
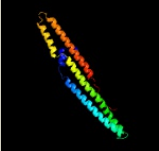

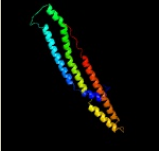

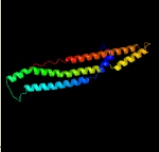

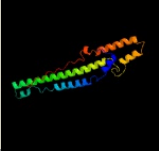

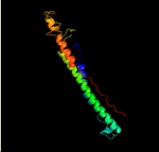

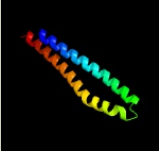

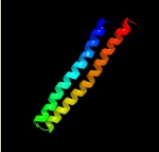







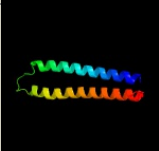


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3621c\_(PPE65)\_4060827\_4062068  
 Date Fri Aug 9 18:20:30 BST 2019  
 Unique Job ID ca385a540feb6829

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	64	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">d2g38b1</a>	 Alignment		100.0	35	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
5	<a href="#">c4wj2A_</a>	 Alignment		98.5	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		97.7	13	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	<a href="#">c4iogD_</a>	 Alignment		97.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
8	<a href="#">c3gvmA_</a>	 Alignment		97.6	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	<a href="#">c3zbhC_</a>	 Alignment		97.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		96.8	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		95.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	<a href="#">c4lwsA_</a>	Alignment		95.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	<a href="#">d1wa8b1</a>	Alignment		95.3	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		94.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	<a href="#">c2kg7B_</a>	Alignment		90.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c4i0xJ_</a>	Alignment		69.6	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J; <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	<a href="#">d1ui5a2</a>	Alignment		22.9	24	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
18	<a href="#">c5frgA_</a>	Alignment		17.3	75	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
19	<a href="#">c1bkvA_</a>	Alignment		14.7	50	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvB_</a>	Alignment		14.1	50	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c1bkvC_</a>	Alignment	not modelled	14.1	50	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
22	<a href="#">c3h6pB_</a>	Alignment	not modelled	11.3	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> esat-6 like protein esxs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
23	<a href="#">d1zeeal</a>	Alignment	not modelled	11.3	33	<b>Fold:</b> Indolic compounds 2,3-dioxygenase-like <b>Superfamily:</b> Indolic compounds 2,3-dioxygenase-like <b>Family:</b> Indoleamine 2,3-dioxygenase-like
24	<a href="#">c2kg7A_</a>	Alignment	not modelled	10.7	47	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
25	<a href="#">c2ke4A_</a>	Alignment	not modelled	10.1	75	<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
26	<a href="#">c2nviA_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 25mer peptide from vacuolar atp synthase subunit <b>PDBTitle:</b> nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
27	<a href="#">c1vytF_</a>	Alignment	not modelled	8.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
28	<a href="#">c4lzxB_</a>	Alignment	not modelled	8.5	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-free cam

29	<a href="#">c2iu1A</a>	Alignment	not modelled	8.3	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of eif5 c-terminal domain
30	<a href="#">c2fulE</a>	Alignment	not modelled	7.9	28	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae eif5
31	<a href="#">c6aokA</a>	Alignment	not modelled	7.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
32	<a href="#">c2lkqA</a>	Alignment	not modelled	7.5	44	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin lambda-like polypeptide 1; <b>PDBTitle:</b> nmr structure of the lambda 5 22-45 peptide
33	<a href="#">c4m1IB</a>	Alignment	not modelled	7.3	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-bound cam
34	<a href="#">c6cqiA</a>	Alignment	not modelled	7.3	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
35	<a href="#">d1khba2</a>	Alignment	not modelled	7.3	30	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
36	<a href="#">d1fcda3</a>	Alignment	not modelled	6.9	38	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
37	<a href="#">c5i4rA</a>	Alignment	not modelled	6.5	43	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> contact-dependent inhibitor a; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
38	<a href="#">c2i94B</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> nmr structure of recoverin bound to rhodopsin kinase
39	<a href="#">d1vifn1</a>	Alignment	not modelled	6.5	80	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
40	<a href="#">c5l85B</a>	Alignment	not modelled	6.4	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear fragile x mental retardation-interacting protein 1; <b>PDBTitle:</b> solution structure of the complex between human znhit3 and nufip12 proteins
41	<a href="#">c6q5IA</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex*-I24h; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
42	<a href="#">c6q5IB</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex*-I24h; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
43	<a href="#">c1vytE</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
44	<a href="#">c1bzgA</a>	Alignment	not modelled	6.1	0	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone-related protein; <b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
45	<a href="#">c6q5hA</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex*-I24d; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
46	<a href="#">c6q5mB</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex*-I24dab; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
47	<a href="#">c6q5iB</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex*-I24e; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24e
48	<a href="#">c6q5kA</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex*-I24k; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24k
49	<a href="#">c6nbiP</a>	Alignment	not modelled	6.0	80	<b>PDB header:</b> signaling protein <b>Chain:</b> P: <b>PDB Molecule:</b> long-acting parathyroid hormone analog; <b>PDBTitle:</b> cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
50	<a href="#">c2jtwA</a>	Alignment	not modelled	6.0	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane helix 7 of yeast vatpase; <b>PDBTitle:</b> solution structure of tm7 bound to dpc micelles
51	<a href="#">c6q5mA</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex*-I24dab; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
52	<a href="#">c1nauA</a>	Alignment	not modelled	5.9	42	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon; <b>PDBTitle:</b> nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of f3 perdeuterated dodecylphosphocholine micelles
53	<a href="#">c3r47I</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24

54	<a href="#">c3r47J_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> J; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
55	<a href="#">c3r47B_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
56	<a href="#">c6q5jE_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> cc-hex*-I24e; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24e
57	<a href="#">c4dexB_</a>	Alignment	not modelled	5.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> voltage-dependent n-type calcium channel subunit alpha-1b; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 I-II linker.
58	<a href="#">c6q5kB_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> cc-hex*-I24k; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24k
59	<a href="#">c6q5jF_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> cc-hex*-I24e; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24e
60	<a href="#">c3r47C_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
61	<a href="#">c3r47L_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> de novo protein <b>Chain:</b> L; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
62	<a href="#">c3r47M_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> de novo protein <b>Chain:</b> M; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
63	<a href="#">c3r47F_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
64	<a href="#">c1t0jC_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel alpha-1c subunit; <b>PDBTitle:</b> crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
65	<a href="#">c6q5hB_</a>	Alignment	not modelled	5.5	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> cc-hex*-I24d; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
66	<a href="#">c6q5nD_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> D; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
67	<a href="#">c6q5nG_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
68	<a href="#">c6q5nC_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
69	<a href="#">c6q5nE_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
70	<a href="#">c4kvtC_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I24c
71	<a href="#">c4kvtB_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I24c
72	<a href="#">c4kvtE_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I24c
73	<a href="#">c4kvtF_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I24c
74	<a href="#">c4kvtA_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I24c
75	<a href="#">c6q5nK_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> K; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
76	<a href="#">c6q5nB_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
77	<a href="#">c6q5nj_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> J; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
78	<a href="#">c6q5ni_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> I; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
79	<a href="#">c6q5nH_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> H; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle

80	<a href="#">c6q5nL_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> L; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
81	<a href="#">c6q5nA_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
82	<a href="#">c6q5nF_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> cc-hex*-I24nle; <b>PDBTitle:</b> crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
83	<a href="#">c3r47A_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
84	<a href="#">c3r47G_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
85	<a href="#">c3r47E_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
86	<a href="#">c3r47K_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> K; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
87	<a href="#">c3r47H_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> H; <b>PDB Molecule:</b> coiled coil helix I24h; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-h24
88	<a href="#">c3r48F_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> coiled coil helix w22-I24h; <b>PDBTitle:</b> crystal structure of a hetero-hexamer coiled coil
89	<a href="#">c5lzkB_</a>	Alignment	not modelled	5.4	4	<b>PDB header:</b> structural genomics <b>Chain:</b> B; <b>PDB Molecule:</b> protein fam83b; <b>PDBTitle:</b> structure of the domain of unknown function duf1669 from human fam83b
90	<a href="#">c4i6jB_</a>	Alignment	not modelled	5.4	22	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> if-box/Irr-repeat protein 3; <b>PDBTitle:</b> a ubiquitin ligase-substrate complex
91	<a href="#">c3r46F_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
92	<a href="#">c3r46C_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
93	<a href="#">c3r46A_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
94	<a href="#">c3r46B_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
95	<a href="#">c3r46E_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
96	<a href="#">c3r46G_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> coiled coil helix I24d; <b>PDBTitle:</b> crystal structure of a parallel 6-helix coiled coil cc-hex-d24
97	<a href="#">c3sjrB_</a>	Alignment	not modelled	5.3	6	<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 unknown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
98	<a href="#">c3owtC_</a>	Alignment	not modelled	5.3	71	<b>PDB header:</b> protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of s. cerevisiae rap1-sir3 complex
99	<a href="#">c3juia_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit