


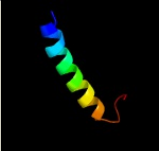

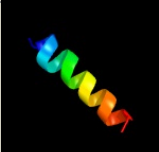

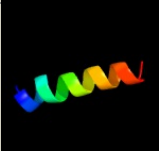

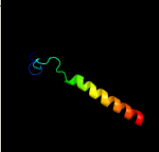

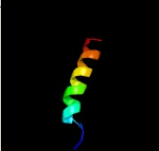



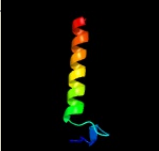



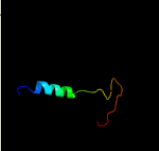

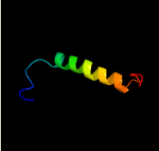



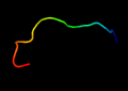
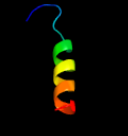

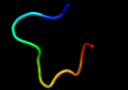
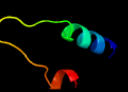
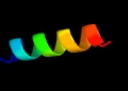


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0420c_(-)_506564_506974
Date	Tue Jul 23 14:50:49 BST 2019
Unique Job ID	e417f24f88dc8bf0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5t42A_</a>	 Alignment		58.0	48	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
2	<a href="#">c2lomA_</a>	 Alignment		25.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1a; <b>PDBTitle:</b> backbone structure of human membrane protein higd1a
3	<a href="#">c5xnmj_</a>	 Alignment		25.2	47	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
4	<a href="#">c3jcu_</a>	 Alignment		19.4	42	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
5	<a href="#">c1p84E_</a>	 Alignment		16.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
6	<a href="#">c6dlnB_</a>	 Alignment		16.5	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein gp41; <b>PDBTitle:</b> oligomeric structure of the hiv gp41 mper-tmd in phospholipid bilayers
7	<a href="#">c5ydfA_</a>	 Alignment		13.6	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> parafibromin; <b>PDBTitle:</b> crystal structure of a disease-related gene, hcdc73(1-100)
8	<a href="#">c4gd3T_</a>	 Alignment		12.9	18	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> hydrogenase-1 small chain; <b>PDBTitle:</b> structure of e. coli hydrogenase-1 in complex with cytochrome b
9	<a href="#">d1u2ca2</a>	 Alignment		11.1	29	<b>Fold:</b> Dystroglycan, domain 2 <b>Superfamily:</b> Dystroglycan, domain 2 <b>Family:</b> Dystroglycan, domain 2
10	<a href="#">c5kk2E_</a>	 Alignment		10.8	23	<b>PDB header:</b> membrane protein, transport protein, sig <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-2 subunit; <b>PDBTitle:</b> architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
11	<a href="#">c2lonA_</a>	 Alignment		10.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b

12	<a href="#">c2k9yA_</a>	Alignment		10.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
13	<a href="#">c2k9yB_</a>	Alignment		10.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
14	<a href="#">d1r18a_</a>	Alignment		9.7	31	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
15	<a href="#">d1fvia1</a>	Alignment		9.1	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
16	<a href="#">c2mi2A_</a>	Alignment		9.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sec-independent protein translocase protein tatb; <b>PDBTitle:</b> solution structure of the e. coli tatb protein in dpc micelles
17	<a href="#">c3jcuw_</a>	Alignment		8.4	40	<b>PDB header:</b> membrane protein <b>Chain:</b> W: <b>PDB Molecule:</b> photosystem ii reaction center w protein, chloroplastic; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
18	<a href="#">c6q56C_</a>	Alignment		7.8	0	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 trna methyltransferase trmk
19	<a href="#">c3jbrE_</a>	Alignment		7.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-1 subunit; <b>PDBTitle:</b> cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
20	<a href="#">c6ithA_</a>	Alignment		7.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
21	<a href="#">c6ckgA_</a>	Alignment	not modelled	7.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate 3-kinase; <b>PDBTitle:</b> d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
22	<a href="#">d2gpia1</a>	Alignment	not modelled	7.5	29	<b>Fold:</b> Shew3726-like <b>Superfamily:</b> Shew3726-like <b>Family:</b> Shew3726-like
23	<a href="#">c4alyB_</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> p35 antigen; <b>PDBTitle:</b> borrelia burgdorferi outer surface lipoprotein bba64
24	<a href="#">d1vbfa_</a>	Alignment	not modelled	7.2	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
25	<a href="#">c2d7uA_</a>	Alignment	not modelled	7.1	6	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
26	<a href="#">c2n9oA_</a>	Alignment	not modelled	7.0	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf126; <b>PDBTitle:</b> solution structure of rnf126 n-terminal zinc finger domain
27	<a href="#">c6e8wC_</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein gp160; <b>PDBTitle:</b> mper-tm domain of hiv-1 envelope glycoprotein (env)
28	<a href="#">c5xlxD_</a>	Alignment	not modelled	6.8	38	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> chemotaxis protein methyltransferase 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of cher1 containing sah
						<b>PDB header:</b> transferase

29	<a href="#">c5ftwA_</a>	Alignment	not modelled	6.8	25	<b>Chain:</b> A; <b>PDB Molecule:</b> chemotaxis protein methyltransferase; <b>PDBTitle:</b> crystal structure of glutamate o-methyltransferase in2 complex with s- adenosyl-l-homocysteine (sah) from3 bacillus subtilis
30	<a href="#">c6fmlJ_</a>	Alignment	not modelled	6.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> J; <b>PDB Molecule:</b> actin related protein 5; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
31	<a href="#">c5nf8A_</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> respiratory supercomplex factor 1, mitochondrial; <b>PDBTitle:</b> solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
32	<a href="#">d1af7a2</a>	Alignment	not modelled	6.2	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Chemotaxis receptor methyltransferase CheR, C-terminal domain
33	<a href="#">c5fcdA_</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
34	<a href="#">c3gnlB_</a>	Alignment	not modelled	6.0	0	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b
35	<a href="#">d1jsxA_</a>	Alignment	not modelled	5.8	33	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB)
36	<a href="#">c4p7cB_</a>	Alignment	not modelled	5.6	26	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
37	<a href="#">c2pbfA_</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase beta-aspartate <b>PDBTitle:</b> crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
38	<a href="#">d1jg1a_</a>	Alignment	not modelled	5.4	45	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
39	<a href="#">c4d05A_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent dna ligase; <b>PDBTitle:</b> structure and activity of a minimal-type atp-dependent dna ligase from2 a psychrotolerant bacterium
40	<a href="#">d1knza_</a>	Alignment	not modelled	5.2	41	<b>Fold:</b> NSP3 homodimer <b>Superfamily:</b> NSP3 homodimer <b>Family:</b> NSP3 homodimer
41	<a href="#">c5w7kA_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag