
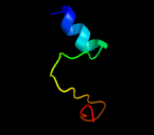
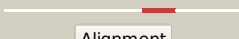
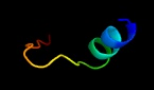
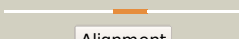
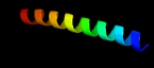

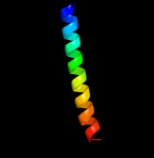



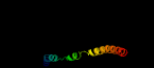

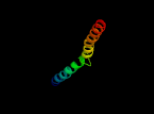

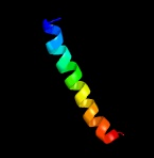

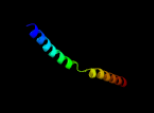

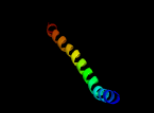


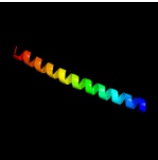
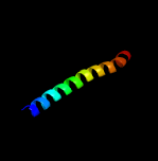
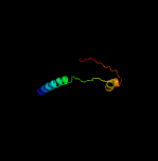

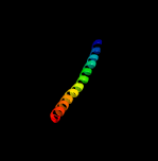

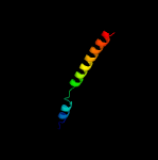
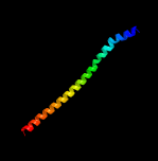
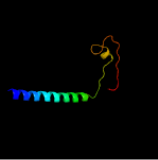


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1024 (- )_1145862_1146548
Date	Wed Jul 31 22:05:09 BST 2019
Unique Job ID	63bf769ec2181981

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5z2wB_</a>	 Alignment		95.9	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> crystal structure of the bacterial cell division protein ftsq and ftsb
2	<a href="#">c6h9nB_</a>	 Alignment		93.3	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
3	<a href="#">c5fv8A_</a>	 Alignment		89.0	43	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
4	<a href="#">c5fv8B_</a>	 Alignment		88.9	43	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
5	<a href="#">d2pila_</a>	 Alignment		88.6	9	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pilin
6	<a href="#">c6b8hb_</a>	 Alignment		86.5	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> atp synthase subunit alpha, mitochondrial; <b>PDBTitle:</b> mosaic model of yeast mitochondrial atp synthase monomer
7	<a href="#">c5t4oJ_</a>	 Alignment		84.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> atp synthase subunit b; <b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1
8	<a href="#">c1u2uA_</a>	 Alignment		84.0	30	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> nmr solution structure of a designed heterodimeric leucine2 zipper
9	<a href="#">c5wq4F_</a>	 Alignment		83.8	16	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> optneurin; <b>PDBTitle:</b> crystal structure of optn and linear diubiquitin complex
10	<a href="#">c3sokB_</a>	 Alignment		81.9	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> fimbrial protein; <b>PDBTitle:</b> dichelobacter nodosus pilin fima
11	<a href="#">c2yy0D_</a>	 Alignment		79.7	10	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens

12	<a href="#">c2xzfA_</a>	Alignment		78.6	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
13	<a href="#">c5vgzC_</a>	Alignment		78.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> conformational landscape of the p28-bound human proteasome regulatory2 particle
14	<a href="#">c5tuvB_</a>	Alignment		78.4	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f5; <b>PDBTitle:</b> crystal structure of the e2f5-dp1-p107 ternary complex
15	<a href="#">d1oqwa_</a>	Alignment		78.4	16	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pilin
16	<a href="#">c1cz7C_</a>	Alignment		77.8	14	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule motor protein ncd; <b>PDBTitle:</b> the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
17	<a href="#">c6fkip_</a>	Alignment		76.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit beta, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
18	<a href="#">c5b83B_</a>	Alignment		75.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
19	<a href="#">c6fkip_</a>	Alignment		74.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> P: <b>PDB Molecule:</b> atp synthase subunit c, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
20	<a href="#">c5tuuB_</a>	Alignment		74.2	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f4; <b>PDBTitle:</b> crystal structure of the e2f4-dp1 coiled coil and marked-box domains
21	<a href="#">c1fmhA_</a>	Alignment	not modelled	72.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> nmr solution structure of a designed heterodimeric leucine2 zipper
22	<a href="#">c6iu3A_</a>	Alignment	not modelled	70.4	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
23	<a href="#">c2lw1A_</a>	Alignment	not modelled	69.3	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein uup; <b>PDBTitle:</b> the c-terminal domain of the uup protein is a dna-binding coiled coil2 motif
24	<a href="#">c5wdaL_</a>	Alignment	not modelled	69.3	8	<b>PDB header:</b> protein transport <b>Chain:</b> L: <b>PDB Molecule:</b> general secretion pathway protein g; <b>PDBTitle:</b> structure of the pulg pseudopilus
25	<a href="#">c2m7gA_</a>	Alignment	not modelled	68.8	10	<b>PDB header:</b> cell adhesion, structural protein, elect <b>Chain:</b> A: <b>PDB Molecule:</b> geopilin domain 1 protein; <b>PDBTitle:</b> structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
26	<a href="#">c4etpA_</a>	Alignment	not modelled	68.2	22	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kar3; <b>PDBTitle:</b> c-terminal motor and motor homology domain of kar3vik1 fused to a2 synthetic heterodimeric coiled coil
27	<a href="#">c6gv9K_</a>	Alignment	not modelled	67.7	11	<b>PDB header:</b> protein fibril <b>Chain:</b> K: <b>PDB Molecule:</b> prepilin peptidase-dependent protein d; <b>PDBTitle:</b> structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehc)
28	<a href="#">c6e2jB_</a>	Alignment	not modelled	67.1	15	<b>PDB header:</b> protein fibril <b>Chain:</b> B: <b>PDB Molecule:</b> keratin, type i cytoskeletal 10; <b>PDBTitle:</b> crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b

29	<a href="#">c3hnwB_</a>	Alignment	not modelled	66.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
30	<a href="#">c3kinB_</a>	Alignment	not modelled	66.3	15	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin heavy chain; <b>PDBTitle:</b> kinesin (dimeric) from rattus norvegicus
31	<a href="#">c1ij2C_</a>	Alignment	not modelled	65.8	28	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
32	<a href="#">c1u0iA_</a>	Alignment	not modelled	65.6	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> iaal-e3; <b>PDBTitle:</b> iaal-e3/k3 heterodimer
33	<a href="#">c4u4pA_</a>	Alignment	not modelled	65.5	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 2; <b>PDBTitle:</b> crystal structure of the human condensin smc hinge domain heterodimer2 with short coiled coils
34	<a href="#">c1swiA_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with benzene
35	<a href="#">c3k7zA_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
36	<a href="#">c3k7zB_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
37	<a href="#">c1rb6C_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
38	<a href="#">c1rb1A_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
39	<a href="#">c1rb1B_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
40	<a href="#">c1ij3B_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvs1 coiled-coil trimer with serine at the a(16)2 position
41	<a href="#">c1ij3C_</a>	Alignment	not modelled	65.3	28	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvs1 coiled-coil trimer with serine at the a(16)2 position
42	<a href="#">c2wukD_</a>	Alignment	not modelled	65.2	19	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
43	<a href="#">c5zk1A_</a>	Alignment	not modelled	65.0	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic amp-responsive element-binding protein 1; <b>PDBTitle:</b> crystal structure of the crtc2(semet)-creb-cre complex
44	<a href="#">c2o7hF_</a>	Alignment	not modelled	64.9	28	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> crystal structure of trimeric coiled coil gcn4 leucine zipper
45	<a href="#">c1ij2B_</a>	Alignment	not modelled	62.9	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
46	<a href="#">c5jvpC_</a>	Alignment	not modelled	62.8	13	<b>PDB header:</b> motor protein <b>Chain:</b> C: <b>PDB Molecule:</b> chimera protein of centromere-associated protein e and <b>PDBTitle:</b> the neck-linker and alpha 7 helix of homo sapiens cenp-e
47	<a href="#">c4u5tB_</a>	Alignment	not modelled	62.2	24	<b>PDB header:</b> transcription/transcription inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> vbp leucine zipper; <b>PDBTitle:</b> crystal structure of vbp leucine zipper with bound arylstibonic acid
48	<a href="#">c4dzmA_</a>	Alignment	not modelled	60.8	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil peptide cc-di; <b>PDBTitle:</b> a de novo designed coiled coil cc-di
49	<a href="#">c4dzmB_</a>	Alignment	not modelled	60.8	32	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled-coil peptide cc-di; <b>PDBTitle:</b> a de novo designed coiled coil cc-di
50	<a href="#">c3m9bK_</a>	Alignment	not modelled	60.3	24	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
51	<a href="#">c2jeeA_</a>	Alignment	not modelled	60.1	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein zapb; <b>PDBTitle:</b> xray structure of e. coli yiu
52	<a href="#">c3iynQ_</a>	Alignment	not modelled	59.9	23	<b>PDB header:</b> virus <b>Chain:</b> Q: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
53	<a href="#">c3mkxC_</a>	Alignment	not modelled	59.6	17	<b>PDB header:</b> antiviral protein <b>Chain:</b> C: <b>PDB Molecule:</b> bone marrow stromal antigen 2; <b>PDBTitle:</b> crystal structure of bst2/tetherin
54	<a href="#">c2v4hA_</a>	Alignment	not modelled	59.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> nemo cc2-lz domain - 1d5 darpin complex

55	<a href="#">c1dh3A</a>	Alignment	not modelled	57.6	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor creb; <b>PDBTitle:</b> crystal structure of a creb bzip-cre complex reveals the2 basis for creb faintly selective dimerization and dna3 binding
56	<a href="#">c1kddC</a>	Alignment	not modelled	57.5	35	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
57	<a href="#">c1ysaD</a>	Alignment	not modelled	57.2	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> protein (gcn4); <b>PDBTitle:</b> the gcn4 basic region leucine zipper binds dna as a dimer2 of uninterrupted alpha helices: crystal structure of the3 protein-dna complex
58	<a href="#">c1kddF</a>	Alignment	not modelled	57.2	35	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
59	<a href="#">c1kddA</a>	Alignment	not modelled	57.2	35	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
60	<a href="#">c4aniA</a>	Alignment	not modelled	55.9	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein grpe; <b>PDBTitle:</b> structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
61	<a href="#">c1ce0B</a>	Alignment	not modelled	55.9	16	<b>PDB header:</b> hiv-1 envelope protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (leucine zipper model h38-p1); <b>PDBTitle:</b> trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
62	<a href="#">c3ra3D</a>	Alignment	not modelled	53.4	31	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> p2f; <b>PDBTitle:</b> crystal structure of a section of a de novo design gigadalton protein2 fibre
63	<a href="#">c1ztaA</a>	Alignment	not modelled	53.1	26	<b>PDB header:</b> dna-binding motif <b>Chain:</b> A: <b>PDB Molecule:</b> leucine zipper monomer; <b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide
64	<a href="#">c5w3dB</a>	Alignment	not modelled	52.7	15	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein claret segregational; <b>PDBTitle:</b> the structure of kinesin-14 wild-type ncd-actin dimer
65	<a href="#">c4ug1A</a>	Alignment	not modelled	50.6	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> gpsb n-terminal domain
66	<a href="#">c5b83C</a>	Alignment	not modelled	50.1	19	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
67	<a href="#">c6gqaD</a>	Alignment	not modelled	49.9	8	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> cell division regulator s. pneumoniae gpsb
68	<a href="#">c1dipA</a>	Alignment	not modelled	49.1	29	<b>PDB header:</b> acetylation <b>Chain:</b> A: <b>PDB Molecule:</b> delta-sleep-inducing peptide immunoreactive <b>PDBTitle:</b> the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
69	<a href="#">c4e61A</a>	Alignment	not modelled	48.9	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein bim1; <b>PDBTitle:</b> crystal structure of the eb1-like motif of bim1p
70	<a href="#">c2kncB</a>	Alignment	not modelled	48.7	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
71	<a href="#">c2zvnF</a>	Alignment	not modelled	48.6	15	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> F: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> nemo cozi domain incomplex with diubiquitin in p212121 space group
72	<a href="#">c1fosF</a>	Alignment	not modelled	47.2	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> F: <b>PDB Molecule:</b> c-jun proto-oncogene protein; <b>PDBTitle:</b> two human c-fos:c-jun:dna complexes
73	<a href="#">c2e43A</a>	Alignment	not modelled	46.1	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ccaat/enhancer-binding protein beta; <b>PDBTitle:</b> crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
74	<a href="#">c2w6bA</a>	Alignment	not modelled	44.4	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 7; <b>PDBTitle:</b> crystal structure of the trimeric beta-pix coiled-coil2 domain
75	<a href="#">c5m9eA</a>	Alignment	not modelled	43.4	10	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule integrity protein mal3; <b>PDBTitle:</b> interactions between the mal3 eb1-like domain and dis1
76	<a href="#">c6nr5</a>	Alignment	not modelled	43.3	15	<b>PDB header:</b> chaperone <b>Chain:</b> 5: <b>PDB Molecule:</b> prefoldin subunit 5; <b>PDBTitle:</b> htrc-hpfd class2
77	<a href="#">c4b86A</a>	Alignment	not modelled	43.2	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> male-specific lethal 1 homolog; <b>PDBTitle:</b> crystal structure of the msl1-msl2 complex (3.5a)
78	<a href="#">c2gd7B</a>	Alignment	not modelled	42.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hexim1 protein; <b>PDBTitle:</b> the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
79	<a href="#">c1t6fA</a>	Alignment	not modelled	42.4	23	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> geminin; <b>PDBTitle:</b> crystal structure of the coiled-coil dimerization motif of2 geminin
						<b>PDB header:</b> structural protein

80	<a href="#">c3swkB_</a>	Alignment	not modelled	42.3	21	<b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin coil1b fragment
81	<a href="#">c3w8vB_</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4n coiled coil peptide; <b>PDBTitle:</b> crystal structure analysis of the synthetic gcn4 coiled coil peptide
82	<a href="#">c3w8vC_</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4n coiled coil peptide; <b>PDBTitle:</b> crystal structure analysis of the synthetic gcn4 coiled coil peptide
83	<a href="#">c3w8vA_</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4n coiled coil peptide; <b>PDBTitle:</b> crystal structure analysis of the synthetic gcn4 coiled coil peptide
84	<a href="#">c1t2kD_</a>	Alignment	not modelled	41.9	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> cyclic-amp-dependent transcription factor atf-2; <b>PDBTitle:</b> structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
85	<a href="#">c2wg6L_</a>	Alignment	not modelled	41.7	25	<b>PDB header:</b> transcription,hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> general control protein gcn4, proteasome-activating <b>PDBTitle:</b> proteasome-activating nucleotidase (pan) n-domain (57-134) from2 archaeoglobus fulgidus fused to gcn4, p61a mutant
86	<a href="#">c1fosE_</a>	Alignment	not modelled	41.4	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> p55-c-fos proto-oncogene protein; <b>PDBTitle:</b> two human c-fos:c-jun:dna complexes
87	<a href="#">c1kd9A_</a>	Alignment	not modelled	40.2	31	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
88	<a href="#">c1kd9F_</a>	Alignment	not modelled	40.2	31	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
89	<a href="#">c1kd9C_</a>	Alignment	not modelled	40.2	31	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
90	<a href="#">d1ivsa1</a>	Alignment	not modelled	40.0	22	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Valyl-tRNA synthetase (ValRS) C-terminal domain
91	<a href="#">c5h69B_</a>	Alignment	not modelled	39.6	24	<b>PDB header:</b> dna binding protein, cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of an asymmetric dimer of the geobacillus2 stearothermophilus smc hinge domain
92	<a href="#">c2eqbC_</a>	Alignment	not modelled	38.9	15	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> C: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
93	<a href="#">c4pxjB_</a>	Alignment	not modelled	38.8	29	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> c-jun-amino-terminal kinase-interacting protein 3; <b>PDBTitle:</b> crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
94	<a href="#">c4dznB_</a>	Alignment	not modelled	38.3	26	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
95	<a href="#">c4dznC_</a>	Alignment	not modelled	38.3	26	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
96	<a href="#">c4dznA_</a>	Alignment	not modelled	38.3	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
97	<a href="#">c3q4fG_</a>	Alignment	not modelled	36.6	13	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein xrcc4; <b>PDBTitle:</b> crystal structure of xrcc4/xf-cernunnos complex
98	<a href="#">c2j5uB_</a>	Alignment	not modelled	35.9	29	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
99	<a href="#">c4ug3C_</a>	Alignment	not modelled	35.7	8	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> b. subtilis gpsb n-terminal domain
100	<a href="#">c1kd8A_</a>	Alignment	not modelled	35.2	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
101	<a href="#">c1kd8C_</a>	Alignment	not modelled	35.2	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
102	<a href="#">c1kd8F_</a>	Alignment	not modelled	35.2	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
103	<a href="#">c6n6sB_</a>	Alignment	not modelled	35.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tnfaip3-interacting protein 1; <b>PDBTitle:</b> crystal structure of abin-1 uban
104	<a href="#">c3qh9A_</a>	Alignment	not modelled	33.8	27	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> liprin-beta-2; <b>PDBTitle:</b> human liprin-beta2 coiled-coil

105	<a href="#">c1ci6A_</a>	Alignment	not modelled	33.5	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor atf-4; <b>PDBTitle:</b> transcription factor atf4-c/ebp beta bzip heterodimer
106	<a href="#">c6h9oB_</a>	Alignment	not modelled	33.4	21	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
107	<a href="#">c2xdjC_</a>	Alignment	not modelled	33.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein ybgf; <b>PDBTitle:</b> crystal structure of the n-terminal domain of e.coli ybgf
108	<a href="#">c6h9mA_</a>	Alignment	not modelled	33.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil domain-containing protein 90b, mitochondrial, <b>PDBTitle:</b> coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
109	<a href="#">c2w6aB_</a>	Alignment	not modelled	32.8	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> arf gtpase-activating protein git1; <b>PDBTitle:</b> x-ray structure of the dimeric git1 coiled-coil domain
110	<a href="#">c1wt6B_</a>	Alignment	not modelled	32.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> myotonin-protein kinase; <b>PDBTitle:</b> coiled-coil domain of dmpk
111	<a href="#">c5vgzF_</a>	Alignment	not modelled	31.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> conformational landscape of the p28-bound human proteasome regulatory2 particle
112	<a href="#">c3tnuA_</a>	Alignment	not modelled	31.9	21	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 14; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
113	<a href="#">c4uzxA_</a>	Alignment	not modelled	31.9	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein tho1; <b>PDBTitle:</b> high-resolution nmr structures of the domains of saccharomyces2 cerevisiae tho1
114	<a href="#">c3ra3B_</a>	Alignment	not modelled	31.8	33	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> p2f; <b>PDBTitle:</b> crystal structure of a section of a de novo design gigadalton protein2 fibre
115	<a href="#">c1a92B_</a>	Alignment	not modelled	31.4	26	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> delta antigen; <b>PDBTitle:</b> oligomerization domain of hepatitis delta antigen
116	<a href="#">c6h9oD_</a>	Alignment	not modelled	30.6	23	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
117	<a href="#">c3nmdA_</a>	Alignment	not modelled	29.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp dependent protein kinase; <b>PDBTitle:</b> crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
118	<a href="#">c2xdjF_</a>	Alignment	not modelled	29.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein ybgf; <b>PDBTitle:</b> crystal structure of the n-terminal domain of e.coli ybgf
119	<a href="#">c1ci6B_</a>	Alignment	not modelled	29.3	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor c/ebp beta; <b>PDBTitle:</b> transcription factor atf4-c/ebp beta bzip heterodimer
120	<a href="#">c2x7aB_</a>	Alignment	not modelled	29.3	24	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> bone marrow stromal antigen 2; <b>PDBTitle:</b> structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain