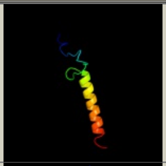
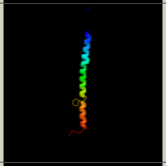
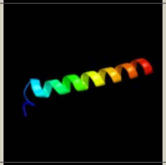
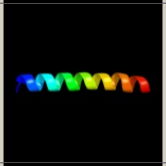
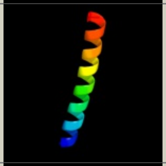
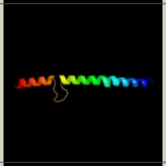
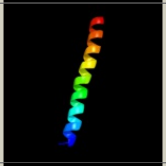
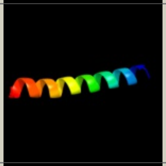
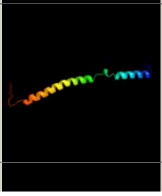
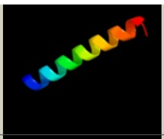
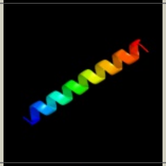
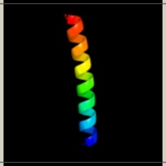
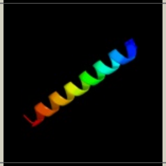
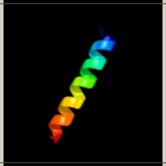
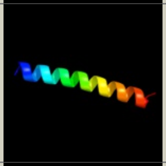
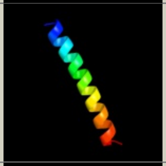
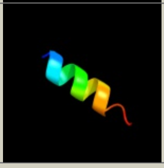
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q46868
Date	Thu Jan 5 12:35:27 GMT 2012
Unique Job ID	d2e6312573615073

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1dipA_	Alignment		86.2	38	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
2	c3p8cE_	Alignment		75.5	31	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
3	c3gw6F_	Alignment		71.2	31	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**endo-n-acetylneuraminidase; **PDBTitle:** intramolecular chaperone
4	c1cosA_	Alignment		56.7	30	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
5	c1cosB_	Alignment		55.6	29	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
6	c3pp5A_	Alignment		55.4	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
7	c1coiA_	Alignment		54.0	27	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
8	c1qceB_	Alignment		53.4	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein (gp41); **PDBTitle:** solution nmr structure of ectodomain of siv gp41,2 restrained regularized mean structure plus 29 simulated3 annealing structures
9	c1cosC_	Alignment		52.8	30	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
10	c2l7kA_	Alignment		52.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
11	c3p8cD_	Alignment		46.8	16	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**wiskott-aldrich syndrome protein family member 1; **PDBTitle:** structure and control of the actin regulatory wave complex

12	c1aq5C_	Alignment		40.7	28	**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
13	c2jgoB_	Alignment		38.0	26	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
14	c2jgoA_	Alignment		38.0	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
15	c3ljmC_	Alignment		38.0	26	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
16	c3ljmA_	Alignment		38.0	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
17	c2ergA_	Alignment		37.9	27	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**regulatory protein leu3; **PDBTitle:** crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex
18	c2jgoC_	Alignment		36.6	25	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
19	c3ljmB_	Alignment		36.6	25	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
20	c3h5fC_	Alignment		34.0	27	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
21	c3h5fB_	Alignment	not modelled	34.0	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
22	c3h5gA_	Alignment	not modelled	34.0	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
23	c3h5gB_	Alignment	not modelled	34.0	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
24	c3h5gC_	Alignment	not modelled	34.0	27	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
25	c3h5fA_	Alignment	not modelled	34.0	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
26	c1d7mA_	Alignment	not modelled	33.5	39	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**cortexillin i; **PDBTitle:** coiled-coil dimerization domain from cortexillin i
27	d1grja1	Alignment	not modelled	33.1	29	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
28	c1g6uB_	Alignment	not modelled	31.7	36	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
29	c3p7kA_	Alignment	not modelled	31.4	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gp41 peptide;

						PDBTitle: gp41 peptide
30	c3iynR_	Alignment	not modelled	30.3	16	**PDB header:**virus **Chain:** R: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
31	d2f23a1	Alignment	not modelled	29.4	29	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
32	d1ohua_	Alignment	not modelled	28.9	24	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
33	c1favA_	Alignment	not modelled	28.4	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 envelope protein chimera; **PDBTitle:** the structure of an hiv-1 specific cell entry inhibitor in complex2 with the hiv-1 gp41 trimeric core
34	c3m06F_	Alignment	not modelled	27.1	14	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of traf2
35	c2kscA_	Alignment	not modelled	25.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
36	c2pnvA_	Alignment	not modelled	25.5	22	**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
37	c3a7pB_	Alignment	not modelled	24.2	24	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
38	c1u0iA_	Alignment	not modelled	23.7	35	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
39	c2zfcB_	Alignment	not modelled	23.3	14	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hiv-1 gp41; **PDBTitle:** x-ray crystal structure of an engineered n-terminal hiv-12 gp41 trimer with enhanced stability and potency
40	c3cvfA_	Alignment	not modelled	19.4	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
41	c3efgA_	Alignment	not modelled	19.1	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein slyx homolog; **PDBTitle:** structure of slyx protein from xanthomonas campestris pv. campestris2 str. atcc 33913
42	c2vrsC_	Alignment	not modelled	18.9	20	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**sigma-c capsid protein; **PDBTitle:** structure of avian reovirus sigma c 117-326, c2 crystal form
43	c3rylB_	Alignment	not modelled	18.6	31	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**protein vpa1370; **PDBTitle:** dimerization domain of vibrio parahemolyticus vopl
44	c1grjA_	Alignment	not modelled	17.6	29	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
45	c3bpqC_	Alignment	not modelled	16.7	29	**PDB header:**toxin **Chain:** C: **PDB Molecule:**antitoxin relb3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
46	c3hnwB_	Alignment	not modelled	16.3	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
47	d1zy3a1	Alignment	not modelled	16.0	20	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
48	c2yggA_	Alignment	not modelled	15.8	40	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** complex of cambr and cam
49	c2kp8A_	Alignment	not modelled	15.7	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**model peptide; **PDBTitle:** ligand bound to a model peptide that mimics the open2 fusogenic form
50	d2oa5a1	Alignment	not modelled	15.5	20	**Fold:**BLRF2-like **Superfamily:**BLRF2-like **Family:**BLRF2-like
51	c3pbjF_	Alignment	not modelled	15.4	39	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
52	c3pbjB_	Alignment	not modelled	15.4	39	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
53	c3pbjD_	Alignment	not modelled	15.3	39	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
54	c3pbjC_	Alignment	not modelled	15.3	39	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
55	c3pbjA_	Alignment	not modelled	15.3	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a

						designed2 metalloprotein
56	c3c4mA_	Alignment	not modelled	15.0	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of maltose-binding periplasmic protein and **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
57	c3dbzB_	Alignment	not modelled	15.0	15	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** human surfactant protein d
58	d1q1va_	Alignment	not modelled	14.5	27	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
59	d1ivsa1	Alignment	not modelled	14.4	11	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
60	c2o2fA_	Alignment	not modelled	14.2	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
61	c2l5gA_	Alignment	not modelled	13.9	33	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**g protein pathway suppressor 2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
62	c1envA_	Alignment	not modelled	13.9	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 envelope protein chimera consisting of a fragment of **PDBTitle:** atomic structure of the ectodomain from hiv-1 gp41
63	c2xa0A_	Alignment	not modelled	13.6	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
64	c1go4F_	Alignment	not modelled	13.3	27	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**mad1 (mitotic arrest deficient)-like 1; **PDBTitle:** crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
65	c3pbjE_	Alignment	not modelled	13.3	28	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
66	c1by0A_	Alignment	not modelled	13.1	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
67	c2x6pB_	Alignment	not modelled	12.5	26	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
68	c2x6pA_	Alignment	not modelled	12.5	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
69	d2p6va1	Alignment	not modelled	12.4	19	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
70	d1cxzb_	Alignment	not modelled	12.0	21	**Fold:**Long alpha-hairpin **Superfamily:**HR1 repeat **Family:**HR1 repeat
71	c1x8yA_	Alignment	not modelled	11.9	31	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
72	c2x6pC_	Alignment	not modelled	11.8	25	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
73	d1k4ta1	Alignment	not modelled	11.7	20	**Fold:**Long alpha-hairpin **Superfamily:**Eukaryotic DNA topoisomerase I, dispensable insert domain **Family:**Eukaryotic DNA topoisomerase I, dispensable insert domain
74	d1urfa_	Alignment	not modelled	11.6	13	**Fold:**Long alpha-hairpin **Superfamily:**HR1 repeat **Family:**HR1 repeat
75	d2rfra1	Alignment	not modelled	11.2	38	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
76	d1pq1a_	Alignment	not modelled	11.2	17	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
77	d2oa4a1	Alignment	not modelled	10.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
78	c2akfB_	Alignment	not modelled	10.6	34	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
79	c2akfA_	Alignment	not modelled	10.6	34	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
80	c2akfC_	Alignment	not modelled	10.6	34	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
81	c3gvmA_	Alignment	not modelled	10.5	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae

82	c2elfA_	Alignment	not modelled	9.7	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
83	c2p4vA_	Alignment	not modelled	9.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
84	c3exmA_	Alignment	not modelled	9.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
85	c1kzzA_	Alignment	not modelled	9.3	25	**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
86	c3myrB_	Alignment	not modelled	9.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
87	c2qnlA_	Alignment	not modelled	9.1	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
88	c2jrtA_	Alignment	not modelled	9.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
89	c2vofA_	Alignment	not modelled	9.1	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
90	c2a5yA_	Alignment	not modelled	9.0	24	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator ced-9; **PDBTitle:** structure of a ced-4/ced-9 complex
91	c3m0dC_	Alignment	not modelled	8.9	22	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1; **PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex
92	c1jekA_	Alignment	not modelled	8.8	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**env polyprotein; **PDBTitle:** visna tm core structure
93	d2it9a1	Alignment	not modelled	8.6	12	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
94	d1pzra_	Alignment	not modelled	8.5	30	**Fold:**HLH-like **Superfamily:**Docking domain B of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain B of the erythromycin polyketide synthase (DEBS)
95	c1jocA_	Alignment	not modelled	8.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
96	c1p9iA_	Alignment	not modelled	8.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cortexillin i/gcn4 hybrid peptide; **PDBTitle:** coiled-coil x-ray structure at 1.17 a resolution
97	c3ci9B_	Alignment	not modelled	7.8	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
98	c2yv6A_	Alignment	not modelled	7.7	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2 homologous antagonist/killer; **PDBTitle:** crystal structure of human bcl-2 family protein bak
99	c1pyiA_	Alignment	not modelled	7.6	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (pyrimidine pathway regulator 1); **PDBTitle:** crystal structure of a ppr1-dna complex: dna recognition by2 proteins containing a zn2cys6 binuclear cluster