6	**PDB header:** **PDB COMPND:**
23	c3u59C_	Alignment	not modelled	89.0	17	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
24	c1deqD_	Alignment	not modelled	87.4	11	**PDB header:** **PDB COMPND:**
25	c3ol1A_	Alignment	not modelled	86.7	6	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
26	c2b9cA_	Alignment	not modelled	86.2	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**striated-muscle alpha tropomyosin; **PDBTitle:** structure of tropomyosin's mid-region: bending and binding2 sites for actin
27	c3hnwB_	Alignment		85.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750

28	c3hizB_	Alignment	not modelled	77.6	6	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
29	c2rd0B_	Alignment	not modelled	72.3	8	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
30	c2i1jA_	Alignment	not modelled	70.9	11	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
31	c2v1yB_	Alignment	not modelled	62.0	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
32	c3ojaA_	Alignment	not modelled	61.6	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
33	c1gk4A_	Alignment	not modelled	54.1	10	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
34	c2no2A_	Alignment	not modelled	51.9	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
35	d2pila_	Alignment	not modelled	49.8	13	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
36	c3dtpA_	Alignment	not modelled	48.5	7	**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
37	c3ipkA_	Alignment	not modelled	47.3	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
38	c1hciB_	Alignment	not modelled	45.2	12	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
39	c2wpqA_	Alignment	not modelled	41.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
40	c3sokB_	Alignment	not modelled	38.8	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
41	c2voyB_	Alignment	not modelled	38.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
42	c1y4cA_	Alignment	not modelled	36.8	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
43	c1sjjB_	Alignment	not modelled	32.9	8	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
44	c1wt6B_	Alignment	not modelled	32.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**myotonin-protein kinase; **PDBTitle:** coiled-coil domain of dmpk
45	d1oqwa_	Alignment	not modelled	32.5	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
46	c2e7sM_	Alignment	not modelled	32.2	6	**PDB header:**endocytosis/exocytosis **Chain:** M: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the yeast sec2p gef domain
47	c2jeeA_	Alignment	not modelled	31.5	6	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
48	d2ap3a1	Alignment	not modelled	31.4	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**MW0975(SA0943)-like **Family:**MW0975(SA0943)-like
49	c2y3aB_	Alignment	not modelled	28.3	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
50	c2dq3A_	Alignment	not modelled	26.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
51	c3u1aC_	Alignment	not modelled	23.4	14	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
52	c3q0xA_	Alignment	not modelled	22.4	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centriole protein; **PDBTitle:** n-terminal coiled-coil dimer domain of c. reinhardtii sas-

						6 homolog2 bld12p
53	c3mraA_	Alignment	not modelled	21.1	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nicotinic acetylcholine receptor; **PDBTitle:** m3 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 153 structures
54	c3ajwA_	Alignment	not modelled	19.1	4	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar flij protein; **PDBTitle:** structure of flij, a soluble component of flagellar type iii export2 apparatus
55	c1m1jA_	Alignment	not modelled	18.4	7	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
56	c2oevA_	Alignment	not modelled	18.3	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
57	c2qa7B_	Alignment	not modelled	16.7	5	**PDB header:**actin binding **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
58	d1gl4a1	Alignment	not modelled	16.6	50	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Domain G2 of nidogen-1
59	c1h4uA_	Alignment	not modelled	15.6	50	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
60	d1jb0m_	Alignment	not modelled	15.4	32	**Fold:**Single transmembrane helix **Superfamily:**Subunit XII of photosystem I reaction centre, PsaM **Family:**Subunit XII of photosystem I reaction centre, PsaM
61	c1jb0M_	Alignment	not modelled	15.4	32	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem 1 reaction centre subunit xii; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
62	d2axti1	Alignment	not modelled	15.3	11	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
63	c3tnfB_	Alignment	not modelled	14.8	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**lida; **PDBTitle:** lida from legionella in complex with active rab8a
64	c2jo1A_	Alignment	not modelled	13.7	13	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
65	c1x8yA_	Alignment	not modelled	13.5	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
66	c3a7pB_	Alignment	not modelled	13.1	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
67	c3cvfA_	Alignment	not modelled	12.4	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
68	d1seta1	Alignment	not modelled	12.2	17	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
69	c2jp3A_	Alignment	not modelled	11.7	13	**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
70	c3mk7B_	Alignment	not modelled	11.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
71	c2oexB_	Alignment	not modelled	11.4	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** structure of alix/aip1 v domain
72	c1l8dB_	Alignment	not modelled	11.4	9	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
73	c1afoB_	Alignment	not modelled	11.3	11	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
74	d1q90m_	Alignment	not modelled	11.3	25	**Fold:**Single transmembrane helix **Superfamily:**PetM subunit of the cytochrome b6f complex **Family:**PetM subunit of the cytochrome b6f complex
75	c2jwaA_	Alignment	not modelled	10.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
76	c2wvrB_	Alignment	not modelled	9.9	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**geminin; **PDBTitle:** human cdt1:geminin complex
77	c2dq0A_	Alignment	not modelled	9.5	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
						PDB header:chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase;

78	c3m9bK_	Alignment	not modelled	9.2	22	**PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
79	c3qh9A_	Alignment	not modelled	9.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
80	c1debA_	Alignment	not modelled	8.7	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
81	c2zxeG_	Alignment	not modelled	8.5	31	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
82	c2xdjF_	Alignment	not modelled	7.8	11	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
83	c3pcqM_	Alignment	not modelled	7.6	32	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem i reaction center subunit xii; **PDBTitle:** femtosecond x-ray protein nanocrystallography
84	c2ap7A_	Alignment	not modelled	7.6	37	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h2; **PDBTitle:** solution structure of bombinin h2 in dpc micelles
85	c2eqbC_	Alignment	not modelled	7.3	13	**PDB header:**endocytosis/exocytosis **Chain:** C: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
86	c2hacA_	Alignment	not modelled	7.2	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 zeta chain; **PDBTitle:** structure of zeta-zeta transmembrane dimer
87	c3l9oA_	Alignment	not modelled	7.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
88	c3movB_	Alignment	not modelled	7.1	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
89	c3n4xB_	Alignment	not modelled	7.0	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
90	c1fosF_	Alignment	not modelled	7.0	14	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
91	c3n23E_	Alignment	not modelled	6.6	25	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
92	c3lssA_	Alignment	not modelled	6.5	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
93	c2zxxA_	Alignment	not modelled	6.1	17	**PDB header:**cell cycle/replication **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of cdt1/geminin complex
94	c3pdsA_	Alignment	not modelled	6.1	4	**PDB header:**membrane protein/hydrolase **Chain:** A: **PDB Molecule:**fusion protein beta-2 adrenergic receptor/lysozyme; **PDBTitle:** irreversible agonist-beta2 adrenoceptor complex
95	c1ic2B_	Alignment	not modelled	5.9	18	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**tropomyosin alpha chain, skeletal muscle; **PDBTitle:** deciphering the design of the tropomyosin molecule
96	c1f5nA_	Alignment	not modelled	5.8	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
97	d1v54i_	Alignment	not modelled	5.6	22	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
98	c1pi8A_	Alignment	not modelled	5.5	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
99	c2gohA_	Alignment	not modelled	5.5	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles