Phyre2

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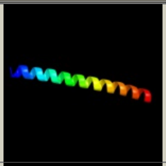
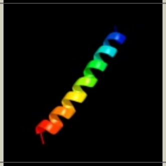
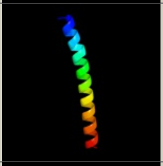
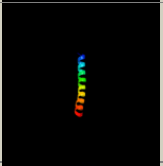
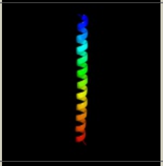
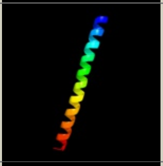
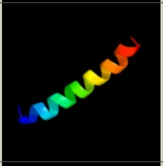
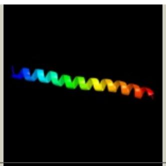
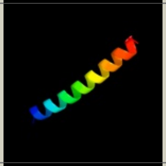
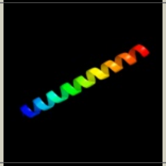
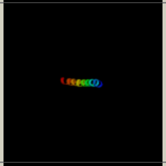
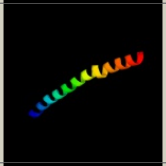
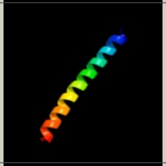
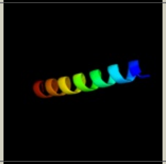
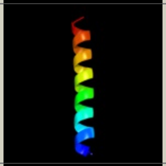
Description	P0A6S5
Date	Wed Jan 25 15:20:16 GMT 2012
Unique Job ID	f5cc17cae7ee79d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xzrA_	Alignment		80.8	5	**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
2	c1ci6B_	Alignment		78.6	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
3	c2yy0D_	Alignment		77.5	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
4	c2e43A_	Alignment		74.6	23	**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
5	c1fosF_	Alignment		72.5	21	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
6	c1ci6A_	Alignment		72.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
7	c2xdjF_	Alignment		71.8	9	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
8	c1fosE_	Alignment		69.8	28	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
9	c1u2uA_	Alignment		69.7	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
10	c3mudA_	Alignment		69.7	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**dna repair protein xrcc4, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
11	c1t2kD_	Alignment		67.5	15	**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

12	c1gk7A_	Alignment		67.4	28	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 1a fragment (1a)
13	c1ce0B_	Alignment		64.9	14	**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
14	c3m9bK_	Alignment		63.0	18	**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
15	c1dh3A_	Alignment		62.3	22	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription factor creb; **PDBTitle:** crystal structure of a creb bzip-cre complex reveals the2 basis for creb faimly selective dimerization and dna3 binding
16	c1cz7C_	Alignment		60.6	23	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**microtubule motor protein ncd; **PDBTitle:** the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
17	d1nkpa_	Alignment		58.6	21	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
18	c1ij3C_	Alignment		57.1	15	**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
19	c1ij3B_	Alignment		57.1	15	**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
20	c1ij2C_	Alignment		56.9	15	**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
21	c1rb1B_	Alignment	not modelled	56.6	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
22	c1swiA_	Alignment	not modelled	56.6	15	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
23	c1rb6C_	Alignment	not modelled	56.6	15	**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
24	c3k7zB_	Alignment	not modelled	56.6	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
25	c1rb1A_	Alignment	not modelled	56.6	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
26	c3k7zA_	Alignment	not modelled	56.6	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
27	c1gd2G_	Alignment	not modelled	56.0	18	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
28	d1ivsa1	Alignment	not modelled	55.8	17	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
						PDB header:transcription

29	c1fmhA_	Alignment	not modelled	55.5	35	**Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
30	d1nkpb_	Alignment	not modelled	55.1	18	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
31	c2gd7B_	Alignment	not modelled	54.5	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hexim1 protein; **PDBTitle:** the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
32	c1ij2B_	Alignment	not modelled	54.0	15	**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
33	c2w6bA_	Alignment	not modelled	53.9	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the trimeric beta-pix coiled-coil2 domain
34	c2o7hF_	Alignment	not modelled	53.0	15	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
35	d2azeb1	Alignment	not modelled	52.4	11	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
36	c2wt7B_	Alignment	not modelled	52.1	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
37	c1wpaA_	Alignment	not modelled	52.1	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** 1.5 angstrom crystal structure of human occludin fragment2 413-522
38	c2j5uB_	Alignment	not modelled	51.9	18	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
39	c2wvrB_	Alignment	not modelled	51.7	15	**PDB header:**replication **Chain:** B: **PDB Molecule:**geminin; **PDBTitle:** human cdt1:geminin complex
40	d1r05a_	Alignment	not modelled	50.8	24	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
41	c1ztaA_	Alignment	not modelled	49.8	20	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
42	c2oqqB_	Alignment	not modelled	49.2	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
43	c2jeeA_	Alignment	not modelled	48.8	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
44	c3n4xB_	Alignment	not modelled	46.2	16	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
45	c2wg6L_	Alignment	not modelled	45.6	17	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
46	c3a5tB_	Alignment	not modelled	45.3	23	**PDB header:**transcription regulator/dna **Chain:** B: **PDB Molecule:**transcription factor mafg; **PDBTitle:** crystal structure of mafg-dna complex
47	c1wt6B_	Alignment	not modelled	44.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**myotonin-protein kinase; **PDBTitle:** coiled-coil domain of dmpk
48	c1xawA_	Alignment	not modelled	44.3	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
49	c3mkxC_	Alignment	not modelled	41.2	14	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
50	d1an2a_	Alignment	not modelled	40.1	18	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
51	c3kinB_	Alignment	not modelled	39.4	16	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**kinesin heavy chain; **PDBTitle:** kinesin (dimeric) from rattus norvegicus
52	c3q4fG_	Alignment	not modelled	39.0	32	**PDB header:**dna binding protein/protein binding **Chain:** G: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of xrcc4/xlf-cernunnos complex
53	c3oa7A_	Alignment	not modelled	38.5	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**head morphogenesis protein, chaotic nuclear migration **PDBTitle:** structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
54	c2w6aB_	Alignment	not modelled	32.8	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
						PDB header:transcription regulation

55	c1junB_	Alignment	not modelled	32.6	21	**Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
56	c3he5A_	Alignment	not modelled	32.3	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip1; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
57	c2wukD_	Alignment	not modelled	32.2	15	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
58	c2zxxA_	Alignment	not modelled	31.8	15	**PDB header:**cell cycle/replication **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of cdt1/geminin complex
59	d1nlwe_	Alignment	not modelled	31.8	17	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
60	c1dipA_	Alignment	not modelled	31.5	15	**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
61	c2x7aB_	Alignment	not modelled	29.7	12	**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
62	d1uklc_	Alignment	not modelled	29.4	25	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
63	d1fxkc_	Alignment	not modelled	29.2	12	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
64	c1x4qA_	Alignment	not modelled	27.3	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 small nuclear ribonucleoprotein prp3; **PDBTitle:** solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
65	c1t6fA_	Alignment	not modelled	26.9	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of the coiled-coil dimerization motif of2 geminin
66	c2a93B_	Alignment	not modelled	26.8	21	**PDB header:**leucine zippers **Chain:** B: **PDB Molecule:**c-myc-max heterodimeric leucine zipper; **PDBTitle:** nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
67	c2v4hA_	Alignment	not modelled	26.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
68	d2e74h1	Alignment	not modelled	25.7	29	**Fold:**Single transmembrane helix **Superfamily:**PetN subunit of the cytochrome b6f complex **Family:**PetN subunit of the cytochrome b6f complex
69	c2e74H_	Alignment	not modelled	25.0	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
70	c2efrB_	Alignment	not modelled	24.2	18	**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
71	c3tlxA_	Alignment	not modelled	24.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 2; **PDBTitle:** crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
72	c2e75H_	Alignment	not modelled	23.6	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
73	c2e76H_	Alignment	not modelled	23.6	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
74	d2oa5a1	Alignment	not modelled	23.5	18	**Fold:**BLRF2-like **Superfamily:**BLRF2-like **Family:**BLRF2-like
75	c1deqO_	Alignment	not modelled	23.3	9	**PDB header:** **PDB COMPND:**
76	d1nlwa_	Alignment	not modelled	23.1	10	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
77	c3he4F_	Alignment	not modelled	22.8	24	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**synzip5; **PDBTitle:** heterospecific coiled-coil pair synzip5:synzip6
78	c3hnwB_	Alignment	not modelled	22.5	15	**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
79	c3ol1A_	Alignment	not modelled	22.4	8	**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
80	c3hizB_	Alignment	not modelled	22.0	10	**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
81	c1jccC_	Alignment	not modelled	21.9	13	**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
82	c1vf5H_	Alignment	not modelled	21.6	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
83	c1vf5U_	Alignment	not modelled	21.6	29	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
84	c1ihqA_	Alignment	not modelled	21.3	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**chimeric peptide glytm1bzip: tropomyosin alpha **PDBTitle:** glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
85	c1l8dB_	Alignment	not modelled	20.7	24	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
86	c2l5gA_	Alignment	not modelled	20.7	13	**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
87	c1hf9B_	Alignment	not modelled	20.4	9	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
88	c3qh9A_	Alignment	not modelled	19.2	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
89	c1ik9B_	Alignment	not modelled	18.2	15	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
90	c2zt9H_	Alignment	not modelled	17.5	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
91	c1p9iA_	Alignment	not modelled	17.1	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cortexillin i/gcn4 hybrid peptide; **PDBTitle:** coiled-coil x-ray structure at 1.17 a resolution
92	c3he4A_	Alignment	not modelled	16.9	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip6; **PDBTitle:** heterospecific coiled-coil pair synzip5:synzip6
93	c1u2uB_	Alignment	not modelled	16.9	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
94	c2d2cU_	Alignment	not modelled	16.8	29	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
95	c2d2cH_	Alignment	not modelled	16.8	29	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
96	c1u0iA_	Alignment	not modelled	16.7	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
97	c2zvnF_	Alignment	not modelled	16.4	17	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p2121212 space group
98	c3a7pB_	Alignment	not modelled	15.8	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
99	c2ke4A_	Alignment	not modelled	14.9	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4