Phyre^2

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Description	P69776
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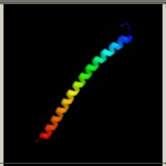
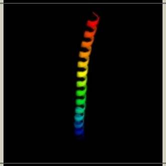
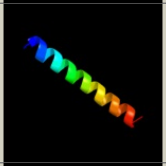
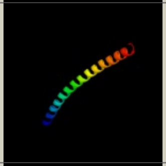
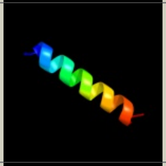
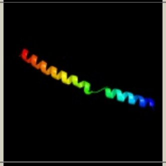
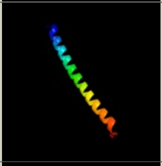
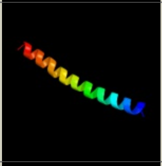
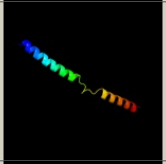
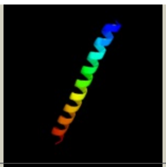
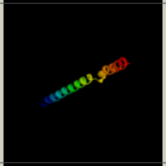
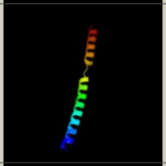
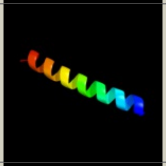
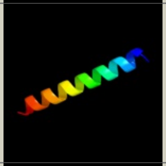
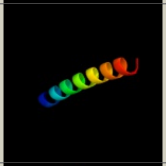
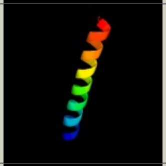
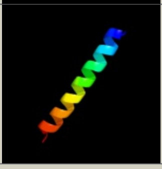
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jccC_	Alignment		99.8	87	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
2	c1t8zA_	Alignment		99.6	72	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** atomic structure of a novel tryptophan-zipper pentamer
3	c2gr7C_	Alignment		78.2	25	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
4	d2gr7a1	Alignment		78.2	25	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
5	c2pohA_	Alignment		67.8	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head completion protein; **PDBTitle:** structure of phage p22 tail needle gp26
6	c1avyA_	Alignment		53.9	29	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
7	c1gk6B_	Alignment		53.9	24	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
8	c2ykqC_	Alignment		53.3	13	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
9	c1fosF_	Alignment		51.0	30	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
10	c1x8yA_	Alignment		49.3	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
11	c1coiA_	Alignment		46.8	43	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald

12	c2xzrA_	Alignment		44.0	9	**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
13	c1gk4A_	Alignment		40.5	16	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
14	c3movB_	Alignment		40.4	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
15	c1ij2C_	Alignment		39.5	30	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
16	c1rb6C_	Alignment		39.2	30	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
17	c3k7zA_	Alignment		39.2	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
18	c1swiA_	Alignment		39.2	30	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
19	c1rb1B_	Alignment		39.2	30	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
20	c3k7zB_	Alignment		39.2	30	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
21	c1rb1A_	Alignment	not modelled	39.2	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
22	d1k4ta1	Alignment	not modelled	38.7	31	**Fold:**Long alpha-hairpin **Superfamily:**Eukaryotic DNA topoisomerase I, dispensable insert domain **Family:**Eukaryotic DNA topoisomerase I, dispensable insert domain
23	c1ij3C_	Alignment	not modelled	37.9	30	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
24	c1ij3B_	Alignment	not modelled	37.9	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
25	c1ij2B_	Alignment	not modelled	37.5	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
26	c2o7hF_	Alignment	not modelled	34.4	30	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
27	c1ce0B_	Alignment	not modelled	33.7	17	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
28	c3m9bK_	Alignment	not modelled	32.1	24	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil

						domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
29	c3u59C_	Alignment	not modelled	31.7	11	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
30	c3na7A_	Alignment	not modelled	29.7	24	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
31	c2qihA_	Alignment	not modelled	28.1	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
32	c1junB_	Alignment	not modelled	27.7	28	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
33	c2efrB_	Alignment	not modelled	27.6	23	**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
34	c1ztaA_	Alignment	not modelled	26.8	30	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
35	c2wpqA_	Alignment	not modelled	25.9	13	**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)
36	c1ci6B_	Alignment	not modelled	25.0	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
37	c2diuA_	Alignment	not modelled	23.2	46	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rrm domain of kiaa0430 protein
38	c1gd2G_	Alignment	not modelled	23.0	16	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
39	c3okqA_	Alignment	not modelled	22.9	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
40	c1deqD_	Alignment	not modelled	22.6	18	**PDB header:** **PDB COMPND:**
41	c1ei3E_	Alignment	not modelled	22.4	4	**PDB header:** **PDB COMPND:**
42	c2ki0A_	Alignment	not modelled	22.0	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
43	c3bvhE_	Alignment	not modelled	20.5	25	**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	c2hpcF_	Alignment	not modelled	20.2	20	**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.
45	c3emoA_	Alignment	not modelled	19.7	19	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
46	c3sjbC_	Alignment	not modelled	19.5	24	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
47	c2gl2B_	Alignment	not modelled	19.4	26	**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
48	c2x7aB_	Alignment	not modelled	18.4	24	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
49	c1deqO_	Alignment	not modelled	18.0	6	**PDB header:** **PDB COMPND:**
50	c2wt7B_	Alignment	not modelled	18.0	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
51	c2js5B_	Alignment	not modelled	18.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
52	c3bvhC_	Alignment	not modelled	18.0	19	**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
53	c2w83C_	Alignment	not modelled	17.2	22	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**c-jun-amino-terminal kinase-interacting protein **PDBTitle:** crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4

54	c2fxmB_	Alignment	not modelled	16.0	23	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
55	c2d3eD_	Alignment	not modelled	15.8	15	**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
56	c2e43A_	Alignment	not modelled	15.5	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**ccaat/enhancer-binding protein beta; **PDBTitle:** crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
57	c3swfA_	Alignment	not modelled	15.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
58	c2npsD_	Alignment	not modelled	15.3	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**syntaxin-6; **PDBTitle:** crystal structure of the early endosomal snare complex
59	c1j1dF_	Alignment	not modelled	15.0	14	**PDB header:**contractile protein **Chain:** F: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
60	c3hnwB_	Alignment	not modelled	14.8	9	**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
61	c2xdjF_	Alignment	not modelled	14.1	10	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
62	c2xv5A_	Alignment	not modelled	13.9	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-a/c; **PDBTitle:** human lamin a coil 2b fragment
63	c3ghgD_	Alignment	not modelled	13.9	22	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
64	c1z56B_	Alignment	not modelled	13.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ligase interacting factor 1; **PDBTitle:** co-crystal structure of lif1p-lig4p
65	c3ipdB_	Alignment	not modelled	13.6	16	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
66	c1ci6A_	Alignment	not modelled	13.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
67	c1fosE_	Alignment	not modelled	13.4	11	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
68	c2zdiC_	Alignment	not modelled	13.2	12	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
69	c3sjaG_	Alignment	not modelled	13.0	27	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
70	c1j1eC_	Alignment	not modelled	12.6	16	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
71	c1n73A_	Alignment	not modelled	12.5	8	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrin alpha-1 chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
72	c1bb1B_	Alignment	not modelled	12.2	23	**PDB header:**de novo protein design **Chain:** B: **PDB Molecule:**designed, thermostable heterotrimeric coiled **PDBTitle:** crystal structure of a designed, thermostable2 heterotrimeric coiled coil
73	c3eukC_	Alignment	not modelled	12.2	26	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**chromosome partition protein mukb, linker; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
74	c2wukD_	Alignment	not modelled	11.5	14	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
75	c2j7aC_	Alignment	not modelled	11.2	56	**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
76	c1j1eB_	Alignment	not modelled	11.0	16	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**troponin t; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
77	c3ntnB_	Alignment	not modelled	10.9	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**uspa1; **PDBTitle:** crystal structure of uspa1 head and neck domain from moraxella2 catarrhalis
78	c1qoyA_	Alignment	not modelled	10.8	23	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
79	d1vb8a_	Alignment	not modelled	10.8	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Cycloviolacin

80	c1vb8A_	Alignment	not modelled	10.8	50	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**viola hederacea root peptide 1; **PDBTitle:** solution structure of vhr1, the first cyclotide from root2 tissue
81	c2dw3A_	Alignment	not modelled	10.7	50	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
82	c3swyB_	Alignment	not modelled	10.7	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
83	c1t2kD_	Alignment	not modelled	10.6	22	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**cyclic-amp-dependent transcription factor atf-2; **PDBTitle:** structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
84	c1by0A_	Alignment	not modelled	10.3	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
85	c2akfC_	Alignment	not modelled	10.3	35	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
86	c2akfA_	Alignment	not modelled	10.3	35	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
87	c2akfB_	Alignment	not modelled	10.3	35	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
88	c3ghgK_	Alignment	not modelled	10.3	8	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
89	c3n27A_	Alignment	not modelled	10.2	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**fusion glycoprotein f0, linker, fusion glycoprotein f0; **PDBTitle:** molecular basis of the inhibition of henipa viruses
90	c3hizB_	Alignment	not modelled	9.7	13	**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
91	c1nbjA_	Alignment	not modelled	9.6	42	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin o1; **PDBTitle:** high-resolution solution structure of cycloviolacin o1
92	d1nbja_	Alignment	not modelled	9.6	42	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Cycloviolacin
93	c3iynR_	Alignment	not modelled	9.6	22	**PDB header:**virus **Chain:** R: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
94	c2hpcH_	Alignment	not modelled	9.6	25	**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.
95	c3u1aC_	Alignment	not modelled	9.3	13	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
96	c1sfcD_	Alignment	not modelled	9.2	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein (snap-25b); **PDBTitle:** neuronal synaptic fusion complex
97	c1n7sB_	Alignment	not modelled	8.9	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 1a; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
98	c3dbzB_	Alignment	not modelled	8.7	28	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** human surfactant protein d
99	c1m7lA_	Alignment	not modelled	8.5	26	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d