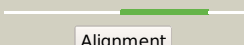
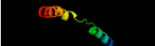
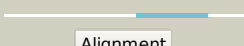

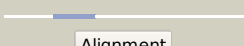
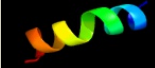
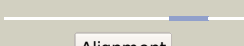




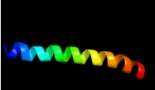

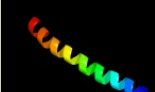








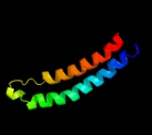
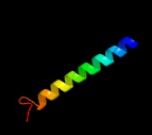



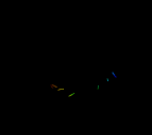
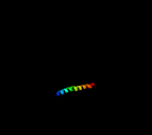




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3760_(-)_4205716_4206018
Date	Fri Aug 9 18:20:46 BST 2019
Unique Job ID	5e155a7092253815

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kncB_	 Alignment		54.8	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
2	c2n2aA_	 Alignment		39.4	26	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains
3	d1kf6d_	 Alignment		25.6	37	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
4	c5fv8B_	 Alignment		24.7	17	PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
5	c5fv8A_	 Alignment		24.6	17	PDB header: structural protein Chain: A: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
6	c5ldxZ_	 Alignment		18.7	9	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class3.
7	c5lc5Z_	 Alignment		18.7	9	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class2
8	c5ldwZ_	 Alignment		18.7	9	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1
9	c2ks1A_	 Alignment		17.3	24	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
10	c2n9bB_	 Alignment		17.1	24	PDB header: motor protein/transcription Chain: B: PDB Molecule: unconventional myosin-x, general control protein gcn4 PDBTitle: solution nmr structure of antiparallel myosin-10:gcn4 tandem coiled-2 coil
11	c3arcl_	 Alignment		15.6	33	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution

12	c2yvxD_	Alignment		15.5	11	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
13	c2jwaA_	Alignment		15.4	24	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
14	c2lw9A_	Alignment		14.7	19	PDB header: motor protein Chain: A: PDB Molecule: unconventionnal myosin-x; PDBTitle: nmr solution structure of myo10 anti-cc
15	d1qjed_	Alignment		14.4	21	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
16	c1cagA_	Alignment		12.7	44	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
17	c1cagC_	Alignment		12.7	44	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
18	c6gcsW_	Alignment		12.4	13	PDB header: oxidoreductase Chain: W: PDB Molecule: nb6m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
19	c6nd1E_	Alignment		11.9	22	PDB header: protein transport Chain: E: PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast
20	c1cgdA_	Alignment		11.8	44	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
21	c1cgdC_	Alignment	not modelled	11.8	44	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
22	c1cgdB_	Alignment	not modelled	11.8	44	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
23	c1cagB_	Alignment	not modelled	11.8	44	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
24	c5lnkq_	Alignment	not modelled	11.5	9	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
25	c6c61N_	Alignment	not modelled	10.8	30	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
26	c5o31Z_	Alignment	not modelled	10.0	9	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: mitochondrial complex i in the deactive state
27	d1m56d_	Alignment	not modelled	9.6	21	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
28	c2k1IA_	Alignment	not modelled	9.5	32	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
29	c2k1IB_	Alignment	not modelled	9.5	32	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1;

29	c2k1bB_	Alignment	not modelled	9.5	32	PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3 PDB header: signaling protein
30	c2k1b_	Alignment	not modelled	9.5	32	Chain: B; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
31	c2k1kA_	Alignment	not modelled	9.5	32	PDB header: signaling protein Chain: A; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
32	c2pcoA_	Alignment	not modelled	9.2	38	PDB header: toxin Chain: A; PDB Molecule: latarcin-1; PDBTitle: spatial structure and membrane permeabilization for2 latarcin-1, a spider antimicrobial peptide
33	c2mmvA_	Alignment	not modelled	7.6	11	PDB header: cell cycle Chain: A; PDB Molecule: cell division protein zapa; PDBTitle: zapa mutant dimer from geobacillus stearotherophilus
34	c2mfrA_	Alignment	not modelled	7.6	26	PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
35	c6hraD_	Alignment	not modelled	7.2	36	PDB header: membrane protein Chain: D; PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
36	c5mrwL_	Alignment	not modelled	7.2	36	PDB header: hydrolase Chain: L; PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
37	c5mrwH_	Alignment	not modelled	7.2	36	PDB header: hydrolase Chain: H; PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
38	c5mrwD_	Alignment	not modelled	7.2	36	PDB header: hydrolase Chain: D; PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
39	c2jo1A_	Alignment	not modelled	7.2	15	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
40	c5jb30_	Alignment	not modelled	6.7	0	PDB header: translation Chain: 0; PDB Molecule: 30s ribosomal protein e141; PDBTitle: cryo-em structure of a full archaeal ribosomal translation initiation2 complex in the p-remote conformation
41	c5jbh0_	Alignment	not modelled	6.7	0	PDB header: transcription Chain: 0; PDB Molecule: 30s ribosomal protein e141; PDBTitle: cryo-em structure of a full archaeal ribosomal translation initiation2 complex in the p-in conformation
42	c3j21h_	Alignment	not modelled	6.6	0	PDB header: ribosome Chain: H; PDB Molecule: 50s ribosomal protein l11p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
43	c3j44h_	Alignment	not modelled	6.6	0	PDB header: ribosome/protein transport Chain: H; PDB Molecule: 50s ribosomal protein l11p; PDBTitle: structure of the methanococcus jannaschii ribosome-secyebeta channel2 complex (50s ribosomal subunit)
44	c4gn0D_	Alignment	not modelled	6.6	15	PDB header: signaling protein Chain: D; PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
45	c5kk2E_	Alignment	not modelled	6.0	12	PDB header: membrane protein, transport protein, sig Chain: E; PDB Molecule: voltage-dependent calcium channel gamma-2 subunit; PDBTitle: architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
46	c2micA_	Alignment	not modelled	5.8	19	PDB header: membrane protein Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
47	c2micB_	Alignment	not modelled	5.8	19	PDB header: membrane protein Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
48	c3b2cl_	Alignment	not modelled	5.7	35	PDB header: structural protein Chain: I; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
49	c3b2cA_	Alignment	not modelled	5.7	35	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
50	c3b2cH_	Alignment	not modelled	5.7	35	PDB header: structural protein Chain: H; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
51	c3b2cC_	Alignment	not modelled	5.7	35	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
52	c1ei8A_	Alignment	not modelled	5.7	35	PDB header: contractile protein Chain: A; PDB Molecule: collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- PDBTitle: structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
53	c2klwC_	Alignment	not modelled	5.7	35	PDB header: de novo protein Chain: C; PDB Molecule: (pog)10;

53	c2kwc_	Alignment	not modelled	5.7	35	PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions PDB header: structural protein
54	c3b2cG_	Alignment	not modelled	5.7	35	Chain: G: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3 PDB header: contractile protein
55	c1ei8B_	Alignment	not modelled	5.7	35	Chain: B: PDB Molecule: collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- PDBTitle: structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide PDB header: structural protein
56	c3b2cF_	Alignment	not modelled	5.7	35	Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3 PDB header: contractile protein
57	c1ei8F_	Alignment	not modelled	5.7	35	Chain: F: PDB Molecule: collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- PDBTitle: structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide PDB header: structural protein
58	c3b2cE_	Alignment	not modelled	5.7	35	Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3 PDB header: structural protein
59	c3b2cD_	Alignment	not modelled	5.7	35	Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3 PDB header: structural protein
60	c3b2cB_	Alignment	not modelled	5.7	35	Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3 PDB header: contractile protein
61	c1ei8D_	Alignment	not modelled	5.7	35	Chain: D: PDB Molecule: collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- PDBTitle: structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide PDB header: contractile protein
62	c1ei8E_	Alignment	not modelled	5.7	35	Chain: E: PDB Molecule: collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- PDBTitle: structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide PDB header: contractile protein