


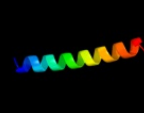

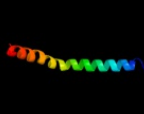

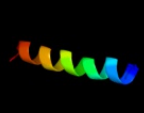

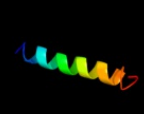

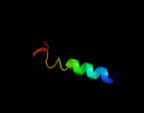
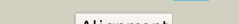

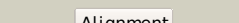

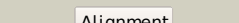
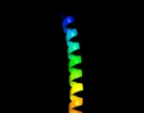


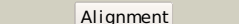
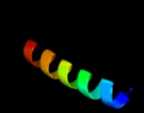
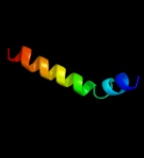



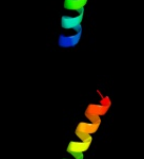


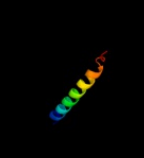
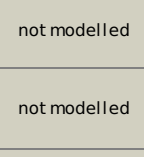


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1a92B_	 Alignment		52.0	21	PDB header: leucine zipper Chain: B: PDB Molecule: delta antigen; PDBTitle: oligomerization domain of hepatitis delta antigen
2	c1ci6B_	 Alignment		50.5	21	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
3	c3errB_	 Alignment		49.0	18	PDB header: ligase Chain: B: PDB Molecule: fusion protein of microtubule binding domain from PDBTitle: microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
4	c1u0iA_	 Alignment		42.7	24	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
5	c3kinB_	 Alignment		40.8	16	PDB header: motor protein Chain: B: PDB Molecule: kinesin heavy chain; PDBTitle: kinesin (dimeric) from rattus norvegicus
6	d1u58a2	 Alignment		39.2	19	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
7	d1uuja_	 Alignment		35.2	35	Fold: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain Superfamily: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain Family: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain
8	c1u2uA_	 Alignment		34.3	12	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
9	c3n4xB_	 Alignment		33.8	14	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
10	c2l5gB_	 Alignment		30.9	27	PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
11	c1zxaB_	 Alignment		30.5	10	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

12	c3eh0C_	Alignment		30.3	10	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
13	c1hf9B_	Alignment		29.9	13	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
14	c2xzaA_	Alignment		28.5	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
15	c2wg6L_	Alignment		27.5	15	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
16	c1ihqA_	Alignment		27.5	17	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
17	c1debA_	Alignment		26.3	8	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from2 apc
18	c2kncB_	Alignment		26.3	18	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
19	c3kltB_	Alignment		24.6	9	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
20	c3m9bK_	Alignment		23.5	10	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	d1k1fa_	Alignment	not modelled	23.1	29	Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
22	c1by0A_	Alignment	not modelled	22.3	23	PDB header: rna binding protein Chain: A: PDB Molecule: protein (hepatitis delta antigen); PDBTitle: n-terminal leucine-repeat region of hepatitis delta antigen
23	d1fewa_	Alignment	not modelled	21.4	11	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
24	c3sjaG_	Alignment	not modelled	20.1	15	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
25	c3gw6F_	Alignment	not modelled	18.5	32	PDB header: chaperone Chain: F: PDB Molecule: endo-n-acetylneuraminidase; PDBTitle: intramolecular chaperone
26	c3swfA_	Alignment	not modelled	18.5	18	PDB header: transport protein Chain: A: PDB Molecule: cgm-p-gated cation channel alpha-1; PDBTitle: cnga1 621-690 containing clz domain
27	d1f6ga_	Alignment	not modelled	17.6	10	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
28	c2ke4A_	Alignment	not modelled	17.4	14	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
						PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl]

29	c2iu9C_	Alignment	not modelled	17.1	21	glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
30	c3he5D_	Alignment	not modelled	16.8	18	PDB header: de novo protein Chain: D: PDB Molecule: synzip2; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1
31	c2w6aB_	Alignment	not modelled	16.3	17	PDB header: signaling protein Chain: B: PDB Molecule: arf gtpase-activating protein git1; PDBTitle: x-ray structure of the dimeric git1 coiled-coil domain
32	dlivsaa1	Alignment	not modelled	15.7	19	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
33	c3sjbC_	Alignment	not modelled	14.2	15	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
34	c3a7pB_	Alignment	not modelled	14.2	15	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
35	c1junB_	Alignment	not modelled	13.6	31	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
36	c1gk4A_	Alignment	not modelled	13.4	11	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
37	c3qngD_	Alignment	not modelled	13.1	21	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
38	c3he4A_	Alignment	not modelled	12.5	17	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
39	c2e43A_	Alignment	not modelled	12.5	19	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
40	c2gd5B_	Alignment	not modelled	12.5	12	PDB header: protein transport Chain: B: PDB Molecule: charged multivesicular body protein 3; PDBTitle: structural basis for budding by the escrtiii factor chmp3
41	c3cvfA_	Alignment	not modelled	11.8	15	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
42	dluklc_	Alignment	not modelled	11.1	5	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
43	c1kddC_	Alignment	not modelled	10.4	19	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
44	c1kddF_	Alignment	not modelled	10.1	19	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
45	c3movB_	Alignment	not modelled	10.0	10	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
46	c1gk7A_	Alignment	not modelled	9.5	21	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
47	c2ergA_	Alignment	not modelled	9.5	23	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
48	c1t3ja_	Alignment	not modelled	9.3	20	PDB header: membrane protein Chain: A: PDB Molecule: mitofusin 1; PDBTitle: mitofusin domain hr2 v686m/i708m mutant
49	dlk4ta1	Alignment	not modelled	9.1	19	Fold: Long alpha-hairpin Superfamily: Eukaryotic DNA topoisomerase I, dispensable insert domain Family: Eukaryotic DNA topoisomerase I, dispensable insert domain
50	dllef1c_	Alignment	not modelled	9.0	26	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Moesin tail domain Family: Moesin tail domain
51	c3hnnwB_	Alignment	not modelled	8.9	5	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
52	c3pmoA_	Alignment	not modelled	8.9	20	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; PDBTitle: the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
53	c1x8ya_	Alignment	not modelled	8.5	5	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
54	dltbga_	Alignment	not modelled	8.3	18	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like

						Family:WD40-repeat
55	c2hpcF_	Alignment	not modelled	8.3	3	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.
56	c1kddA_	Alignment	not modelled	8.1	17	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
57	c2voyB_	Alignment	not modelled	8.1	23	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
58	c1wazA_	Alignment	not modelled	7.9	16	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
59	c3frvA_	Alignment	not modelled	7.9	15	PDB header: protein transport Chain: A: PDB Molecule: charged multivesicular body protein 3; PDBTitle: structure of human chmp3 (residues 1-150)
60	c1ci6A_	Alignment	not modelled	7.6	8	PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
61	c3a0hl_	Alignment	not modelled	7.5	19	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of i-substituted photosystem ii complex
62	c3a0hL_	Alignment	not modelled	7.5	19	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of i-substituted photosystem ii complex
63	c1kd9C_	Alignment	not modelled	7.3	22	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
64	c1kd9F_	Alignment	not modelled	7.3	22	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
65	c1kd9A_	Alignment	not modelled	7.3	22	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
66	c1mofA_	Alignment	not modelled	7.3	23	PDB header: viral protein Chain: A: PDB Molecule: moloney murine leukemia virus p15; PDBTitle: coat protein
67	c2lf0A_	Alignment	not modelled	7.3	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yibl; PDBTitle: solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
68	c2z5hB_	Alignment	not modelled	7.1	19	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
69	c1aq5C_	Alignment	not modelled	6.7	11	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
70	c3a7oB_	Alignment	not modelled	6.6	14	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of the coiled-coil domain of2 saccharomyces cerevisiae atg16
71	c2wvrB_	Alignment	not modelled	6.6	9	PDB header: replication Chain: B: PDB Molecule: geminin; PDBTitle: human cdt1:geminin complex
72	c1gk6B_	Alignment	not modelled	6.6	13	PDB header: vimentin Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
73	c2l5gA_	Alignment	not modelled	6.5	28	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
74	d1ab4a_	Alignment	not modelled	6.5	10	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
75	c2yy0D_	Alignment	not modelled	6.4	17	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
76	d1vp7a_	Alignment	not modelled	6.4	12	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
77	c2h3oA_	Alignment	not modelled	6.3	19	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
78	c3ifzA_	Alignment	not modelled	6.3	13	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of the first part of the mycobacterium

						tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
79	c2a93B	Alignment	not modelled	6.2	17	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
80	c1rb6C	Alignment	not modelled	6.1	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
81	c3k7zA	Alignment	not modelled	6.1	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
82	c1rb1A	Alignment	not modelled	6.1	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
83	c3k7zB	Alignment	not modelled	6.1	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
84	c1rb1B	Alignment	not modelled	6.1	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
85	c1swiA	Alignment	not modelled	6.1	15	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with2 benzene
86	c1ij3B	Alignment	not modelled	5.9	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
87	c1ij3C	Alignment	not modelled	5.9	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
88	c1dipA	Alignment	not modelled	5.9	13	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
89	c2k6sB	Alignment	not modelled	5.9	21	PDB header: protein transport Chain: B: PDB Molecule: rab11fip2 protein; PDBTitle: structure of rab11-fip2 c-terminal coiled-coil domain
90	c2wl2B	Alignment	not modelled	5.8	10	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
91	c2pnvA	Alignment	not modelled	5.8	7	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
92	c1kd8C	Alignment	not modelled	5.8	20	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
93	c1kd8A	Alignment	not modelled	5.8	20	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
94	c1kd8F	Alignment	not modelled	5.8	20	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
95	c1ij2C	Alignment	not modelled	5.7	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
96	d2jn6a1	Alignment	not modelled	5.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
97	c3e98B	Alignment	not modelled	5.5	10	PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
98	d1wmib1	Alignment	not modelled	5.5	9	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: RelB-like Family: RelB-like
99	d1vcsa1	Alignment	not modelled	5.5	8	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins