
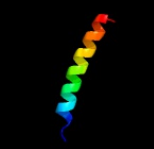

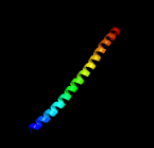



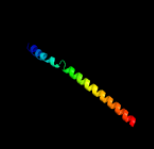





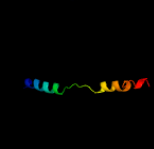

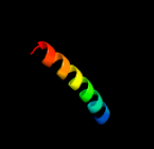
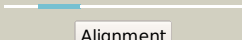

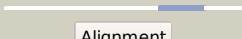
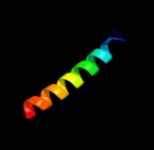
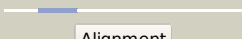



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2548A\_(RVBD2548A)\_2869263\_2869637  
 Date Wed Aug 7 12:50:18 BST 2019  
 Unique Job ID ddeda1214f98a036

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1coiA_</a>	 Alignment		78.6	52	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coil-vald; <b>PDBTitle:</b> designed trimeric coiled coil-vald
2	<a href="#">c3cvfA_</a>	 Alignment		61.0	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> homer protein homolog 3; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer3
3	<a href="#">c6h9mA_</a>	 Alignment		50.6	26	<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
4	<a href="#">c5xauC_</a>	 Alignment		43.2	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> laminin subunit gamma-1; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511
5	<a href="#">c6dmpA_</a>	 Alignment		37.3	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed orthogonal protein dhd13_xaaa_a; <b>PDBTitle:</b> de novo design of a protein heterodimer with specificity mediated by2 hydrogen bond networks
6	<a href="#">c5uxtB_</a>	 Alignment		35.9	48	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
7	<a href="#">c4widA_</a>	 Alignment		34.6	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> rhul123; <b>PDBTitle:</b> crystal structure of the immediate-early 1 protein (ie1) at 2.312 angstrom (tetragonal form after crystal dehydration)
8	<a href="#">c5uxtC_</a>	 Alignment		34.6	48	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
9	<a href="#">c5uxtA_</a>	 Alignment		33.9	48	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
10	<a href="#">c3sjrB_</a>	 Alignment		29.0	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 conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
11	<a href="#">c2pnvA_</a>	 Alignment		25.7	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus

12	<a href="#">c4zmhA_</a>	Alignment		23.2	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a five-domain gh115 alpha-glucuronidase from the2 marine bacterium saccharophagus degradans 2-40t
13	<a href="#">c1cosC_</a>	Alignment		20.7	40	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> C; <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-helical bundle
14	<a href="#">c1cosB_</a>	Alignment		20.7	40	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> B; <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-helical bundle
15	<a href="#">c1cosA_</a>	Alignment		20.7	40	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A; <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-helical bundle
16	<a href="#">c3swyB_</a>	Alignment		20.1	58	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> cyclic nucleotide-gated cation channel alpha-3; <b>PDBTitle:</b> cnga3 626-672 containing clz domain
17	<a href="#">c2a93B_</a>	Alignment		19.6	41	<b>PDB header:</b> leucine zippers <b>Chain:</b> B; <b>PDB Molecule:</b> c-myc-max heterodimeric leucine zipper; <b>PDBTitle:</b> nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
18	<a href="#">c5k92C_</a>	Alignment		17.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> apo-(csl16c)3; <b>PDBTitle:</b> crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide
19	<a href="#">c5k92B_</a>	Alignment		17.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> apo-(csl16c)3; <b>PDBTitle:</b> crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide
20	<a href="#">c5k92A_</a>	Alignment		17.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> apo-(csl16c)3; <b>PDBTitle:</b> crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide
21	<a href="#">c5by3A_</a>	Alignment	not modelled	17.2	27	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> btgh115a; <b>PDBTitle:</b> a novel family gh115 4-o-methyl-alpha-glucuronidase, btgh115a, with2 specificity for decorated arabinogalactans
22	<a href="#">c4u5tB_</a>	Alignment	not modelled	16.8	35	<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
23	<a href="#">c4e18B_</a>	Alignment	not modelled	16.3	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> catenin alpha-1; <b>PDBTitle:</b> alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
24	<a href="#">c2jgoA_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser I9c
25	<a href="#">c2jgoC_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser I9c
26	<a href="#">c2jgoB_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser I9c
27	<a href="#">c3ljmA_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser I9c
28	<a href="#">c3ljmC_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser I9c
29	<a href="#">c3ljmB_</a>	Alignment	not modelled	16.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> coil ser I9c;

						<b>PDBTitle:</b> structure of de novo designed apo peptide coil ser l9c
30	<a href="#">c3iynR_</a>	Alignment	not modelled	15.4	18	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
31	<a href="#">c2wpyA_</a>	Alignment	not modelled	14.8	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
32	<a href="#">c4g1aC_</a>	Alignment	not modelled	14.3	38	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> aaq-c16c19 peptide; <b>PDBTitle:</b> metal-binding properties of a self-assembled coiled coil: formation of2 a polynuclear cd-thiolated cluster
33	<a href="#">c6a9wA_</a>	Alignment	not modelled	14.2	27	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> primase; <b>PDBTitle:</b> structure of the bifunctional dna primase-polymerase from phage nrs-1
34	<a href="#">c2oqqB_</a>	Alignment	not modelled	14.2	43	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor hy5; <b>PDBTitle:</b> crystal structure of hy5 leucine zipper homodimer from arabidopsis2 thaliana
35	<a href="#">c3w8vC_</a>	Alignment	not modelled	14.1	35	<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
36	<a href="#">c3w8vB_</a>	Alignment	not modelled	14.1	35	<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
37	<a href="#">c3w8vA_</a>	Alignment	not modelled	14.1	35	<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
38	<a href="#">c5kb0A_</a>	Alignment	not modelled	14.1	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> pb(ii)zn(ii)(grand coil ser-l16c130h)3+; <b>PDBTitle:</b> crystal structure of a tris-thiolate pb(ii) complex in a de novo2 three-stranded coiled coil peptide
39	<a href="#">c1ztaA_</a>	Alignment	not modelled	13.5	34	<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
40	<a href="#">c1ce0B_</a>	Alignment	not modelled	12.3	25	<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
41	<a href="#">c1ij2C_</a>	Alignment	not modelled	12.3	32	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
42	<a href="#">c2hw2A_</a>	Alignment	not modelled	12.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rifampin adp-ribosyl transferase; <b>PDBTitle:</b> crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
43	<a href="#">c1rb6C_</a>	Alignment	not modelled	11.9	32	<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
44	<a href="#">c3k7zA_</a>	Alignment	not modelled	11.9	32	<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
45	<a href="#">c1rb1B_</a>	Alignment	not modelled	11.9	32	<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
46	<a href="#">c1rb1A_</a>	Alignment	not modelled	11.9	32	<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
47	<a href="#">c1swiA_</a>	Alignment	not modelled	11.9	32	<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
48	<a href="#">c3k7zB_</a>	Alignment	not modelled	11.9	32	<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
49	<a href="#">d1vkoa1</a>	Alignment	not modelled	11.7	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	<a href="#">c1ij3C_</a>	Alignment	not modelled	11.7	32	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
51	<a href="#">c1ij3B_</a>	Alignment	not modelled	11.7	32	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
52	<a href="#">c1ij2B_</a>	Alignment	not modelled	11.5	32	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
53	<a href="#">c3vgxC_</a>	Alignment	not modelled	11.4	27	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein gp160; <b>PDBTitle:</b> structure of gp41 t21/cp621-652
54	<a href="#">c4cgbE_</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2
55	<a href="#">c5cffD_</a>	Alignment	not modelled	11.0	29	<b>PDB header:</b> transcription/rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> miranda;

