



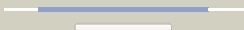










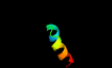



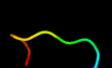

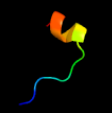
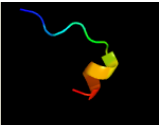




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0318c_(-)_386305_387099
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	74f0420bcc6b0758

Detailed template information

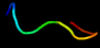
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5tsaA_</a>	 Alignment		100.0	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein; <b>PDBTitle:</b> crystal structure of the zrt-/irt-like protein from bordetella2 bronchiseptica with bound zn2+
2	<a href="#">c5oonA_</a>	 Alignment		73.4	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl-diphosphatase; <b>PDBTitle:</b> structure of undecaprenyl-pyrophosphate phosphatase, bac
3	<a href="#">c6oh2A_</a>	 Alignment		20.2	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cmp-sialic acid transporter; <b>PDBTitle:</b> x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase
4	<a href="#">d3bqoa1</a>	 Alignment		12.8	32	<b>Fold:</b> Telomeric repeat binding factor (TRF) dimerisation domain <b>Superfamily:</b> Telomeric repeat binding factor (TRF) dimerisation domain <b>Family:</b> Telomeric repeat binding factor (TRF) dimerisation domain
5	<a href="#">c6ajjA_</a>	 Alignment		12.4	17	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
6	<a href="#">c3bu8B_</a>	 Alignment		12.2	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> telomeric repeat-binding factor 2; <b>PDBTitle:</b> crystal structure of trf2 trfh domain and tin2 peptide2 complex
7	<a href="#">c3hc1A_</a>	 Alignment		11.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hdod domain protein; <b>PDBTitle:</b> crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducers at 1.90 a resolution
8	<a href="#">d1h6pa_</a>	 Alignment		11.2	26	<b>Fold:</b> Telomeric repeat binding factor (TRF) dimerisation domain <b>Superfamily:</b> Telomeric repeat binding factor (TRF) dimerisation domain <b>Family:</b> Telomeric repeat binding factor (TRF) dimerisation domain
9	<a href="#">c3j39M_</a>	 Alignment		7.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
10	<a href="#">c3zf7P_</a>	 Alignment		7.8	30	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> probable 60s ribosomal protein l14; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
11	<a href="#">c2d11E_</a>	 Alignment		7.3	43	<b>PDB header:</b> cell adhesion <b>Chain:</b> E: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide

12	<a href="#">c2d11F_</a>	Alignment		7.3	43	<b>PDB header:</b> cell adhesion <b>Chain:</b> F; <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
13	<a href="#">c3j3bM_</a>	Alignment		7.2	40	<b>PDB header:</b> ribosome <b>Chain:</b> M; <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
14	<a href="#">d1zq1c1</a>	Alignment		6.9	33	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like

15

[c3iz5N\\_](#)

Alignment



6.7

50

**PDB header:**ribosome  
**Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e);  
**PDB Title:** localization of the large subunit ribosomal proteins into a  
5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome