Phyre^2

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Description	P0A8R4
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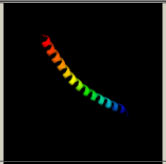
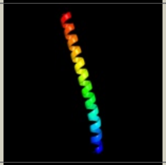
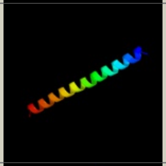
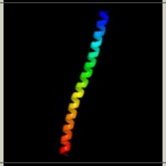
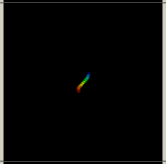
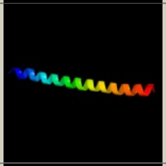
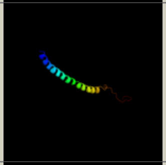
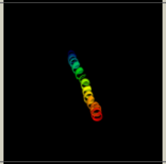
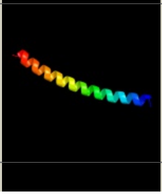
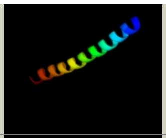
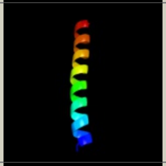
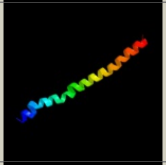
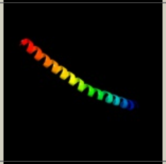
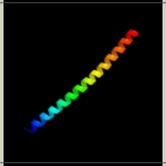
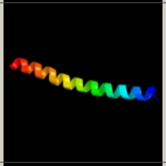
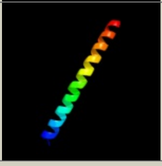
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3efgA_	Alignment		98.1	41	**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
2	c3m06F_	Alignment		93.3	27	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of traf2
3	c2xdjF_	Alignment		92.0	14	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
4	c1gd2G_	Alignment		89.2	17	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
5	c3a7pB_	Alignment		88.9	22	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
6	c1m1jA_	Alignment		87.2	24	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
7	c2ykqC_	Alignment		87.2	21	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
8	c1deqD_	Alignment		86.0	19	**PDB header:** **PDB COMPND:**
9	c1deqF_	Alignment		83.7	15	**PDB header:** **PDB COMPND:**
10	c1deqO_	Alignment		82.8	7	**PDB header:** **PDB COMPND:**
11	c2wt7B_	Alignment		81.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna

12	c1t2kD_	Alignment		81.1	24	**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
13	c1zxaB_	Alignment		80.6	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
14	c3ghgK_	Alignment		80.4	8	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
15	c1ei3E_	Alignment		79.7	12	**PDB header:** **PDB COMPND:**
16	c3m0dC_	Alignment		79.6	30	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1; **PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex
17	c3movB_	Alignment		76.7	25	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
18	c1fosF_	Alignment		73.6	24	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
19	c1ci6A_	Alignment		73.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
20	c3m9bK_	Alignment		73.1	29	**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
21	c1aq5C_	Alignment	not modelled	72.6	20	**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
22	c1n73A_	Alignment	not modelled	72.6	18	**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
23	c2hpcF_	Alignment	not modelled	72.4	12	**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.
24	c2z5hB_	Alignment	not modelled	72.0	15	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin **PDBTitle:** crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
25	c1ei3C_	Alignment	not modelled	64.9	15	**PDB header:** **PDB COMPND:**
26	c2e43A_	Alignment	not modelled	64.2	21	**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
27	c1x8yA_	Alignment	not modelled	63.1	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
28	c2v4hA_	Alignment	not modelled	62.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
						PDB header:tnf signaling

29	c1ca9D_	Alignment	not modelled	62.6	19	**Chain:** D: **PDB Molecule:**protein (tnf receptor associated factor 2); **PDBTitle:** structure of tnf receptor associated factor 2 in complex2 with a peptide from tnf-r2
30	c1n73C_	Alignment	not modelled	61.5	14	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
31	c2fxmB_	Alignment	not modelled	58.3	15	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
32	c1gk4A_	Alignment	not modelled	55.6	14	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
33	c3dtpA_	Alignment	not modelled	53.4	29	**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
34	c2zdiA_	Alignment	not modelled	52.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**prefoldin subunit beta; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
35	c1fllA_	Alignment	not modelled	50.7	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** molecular basis for cd40 signaling mediated by traf3
36	c1fosE_	Alignment	not modelled	48.8	18	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
37	c2d3eD_	Alignment	not modelled	47.6	23	**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
38	c2xzrA_	Alignment	not modelled	47.5	21	**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
39	c3mkxC_	Alignment	not modelled	47.4	24	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
40	c3bvhE_	Alignment	not modelled	47.3	24	**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
41	c3cvfA_	Alignment	not modelled	47.1	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
42	c3ghgD_	Alignment	not modelled	46.9	20	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
43	c2a93B_	Alignment	not modelled	45.2	22	**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
44	c2zdiC_	Alignment	not modelled	42.0	15	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
45	c1lwuH_	Alignment	not modelled	39.7	18	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from lamprey fibrinogen complexed with2 the peptide gly-his-arg-pro-amide
46	c1junB_	Alignment	not modelled	39.3	24	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
47	c3a5tB_	Alignment	not modelled	38.7	24	**PDB header:**transcription regulator/dna **Chain:** B: **PDB Molecule:**transcription factor mafg; **PDBTitle:** crystal structure of mafg-dna complex
48	c2fxpA_	Alignment	not modelled	38.4	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike glycoprotein; **PDBTitle:** solution structure of the sars-coronavirus hr2 domain
49	c2efrB_	Alignment	not modelled	37.5	17	**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
50	c3u59C_	Alignment	not modelled	37.5	11	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
51	c3hizB_	Alignment	not modelled	36.4	12	**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
52	c1cosB_	Alignment	not modelled	36.4	48	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
53	c1cosC_	Alignment	not modelled	36.4	48	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
54	c1cosA_	Alignment	not modelled	36.4	48	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine;

		Alignment	not modelled			**PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
55	c3m9hB_	Alignment	not modelled	35.9	29	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
56	c1c1gA_	Alignment	not modelled	35.6	16	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
57	c3ojaB_	Alignment	not modelled	34.7	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
58	c1coiA_	Alignment	not modelled	34.3	39	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
59	c3na7A_	Alignment	not modelled	31.1	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
60	c3bvhC_	Alignment	not modelled	30.8	16	**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
61	d1fxkc_	Alignment	not modelled	30.1	18	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
62	c2xgjA_	Alignment	not modelled	29.1	17	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
63	c3u1aC_	Alignment	not modelled	28.9	19	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
64	c1l4aD_	Alignment	not modelled	28.8	6	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**s-snap25 fusion protein; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
65	c2akfC_	Alignment	not modelled	27.3	16	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
66	c2akfA_	Alignment	not modelled	27.3	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
67	c3h32A_	Alignment	not modelled	27.1	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of d-dimer from human fibrin complexed with gly-his-2 arg-pro-tyr-amide
68	c1pl5A_	Alignment	not modelled	26.0	25	**PDB header:**dna binding protein/transcription **Chain:** A: **PDB Molecule:**regulatory protein sir4; **PDBTitle:** crystal structure analysis of the sir4p c-terminal coiled2 coil
69	c3ci9B_	Alignment	not modelled	26.0	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
70	c1ce9A_	Alignment	not modelled	25.4	29	**PDB header:**helix capping **Chain:** A: **PDB Molecule:**protein (gcn4-pmse); **PDBTitle:** helix capping in the gcn4 leucine zipper
71	c1ce9B_	Alignment	not modelled	25.4	29	**PDB header:**helix capping **Chain:** B: **PDB Molecule:**protein (gcn4-pmse); **PDBTitle:** helix capping in the gcn4 leucine zipper
72	c1ce9C_	Alignment	not modelled	25.4	29	**PDB header:**helix capping **Chain:** C: **PDB Molecule:**protein (gcn4-pmse); **PDBTitle:** helix capping in the gcn4 leucine zipper
73	c1ce9D_	Alignment	not modelled	25.4	29	**PDB header:**helix capping **Chain:** D: **PDB Molecule:**protein (gcn4-pmse); **PDBTitle:** helix capping in the gcn4 leucine zipper
74	c1nyhA_	Alignment	not modelled	25.2	25	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**regulatory protein sir4; **PDBTitle:** crystal structure of the coiled-coil dimerization motif of sir4
75	c3a2aC_	Alignment	not modelled	25.0	29	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**voltage-gated hydrogen channel 1; **PDBTitle:** the structure of the carboxyl-terminal domain of the human voltage-2 gated proton channel hv1
76	c1kwwC_	Alignment	not modelled	25.0	22	**PDB header:**immune system, sugar binding protein **Chain:** C: **PDB Molecule:**mannose-binding protein a; **PDBTitle:** rat mannose protein a complexed with a-me-fuc.
77	c2akfB_	Alignment	not modelled	24.9	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
78	c2ba2A_	Alignment	not modelled	24.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0134 protein mpn010; **PDBTitle:** crystal structure of the duf16 domain of mpn010 from2 mycoplasma pneumoniae
79	c1mofA_	Alignment	not modelled	23.7	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**moloney murine leukemia virus p15; **PDBTitle:** coat protein
80	c2pnvA_	Alignment	not modelled	23.5	24	**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
81	c1bf5A_	Alignment	not modelled	23.1	10	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
82	c1w5jB_	Alignment	not modelled	23.0	21	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
83	c3ol1A_	Alignment	not modelled	22.4	17	**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
84	c2x7aB_	Alignment	not modelled	22.2	14	**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
85	c1l8dB_	Alignment	not modelled	22.1	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
86	c1yvlB_	Alignment	not modelled	22.1	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
87	c2wq1A_	Alignment	not modelled	21.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with three ixxntxx motifs2 coordinating bromide
88	c2wq3A_	Alignment	not modelled	21.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with three ixxntxx motifs2 coordinating chloride and nitrate
89	c2eqbC_	Alignment	not modelled	21.7	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
90	c1w5jA_	Alignment	not modelled	21.4	23	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
91	c1w5jD_	Alignment	not modelled	21.4	23	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
92	c1w5jC_	Alignment	not modelled	21.4	23	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
93	c1y4mC_	Alignment	not modelled	21.3	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**herv-frd_6p24.1 provirus ancestral env polyprotein; **PDBTitle:** crystal structure of human endogenous retrovirus herv-frd envelope2 protein (syncitin-2)
94	c1gcmA_	Alignment	not modelled	20.9	19	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
95	c1w5kB_	Alignment	not modelled	20.7	23	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
96	c1w5kA_	Alignment	not modelled	20.7	23	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
97	c1w5kC_	Alignment	not modelled	20.7	23	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
98	c1w5kD_	Alignment	not modelled	20.7	23	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
99	c1by0A_	Alignment	not modelled	20.3	28	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen