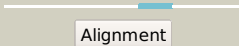





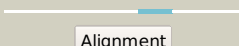

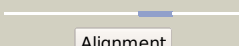

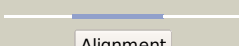

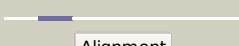

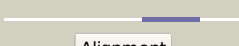









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1947 (-) _2198031_2198432
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	dc76a4b71377f01f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ukzA_</a>	 Alignment		38.2	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin pediocin pa-1 m31l; <b>PDBTitle:</b> nmr solution structure of chemically synthesized antilisterial2 pediocin pa-1 m31l analog.
2	<a href="#">c2n4kA_</a>	 Alignment		36.0	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterocin-hf; <b>PDBTitle:</b> solution structure of enterocin hf, an antilisterial bacteriocin2 produced by enterococcus faecium m3k31
3	<a href="#">c1ry3A_</a>	 Alignment		34.2	43	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin carnobacteriocin b2; <b>PDBTitle:</b> nmr solution structure of the precursor for2 carnobacteriocin b2, an antimicrobial peptide from3 carnobacterium piscicola
4	<a href="#">c3leuA_</a>	 Alignment		30.8	43	<b>PDB header:</b> antibacterial peptide <b>Chain:</b> A: <b>PDB Molecule:</b> leucocin a; <b>PDBTitle:</b> high resolution 1h nmr study of leucocin a in2 dodecylphosphocholine micelles, 19 structures (1:40 ratio3 of leucocin a:dpc) (0.1% tfa)
5	<a href="#">c1og7A_</a>	 Alignment		28.8	29	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin sakacin p; <b>PDBTitle:</b> three-dimensional structure in lipid micelles of the2 pediocin-like antimicrobial peptide sakacin p.
6	<a href="#">c2eghA_</a>	 Alignment		23.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
7	<a href="#">d1kq1a_</a>	 Alignment		18.3	9	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Pleiotropic translational regulator Hfq
8	<a href="#">c2n86A_</a>	 Alignment		17.8	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> spiderine-1a; <b>PDBTitle:</b> nmr structure of otx1a - ick
9	<a href="#">d1u1sa1</a>	 Alignment		17.0	33	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Pleiotropic translational regulator Hfq
10	<a href="#">c4x9zB_</a>	 Alignment		16.9	44	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> alphad-conotoxin gexxa from the venom of conus generalis; <b>PDBTitle:</b> dimeric conotoxin alphad-gexxa
11	<a href="#">c2jcyA_</a>	 Alignment		15.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis

12	<a href="#">c1kq1W_</a>	Alignment		15.6	8	<b>PDB header:</b> translation <b>Chain:</b> W: <b>PDB Molecule:</b> host factor for q beta; <b>PDBTitle:</b> 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
13	<a href="#">c3qhsD_</a>	Alignment		15.3	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein hfq; <b>PDBTitle:</b> crystal structure of full-length hfq from escherichia coli
14	<a href="#">c6gwkX_</a>	Alignment		15.0	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of hfq from caulobacter crescentus
15	<a href="#">d1hk9a_</a>	Alignment		14.7	38	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Pleiotropic translational regulator Hfq
16	<a href="#">c4y91L_</a>	Alignment		14.7	25	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> L: <b>PDB Molecule:</b> rna-binding protein hfq; <b>PDBTitle:</b> crystal structure of a thermotoga maritima hfq homolog
17	<a href="#">c3hsbB_</a>	Alignment		14.4	25	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> protein hfq; <b>PDBTitle:</b> crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
18	<a href="#">c5szeA_</a>	Alignment		12.2	27	<b>PDB header:</b> rna-binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein hfq; <b>PDBTitle:</b> crystal structure of aquifex aeolicus hfq-rna complex at 1.5a
19	<a href="#">c6ewvA_</a>	Alignment		12.0	17	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nrps kj12c-ndd, nrps kj12b-cdd; <b>PDBTitle:</b> solution structure of docking domain complex of rxp nrps: kj12c ndd -2 kj12b cdd
20	<a href="#">c4x9zA_</a>	Alignment		9.2	60	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alphad-conotoxin gexxa from the venom of conus generalis; <b>PDBTitle:</b> dimeric conotoxin alphad-gexxa
21	<a href="#">c1w9zB_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> virus coat protein <b>Chain:</b> B: <b>PDB Molecule:</b> vp9; <b>PDBTitle:</b> structure of bannavirus vp9
22	<a href="#">d2hgsa4</a>	Alignment	not modelled	8.2	23	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Eukaryotic glutathione synthetase ATP-binding domain
23	<a href="#">c2hgsA_</a>	Alignment	not modelled	7.4	21	<b>PDB header:</b> amine/carboxylate ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione synthetase); <b>PDBTitle:</b> human glutathione synthetase
24	<a href="#">d1rh7a_</a>	Alignment	not modelled	7.0	22	<b>Fold:</b> Resistin <b>Superfamily:</b> Resistin <b>Family:</b> Resistin
25	<a href="#">c5oevD_</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione synthetase-like effector 22 (gpa-gss22-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.