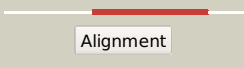
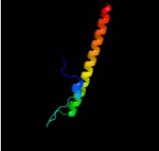
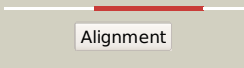
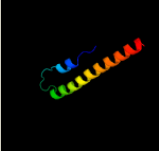
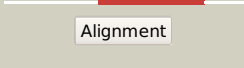
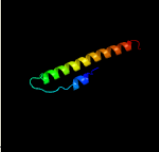
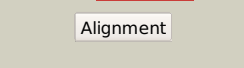

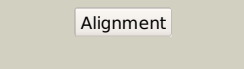

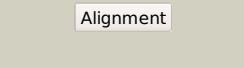
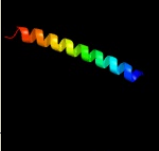
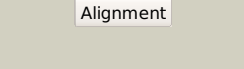

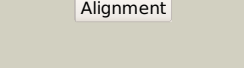

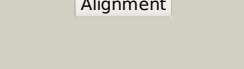
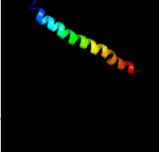
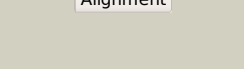
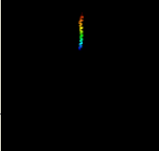
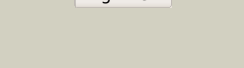
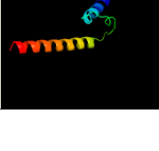
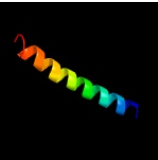





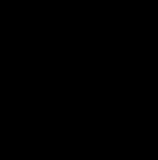

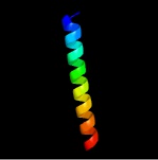


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1209_(-)_1353163_1353531
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	9b08c0a1c9876f42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ug1A_</a>	 Alignment		99.7	21	<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
2	<a href="#">c6gqaD_</a>	 Alignment		99.6	23	<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
3	<a href="#">c2wukD_</a>	 Alignment		99.6	22	<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
4	<a href="#">c4ug3C_</a>	 Alignment		99.6	18	<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
5	<a href="#">c5fv8A_</a>	 Alignment		89.5	24	<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.
6	<a href="#">c5fv8B_</a>	 Alignment		86.6	24	<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.
7	<a href="#">c4l9uA_</a>	 Alignment		76.5	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ras guanyl-releasing protein 1; <b>PDBTitle:</b> structure of c-terminal coiled coil of rasgrp1
8	<a href="#">c3gp4B_</a>	 Alignment		76.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
9	<a href="#">c2ke4A_</a>	 Alignment		75.9	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
10	<a href="#">c3iyqQ_</a>	 Alignment		75.9	24	<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
11	<a href="#">c2vz4A_</a>	 Alignment		75.1	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna

12	<a href="#">c1cosC_</a>	Alignment		66.4	28	<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
13	<a href="#">c3gpvA_</a>	Alignment		65.8	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
14	<a href="#">c5wlgA_</a>	Alignment		65.7	17	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7,microtubule- <b>PDBTitle:</b> crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
15	<a href="#">c1cosA_</a>	Alignment		65.5	28	<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="#">c1cosB_</a>	Alignment		64.2	28	<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
17	<a href="#">c3jynR_</a>	Alignment		63.7	24	<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
18	<a href="#">c3vkhD_</a>	Alignment		63.3	15	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
19	<a href="#">c2x6pA_</a>	Alignment		61.0	28	<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
20	<a href="#">c2x6pB_</a>	Alignment		60.9	28	<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
21	<a href="#">c3qo8A_</a>	Alignment	not modelled	60.4	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from candida albicans
22	<a href="#">c2x6pC_</a>	Alignment	not modelled	59.6	28	<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
23	<a href="#">c1debA_</a>	Alignment	not modelled	59.4	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> adenomatous polyposis coli protein; <b>PDBTitle:</b> crystal structure of the n-terminal coiled coil domain from apc
24	<a href="#">c4l9uB_</a>	Alignment	not modelled	57.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ras guanyl-releasing protein 1; <b>PDBTitle:</b> structure of c-terminal coiled coil of rasgrp1
25	<a href="#">c3cvfA_</a>	Alignment	not modelled	57.3	9	<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
26	<a href="#">d1q08a_</a>	Alignment	not modelled	56.4	18	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
27	<a href="#">c2mxrA_</a>	Alignment	not modelled	56.2	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 12a; <b>PDBTitle:</b> solution structure of coiled coil domain of myosin binding subunit of2 myosin light chain phosphatase
28	<a href="#">c1t6fA_</a>	Alignment	not modelled	55.4	15	<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

29	<a href="#">c2jgoA_</a>	Alignment	not modelled	54.9	24	<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
30	<a href="#">c3ljmC_</a>	Alignment	not modelled	54.9	24	<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
31	<a href="#">c3ljmA_</a>	Alignment	not modelled	54.9	24	<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
32	<a href="#">c2jgoB_</a>	Alignment	not modelled	54.9	24	<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
33	<a href="#">d1q06a_</a>	Alignment	not modelled	54.3	10	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
34	<a href="#">c5k92A_</a>	Alignment	not modelled	53.7	28	<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
35	<a href="#">c5k92C_</a>	Alignment	not modelled	53.7	28	<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
36	<a href="#">c3ljmB_</a>	Alignment	not modelled	53.4	24	<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 I9c
37	<a href="#">c2jgoC_</a>	Alignment	not modelled	53.4	24	<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
38	<a href="#">c1coiA_</a>	Alignment	not modelled	52.8	24	<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
39	<a href="#">c5k92B_</a>	Alignment	not modelled	52.2	28	<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
40	<a href="#">c6akIA_</a>	Alignment	not modelled	51.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of ikbke 1; <b>PDBTitle:</b> crystal structure of striatin3 in complex with sike1 coiled-coil2 domain
41	<a href="#">c2e43A_</a>	Alignment	not modelled	50.1	9	<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
42	<a href="#">c1fosF_</a>	Alignment	not modelled	49.5	11	<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
43	<a href="#">d1nkpa_</a>	Alignment	not modelled	47.9	11	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
44	<a href="#">c3ra3D_</a>	Alignment	not modelled	47.8	15	<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
45	<a href="#">c3n4xB_</a>	Alignment	not modelled	46.5	19	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> monopolin complex subunit csm1; <b>PDBTitle:</b> structure of csm1 full-length
46	<a href="#">c1t2kD_</a>	Alignment	not modelled	46.1	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
47	<a href="#">c3m9bK_</a>	Alignment	not modelled	45.7	12	<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
48	<a href="#">c3rrkA_</a>	Alignment	not modelled	45.7	19	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atpase 116 kda subunit; <b>PDBTitle:</b> crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase
49	<a href="#">d1r05a_</a>	Alignment	not modelled	45.5	14	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
50	<a href="#">c1hf9B_</a>	Alignment	not modelled	44.7	9	<b>PDB header:</b> atpase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> atpase inhibitor (mitochondrial); <b>PDBTitle:</b> c-terminal coiled-coil domain from bovine if1
51	<a href="#">c1jccC_</a>	Alignment	not modelled	43.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> major outer membrane lipoprotein; <b>PDBTitle:</b> crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,i16a,v20a,i23a,v27a,m30a,v34a mutations
52	<a href="#">c6akkA_</a>	Alignment	not modelled	43.3	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of ikbke 1; <b>PDBTitle:</b> crystal structure of the second coiled-coil domain of sike1
53	<a href="#">c2o7hF_</a>	Alignment	not modelled	42.7	19	<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
54	<a href="#">c6g3eA_</a>	Alignment	not modelled	41.7	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate lyase; <b>PDBTitle:</b> crystal structure of edds lyase in complex with formate
						<b>PDB header:</b> motor protein

55	<a href="#">c3vkGA_</a>	Alignment	not modelled	40.2	15	<b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
56	<a href="#">c3ra3B_</a>	Alignment	not modelled	39.1	17	<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
57	<a href="#">c5kb0A_</a>	Alignment	not modelled	39.0	30	<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
58	<a href="#">c1aq5C_</a>	Alignment	not modelled	38.8	16	<b>PDB header:</b> coiled-coil <b>Chain:</b> C: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
59	<a href="#">c1aq5B_</a>	Alignment	not modelled	38.8	16	<b>PDB header:</b> coiled-coil <b>Chain:</b> B: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
60	<a href="#">c1ci6A_</a>	Alignment	not modelled	38.5	17	<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
61	<a href="#">c3kinB_</a>	Alignment	not modelled	38.5	16	<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
62	<a href="#">d1jnra1</a>	Alignment	not modelled	37.0	20	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
63	<a href="#">c1go4F_</a>	Alignment	not modelled	36.9	19	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> mitotic spindle assembly checkpoint protein mad1; <b>PDBTitle:</b> crystal structure of mad1-mad2 reveals a conserved mad2 binding motif2 in mad1 and cdc20.
64	<a href="#">c1g6uB_</a>	Alignment	not modelled	36.5	31	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> domain swapped dimer; <b>PDBTitle:</b> crystal structure of a domain swapped dimer
65	<a href="#">c3vr8E_</a>	Alignment	not modelled	36.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> flavoprotein subunit of complex ii; <b>PDBTitle:</b> mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum
66	<a href="#">c2zhhA_</a>	Alignment	not modelled	36.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
67	<a href="#">c1ij2C_</a>	Alignment	not modelled	35.9	15	<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
68	<a href="#">c1ij3C_</a>	Alignment	not modelled	35.5	15	<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
69	<a href="#">c1ij3B_</a>	Alignment	not modelled	35.5	15	<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
70	<a href="#">c1rb6C_</a>	Alignment	not modelled	35.5	15	<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
71	<a href="#">c3k7zA_</a>	Alignment	not modelled	35.5	15	<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
72	<a href="#">c1rb1A_</a>	Alignment	not modelled	35.5	15	<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
73	<a href="#">c3k7zB_</a>	Alignment	not modelled	35.5	15	<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
74	<a href="#">c1rb1B_</a>	Alignment	not modelled	35.5	15	<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
75	<a href="#">c1swiA_</a>	Alignment	not modelled	35.5	15	<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
76	<a href="#">c6mctL_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
77	<a href="#">c6mctF_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
78	<a href="#">c6mctI_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
79	<a href="#">c6mq2D_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
80	<a href="#">c6mctB_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by

						van der waals2 interaction
81	<a href="#">c6mctA_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
82	<a href="#">c6mctJ_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
83	<a href="#">c6mctG_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
84	<a href="#">c6mctE_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
85	<a href="#">c6mctN_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> N: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
86	<a href="#">c6mctH_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> H: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
87	<a href="#">c6mctM_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
88	<a href="#">c6mctO_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
89	<a href="#">c6mpwA_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-1
90	<a href="#">c6mctD_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
91	<a href="#">c6mctK_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
92	<a href="#">c6mctC_</a>	Alignment	not modelled	35.0	50	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
93	<a href="#">c5gpeB_</a>	Alignment	not modelled	34.6	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr-family; <b>PDBTitle:</b> crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
94	<a href="#">c6nr92_</a>	Alignment	not modelled	34.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> 2: <b>PDB Molecule:</b> prefoldin subunit 2; <b>PDBTitle:</b> htrc-hpfd class5
95	<a href="#">c6mpwC_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-1
96	<a href="#">c6mq2B_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-2
97	<a href="#">c6mpwD_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-1
98	<a href="#">c6mq2E_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-2
99	<a href="#">c6mpwB_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-1
100	<a href="#">c6mq2C_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-2
101	<a href="#">c6mpwE_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-1
102	<a href="#">c6mq2A_</a>	Alignment	not modelled	34.4	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c2212 form-2
103	<a href="#">c2yy0D_</a>	Alignment	not modelled	33.2	21	<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
104	<a href="#">c1fosE_</a>	Alignment	not modelled	32.9	14	<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
105	<a href="#">c1ci6B_</a>	Alignment	not modelled	32.9	11	<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
106	<a href="#">c4y66C_</a>	Alignment	not modelled	32.9	23	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> mnd1;

						<b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
107	<a href="#">c3a5tB_</a>	Alignment	not modelled	32.8	17	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mafg; <b>PDBTitle:</b> crystal structure of mafg-dna complex
108	<a href="#">c1ij2B_</a>	Alignment	not modelled	32.6	15	<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
109	<a href="#">c5zk1A_</a>	Alignment	not modelled	32.4	10	<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
110	<a href="#">c2gl2B_</a>	Alignment	not modelled	32.3	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
111	<a href="#">c3qaoA_</a>	Alignment	not modelled	32.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
112	<a href="#">c1ysaD_</a>	Alignment	not modelled	31.9	13	<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
113	<a href="#">c4om3D_</a>	Alignment	not modelled	31.7	20	<b>PDB header:</b> transcription, dna binding <b>Chain:</b> D: <b>PDB Molecule:</b> transducin-like enhancer protein 1; <b>PDBTitle:</b> crystal structure of human tie1 q-domain residues 20-156
114	<a href="#">c4y66D_</a>	Alignment	not modelled	31.3	14	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> putative tbpip family protein; <b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
115	<a href="#">d1r8da_</a>	Alignment	not modelled	31.2	16	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
116	<a href="#">c2wt7B_</a>	Alignment	not modelled	30.8	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mafb; <b>PDBTitle:</b> crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
117	<a href="#">c1ztaA_</a>	Alignment	not modelled	30.6	16	<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
118	<a href="#">c1dh3A_</a>	Alignment	not modelled	30.2	10	<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 family selective dimerization and dna3 binding
119	<a href="#">c2gd7B_</a>	Alignment	not modelled	30.1	21	<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
120	<a href="#">c4dznC_</a>	Alignment	not modelled	28.9	19	<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