








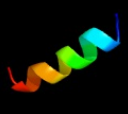

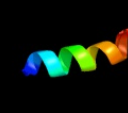





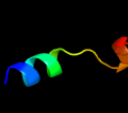










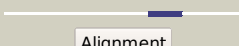

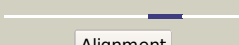

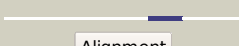

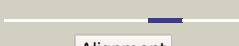





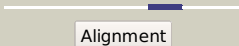
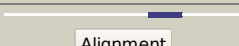

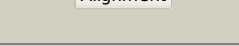
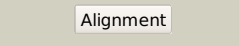

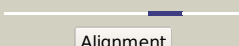



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3770c_(-)_4215378_4215953
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	f2a8f09b1b9e20a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1wazA_</a>	 Alignment		31.6	32	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
2	<a href="#">c2h3oA_</a>	 Alignment		26.5	64	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merft, a membrane protein with two trans-2 membrane helices
3	<a href="#">c5y6aA_</a>	 Alignment		22.7	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> chain a and b; <b>PDBTitle:</b> crystal structure of the anti-crispr protein, acriia1
4	<a href="#">d1dq3a2</a>	 Alignment		19.4	31	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain <b>Family:</b> PI-Pfui intein middle domain
5	<a href="#">c2lj2A_</a>	 Alignment		13.0	60	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
6	<a href="#">c2m67A_</a>	 Alignment		9.7	60	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
7	<a href="#">c2v52M_</a>	 Alignment		6.9	54	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> M: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel2 complexed to g-actin
8	<a href="#">c2v51F_</a>	 Alignment		6.7	53	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> F: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
9	<a href="#">c2v51E_</a>	 Alignment		6.7	53	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> E: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
10	<a href="#">c6q5IA_</a>	 Alignment		6.6	62	<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
11	<a href="#">c6q5hA_</a>	 Alignment		6.6	62	<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

12	<a href="#">c6q5lB_</a>	 Alignment		6.6	62	<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
13	<a href="#">c6q5mB_</a>	 Alignment		6.4	62	<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
14	<a href="#">c6q5lB_</a>	 Alignment		6.4	62	<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
15	<a href="#">c6q5kA_</a>	 Alignment		6.4	62	<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
16	<a href="#">c6q5lE_</a>	 Alignment		6.3	62	<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
17	<a href="#">c6q5mA_</a>	 Alignment		6.2	62	<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
18	<a href="#">c6q5lF_</a>	 Alignment		6.0	62	<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
19	<a href="#">c4kvvC_</a>	 Alignment		5.9	62	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I17c-w224bf; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I17c-w224bf
20	<a href="#">c3r47J_</a>	 Alignment		5.9	62	<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
21	<a href="#">c3r47B_</a>	 Alignment	not modelled	5.9	62	<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
22	<a href="#">c3r47I_</a>	 Alignment	not modelled	5.9	62	<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
23	<a href="#">c6hn9A_</a>	 Alignment	not modelled	5.8	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> nicomicin-1; <b>PDBTitle:</b> nicomicin-1 -- novel antimicrobial peptides from the arctic polychaeta2 nicomache minor provide new molecular insight into biological role of3 the brichos domain
24	<a href="#">c4kvvC_</a>	 Alignment	not modelled	5.8	62	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
25	<a href="#">c5dayA_</a>	 Alignment	not modelled	5.7	42	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nap1-related protein 1; <b>PDBTitle:</b> the structure of nap1-related protein(nrp1) in arabidopsis
26	<a href="#">c6q5kB_</a>	 Alignment	not modelled	5.7	62	<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
27	<a href="#">c3esiD_</a>	 Alignment	not modelled	5.7	55	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
28	<a href="#">c1zqlQ_</a>	 Alignment	not modelled	5.7	9	<b>PDB header:</b> immune system <b>Chain:</b> Q: <b>PDB Molecule:</b> t cell receptor alpha chain; <b>PDBTitle:</b> crystal structure of 3a6 tcr bound to mbp/hla-dr2a

29	<a href="#">c4kvvj_</a>	Alignment	not modelled	5.5	62	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
30	<a href="#">c4kvvG_</a>	Alignment	not modelled	5.5	62	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
31	<a href="#">c4kvvE_</a>	Alignment	not modelled	5.5	62	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
32	<a href="#">c4kvvB_</a>	Alignment	not modelled	5.5	62	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
33	<a href="#">c3r47M_</a>	Alignment	not modelled	5.4	62	<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
34	<a href="#">c3r47F_</a>	Alignment	not modelled	5.4	62	<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
35	<a href="#">c3r47C_</a>	Alignment	not modelled	5.4	62	<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
36	<a href="#">c3r47L_</a>	Alignment	not modelled	5.4	62	<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
37	<a href="#">c6q5hB_</a>	Alignment	not modelled	5.4	62	<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
38	<a href="#">c4kvvK_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
39	<a href="#">c4kvvD_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
40	<a href="#">c4kvvI_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
41	<a href="#">c4kvvA_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
42	<a href="#">c4kvvF_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
43	<a href="#">c6q5nD_</a>	Alignment	not modelled	5.2	62	<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
44	<a href="#">c6q5nG_</a>	Alignment	not modelled	5.2	62	<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
45	<a href="#">c6q5nE_</a>	Alignment	not modelled	5.2	62	<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
46	<a href="#">c6q5nC_</a>	Alignment	not modelled	5.2	62	<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
47	<a href="#">c4ui9D_</a>	Alignment	not modelled	5.2	57	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> anaphase-promoting complex subunit 15; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
48	<a href="#">c6q5iA_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <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
49	<a href="#">c4kvvuA_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I17c-w224bf; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-I17c-w224bf
50	<a href="#">c6agbH_</a>	Alignment	not modelled	5.1	56	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop8; <b>PDBTitle:</b> cryo-em structure of yeast ribonuclease p
51	<a href="#">c3r47A_</a>	Alignment	not modelled	5.1	62	<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
52	<a href="#">c3r47G_</a>	Alignment	not modelled	5.1	62	<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
53	<a href="#">c3r47E_</a>	Alignment	not modelled	5.1	62	<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
54	<a href="#">c4kvvL_</a>	Alignment	not modelled	5.0	62	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
						<b>PDB header:</b> de novo protein

55	<a href="#">c4kvvH_</a>	Alignment	not modelled	5.0	62	<b>Chain:</b> H; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-I24c peptide with an alkylated <b>PDBTitle:</b> crystal structure of an alkylated cys mutant of cc-hex
56	<a href="#">c6q5nL_</a>	Alignment	not modelled	5.0	62	<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
57	<a href="#">c6q5nF_</a>	Alignment	not modelled	5.0	62	<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
58	<a href="#">c6q5nJ_</a>	Alignment	not modelled	5.0	62	<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
59	<a href="#">c6q5nK_</a>	Alignment	not modelled	5.0	62	<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
60	<a href="#">c6q5nA_</a>	Alignment	not modelled	5.0	62	<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
61	<a href="#">c6q5nI_</a>	Alignment	not modelled	5.0	62	<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
62	<a href="#">c6q5nB_</a>	Alignment	not modelled	5.0	62	<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