						<b>PDBTitle:</b> crystal structure of miranda/staufen dsrbd5 complex
56	<a href="#">c5ep6C_</a>	Alignment	not modelled	11.0	20	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 5-azacytidine-induced protein 2; <b>PDBTitle:</b> the crystal structure of nap1 in complex with tbk1
57	<a href="#">c1lq7A_</a>	Alignment	not modelled	10.8	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha3w; <b>PDBTitle:</b> de novo designed protein model of radical enzymes
58	<a href="#">c5ep6A_</a>	Alignment	not modelled	10.7	20	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-azacytidine-induced protein 2; <b>PDBTitle:</b> the crystal structure of nap1 in complex with tbk1
59	<a href="#">c2mi7A_</a>	Alignment	not modelled	10.7	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo protein a3y; <b>PDBTitle:</b> solution nmr structure of alpha3y
60	<a href="#">c2lxyA_</a>	Alignment	not modelled	10.7	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 2-mercaptophenol-alpha3c; <b>PDBTitle:</b> nmr structure of 2-mercaptophenol-alpha3c
61	<a href="#">c2o7hF_</a>	Alignment	not modelled	10.4	32	<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
62	<a href="#">c2qj2A_</a>	Alignment	not modelled	9.8	60	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor e2-alpha; <b>PDBTitle:</b> crystal structure of the basic-helix-loop-helix domains of2 the heterodimer e47/neurod1 bound to dna
63	<a href="#">c4cgbA_</a>	Alignment	not modelled	9.6	33	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2
64	<a href="#">d2p4ka2</a>	Alignment	not modelled	9.3	33	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
65	<a href="#">c4bl6A_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein bicaudal d; <b>PDBTitle:</b> bicaudal-d uses a parallel, homodimeric coiled coil with heterotypic2 registry to co-ordinate recruitment of cargos to dynein
66	<a href="#">c6gapB_</a>	Alignment	not modelled	8.8	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
67	<a href="#">c2x6pC_</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
68	<a href="#">c2x6pA_</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
69	<a href="#">c2x6pB_</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
70	<a href="#">c6gbrA_</a>	Alignment	not modelled	8.4	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
71	<a href="#">c1htmB_</a>	Alignment	not modelled	8.3	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> structure of influenza haemagglutinin at the ph of membrane2 fusion
72	<a href="#">c3cveC_</a>	Alignment	not modelled	8.1	21	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> homer protein homolog 1; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer1
73	<a href="#">c6fueC_</a>	Alignment	not modelled	7.7	64	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> fapf; <b>PDBTitle:</b> periplasmic coiled coil domain of the fapf amyloid transporter
74	<a href="#">c3mtuD_</a>	Alignment	not modelled	7.3	18	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> tropomyosin alpha-1 chain,microtubule-associated protein <b>PDBTitle:</b> structure of the tropomyosin overlap complex from chicken smooth2 muscle
75	<a href="#">c4iffC_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> fusion of phage phi29 gp7 protein and cell division protein <b>PDBTitle:</b> structural organization of ftsb, a transmembrane protein of the2 bacterial divisome
76	<a href="#">c1m7IA_</a>	Alignment	not modelled	7.0	40	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated protein d; <b>PDBTitle:</b> solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
77	<a href="#">c5eofB_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optn ntd and tbk1 ctd complex
78	<a href="#">c1kwwC_</a>	Alignment	not modelled	6.6	13	<b>PDB header:</b> immune system, sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mannose-binding protein a; <b>PDBTitle:</b> rat mannose protein a complexed with a-me-fuc.
79	<a href="#">d1p1ja1</a>	Alignment	not modelled	6.5	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	<a href="#">c3h3mB_</a>	Alignment	not modelled	6.4	7	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar protein flit; <b>PDBTitle:</b> crystal structure of flagellar protein flit from bordetella2 bronchiseptica
81	<a href="#">c2rukA_</a>	Alignment	not modelled	6.4	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> solution structure of the complex between p53

						transactivation domain 22 and tfiih p62 ph domain
82	<a href="#">c1qceB</a>	Alignment	not modelled	6.3	47	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gp41); <b>PDBTitle:</b> solution nmr structure of ectodomain of siv gp41,2 restrained regularized mean structure plus 29 simulated3 annealing structures
83	<a href="#">d1b06a2</a>	Alignment	not modelled	6.3	25	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
84	<a href="#">c6gboG</a>	Alignment	not modelled	6.3	34	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the oligomerization domain of vp35 from ebola2 virus
85	<a href="#">c6e6aB</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> inclusion membrane protein a; <b>PDBTitle:</b> triclinic crystal form of inca g144a point mutant
86	<a href="#">c1iojA</a>	Alignment	not modelled	5.9	36	<b>PDB header:</b> apolipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> apoc-i; <b>PDBTitle:</b> human apolipoprotein c-i, nmr, 18 structures
87	<a href="#">c3w93C</a>	Alignment	not modelled	5.9	58	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> coiled coil peptide; <b>PDBTitle:</b> crystal structure analysis of the synthetic gcn4 ester coiled coil2 peptide
88	<a href="#">c2yfaA</a>	Alignment	not modelled	5.8	21	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis transducer; <b>PDBTitle:</b> x-ray structure of mcps ligand binding domain in complex with malate
89	<a href="#">c3h5fB</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser I16l-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
90	<a href="#">c5u9uA</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> apo-(coilser I16(dcy))3; <b>PDBTitle:</b> de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
91	<a href="#">c5u9uC</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> apo-(coilser I16(dcy))3; <b>PDBTitle:</b> de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
92	<a href="#">c5u9tB</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> zn(ii)cl(coilser I16(dcy))3 2-; <b>PDBTitle:</b> the tris-thiolate zn(ii)s3cl binding site engineered by d-cysteine2 ligands in de novo three-stranded coiled coil environment
93	<a href="#">c3h5gA</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser I16d-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
94	<a href="#">c3h5fA</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser I16l-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
95	<a href="#">c3h5fC</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser I16l-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
96	<a href="#">c3h5gC</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser I16d-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
97	<a href="#">c5u9uB</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> apo-(coilser I16(dcy))3; <b>PDBTitle:</b> de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
98	<a href="#">c3h5gB</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser I16d-pen; <b>PDBTitle:</b> switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
99	<a href="#">c5u9tA</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> zn(ii)cl(coilser I16(dcy))3 2-; <b>PDBTitle:</b> the tris-thiolate zn(ii)s3cl binding site engineered by d-cysteine2 ligands in de novo three-stranded coiled coil environment