

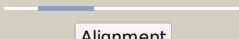
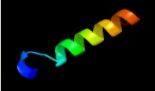
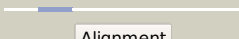















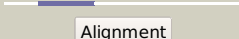

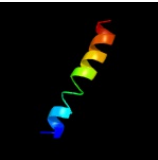
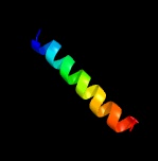
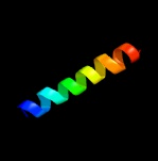
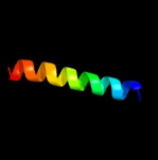
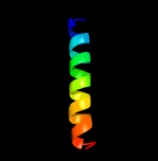


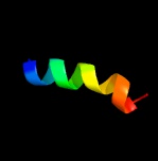
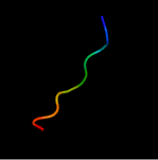


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0544c (- )_635938_636216
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	c765c3a3323d7df9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1fpA_</a>	 Alignment		55.5	41	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> major coat protein assembly; <b>PDBTitle:</b> inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
2	<a href="#">c6bzfG_</a>	 Alignment		24.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation-specific protein 16; <b>PDBTitle:</b> structure of s. cerevisiae zip2:spo16 complex, c2 form
3	<a href="#">c2k1kB_</a>	 Alignment		20.5	64	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
4	<a href="#">c2k1lB_</a>	 Alignment		20.5	64	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
5	<a href="#">c2k1kA_</a>	 Alignment		20.5	64	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
6	<a href="#">c2k1lA_</a>	 Alignment		20.5	64	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
7	<a href="#">d3e11a1</a>	 Alignment		15.7	63	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
8	<a href="#">c4pv1E_</a>	 Alignment		15.4	25	<b>PDB header:</b> electron transport/inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f structure from m. lamosus with the quinone analog2 inhibitor stigmatellin
9	<a href="#">c4i7zE_</a>	 Alignment		15.4	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain
10	<a href="#">c4av3A_</a>	 Alignment		14.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> k(+)-stimulated pyrophosphate-energized sodium pump; <b>PDBTitle:</b> crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site
11	<a href="#">c2e74E_</a>	 Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from m.lamosus

12	<a href="#">c4h0IE_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f complex crystal structure from mastigocladus laminosus2 with n-side inhibitor nqno
13	<a href="#">c2e76E_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
14	<a href="#">c1vf5R_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
15	<a href="#">c4h13E_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
16	<a href="#">c2e75E_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
17	<a href="#">c1vf5E_</a>	Alignment		12.9	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
18	<a href="#">d2e74e1</a>	Alignment		12.9	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetL subunit of the cytochrome b6f complex <b>Family:</b> PetL subunit of the cytochrome b6f complex
19	<a href="#">c4a01B_</a>	Alignment		12.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proton pyrophosphatase; <b>PDBTitle:</b> crystal structure of the h-translocating pyrophosphatase
20	<a href="#">c2zp2B_</a>	Alignment		12.4	50	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> c-terminal domain of kipi from bacillus subtilis
21	<a href="#">d1v54d_</a>	Alignment	not modelled	11.3	10	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
22	<a href="#">c3cjsA_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> minimal recognition complex between prma and ribosomal protein l11
23	<a href="#">d1bm8a_</a>	Alignment	not modelled	9.7	42	<b>Fold:</b> DNA-binding domain of Mlu1-box binding protein MBP1 <b>Superfamily:</b> DNA-binding domain of Mlu1-box binding protein MBP1 <b>Family:</b> DNA-binding domain of Mlu1-box binding protein MBP1
24	<a href="#">d2phcb1</a>	Alignment	not modelled	9.5	44	<b>Fold:</b> Cyclophilin-like <b>Superfamily:</b> Cyclophilin-like <b>Family:</b> PH0987 C-terminal domain-like
25	<a href="#">c3i71B_</a>	Alignment	not modelled	9.1	44	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutk; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
26	<a href="#">c5dudB_</a>	Alignment	not modelled	9.0	44	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ybgj; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
27	<a href="#">c3mmiD_</a>	Alignment	not modelled	8.2	44	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> allophanate hydrolase subunit 1; <b>PDBTitle:</b> allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
28	<a href="#">d1nekc_</a>	Alignment	not modelled	8.1	14	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)

29	<a href="#">c2uwjG_</a>	Alignment	not modelled	7.2	40	<b>PDB header:</b> chaperone <b>Chain:</b> G: <b>PDB Molecule:</b> type iii export protein pscg; <b>PDBTitle:</b> structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
30	<a href="#">c2phcB_</a>	Alignment	not modelled	7.0	44	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ph0987; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
31	<a href="#">c3kziE_</a>	Alignment	not modelled	7.0	31	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b559 subunit alpha; <b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii
32	<a href="#">c2y69Q_</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> electron transport <b>Chain:</b> Q: <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
33	<a href="#">c5ncnB_</a>	Alignment	not modelled	6.8	33	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell cycle protein kinase dbf2; <b>PDBTitle:</b> crystal structure dbf2(ntr)-mob1 complex
34	<a href="#">c4ux5B_</a>	Alignment	not modelled	6.7	42	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mbp1; <b>PDBTitle:</b> structure of dna complex of pcg2
35	<a href="#">c2n28A_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu
36	<a href="#">d2axte1</a>	Alignment	not modelled	6.5	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Cytochrome b559 subunits <b>Family:</b> Cytochrome b559 subunits
37	<a href="#">c3jcue_</a>	Alignment	not modelled	6.4	31	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b559 subunit alpha; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
38	<a href="#">d1l3ga_</a>	Alignment	not modelled	6.3	38	<b>Fold:</b> DNA-binding domain of Mlu1-box binding protein MBP1 <b>Superfamily:</b> DNA-binding domain of Mlu1-box binding protein MBP1 <b>Family:</b> DNA-binding domain of Mlu1-box binding protein MBP1
39	<a href="#">c3m9qA_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein male-specific lethal-3; <b>PDBTitle:</b> drosophila msl3 chromodomain