

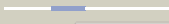






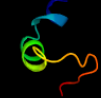


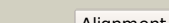

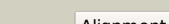


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2600_(-)_2928000_2928401
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	457e60641ce7a8e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4mkqA_	 Alignment		35.4	7	PDB header: toxin Chain: A: PDB Molecule: monalysin; PDBTitle: crystal structure of the pore-forming toxin monalysin mutant deleted2 of the membrane-spanning domain
2	c4mnoA_	 Alignment		25.4	54	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
3	c1yceD_	 Alignment		20.9	31	PDB header: membrane protein Chain: D: PDB Molecule: subunit c; PDBTitle: structure of the rotor ring of f-type na+-atpase from ilyobacter2 tartaricus
4	c2oqkA_	 Alignment		18.6	21	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
5	c1vw48_	 Alignment		17.8	17	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
6	c5e06A_	 Alignment		16.9	33	PDB header: nuclear protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: structure of sin nombre virus nucleoprotein in long-axis crystal form
7	c2dgyA_	 Alignment		16.0	31	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
8	d1jt8a_	 Alignment		14.2	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
9	c5dn6P_	 Alignment		13.7	27	PDB header: hydrolase Chain: P: PDB Molecule: atp synthase f0 subcomplex c subunit; PDBTitle: atp synthase from paracoccus denitrificans
10	c4mjtH_	 Alignment		13.1	7	PDB header: toxin Chain: H: PDB Molecule: monalysin; PDBTitle: crystal structure of the oligomeric pore-forming toxin pro-monalysin
11	c4v1gA_	 Alignment		12.1	23	PDB header: hydrolase Chain: A: PDB Molecule: f0f1 atp synthase subunit c; PDBTitle: crystal structure of a mycobacterial atp synthase rotor ring

12	c5fsgA_	Alignment		11.1	42	<p>PDB header:viral protein Chain: A: PDB Molecule:maltose-binding periplasmic protein, hantavirus PDBTitle: structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design</p>
13	c4bpp0_	Alignment		10.1	33	<p>PDB header:ribosome Chain: 0: PDB Molecule:translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4</p>
14	c6f36E_	Alignment		9.3	21	<p>PDB header:proton transport Chain: E: PDB Molecule:mitochondrial atp synthase subunit c; PDBTitle: polytomella fo model</p>
15	c4rndB_	Alignment		9.2	18	<p>PDB header:hydrolase Chain: B: PDB Molecule:v-type proton atpase subunit f; PDBTitle: crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.</p>
16	c2w5jM_	Alignment		8.6	31	<p>PDB header:hydrolase Chain: M: PDB Molecule:atp synthase c chain, chloroplastic; PDBTitle: structure of the c14-rotor ring of the proton translocating2 chloroplast atp synthase</p>
17	c3fbzA_	Alignment		7.5	18	<p>PDB header:structural protein Chain: A: PDB Molecule:putative uncharacterized protein; PDBTitle: crystal structure of orf140 of the archaeal virus acidianus2 filamentous virus 1 (afv1)</p>
18	d1d7qa_	Alignment		6.7	36	<p>Fold:OB-fold Superfamily:Nucleic acid-binding proteins Family:Cold shock DNA-binding domain-like</p>
19	c2vy2A_	Alignment		5.7	46	<p>PDB header:transcription Chain: A: PDB Molecule:protein leafy; PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter</p>
20	c2ldeA_	Alignment		5.3	14	<p>PDB header:toxin Chain: A: PDB Molecule:sarafotoxin-i3; PDBTitle: solution structure of the long sarafotoxin srtx-i3</p>
21	c3j81i_	Alignment	not modelled	5.1	31	<p>PDB header:ribosome Chain: I: PDB Molecule:es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex</p>