










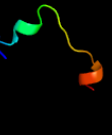

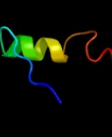



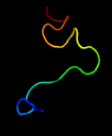










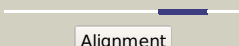
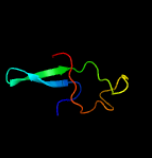
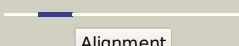

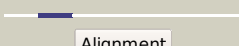

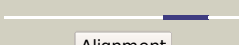
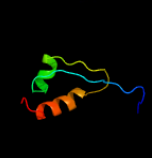

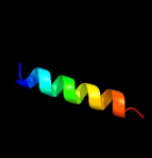



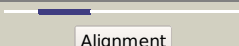
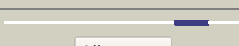



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3576\_(lppH)\_4018537\_4019250  
 Date Fri Aug 9 18:20:25 BST 2019  
 Unique Job ID da0221d8dccb90b8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4esqA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine protein kinase; <b>PDBTitle:</b> crystal structure of the extracellular domain of pknh from2 mycobacterium tuberculosis
2	<a href="#">c2b3gB_</a>	 Alignment		42.4	32	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> p53n (fragment 33-60) bound to rpa70n
3	<a href="#">d2fiua1</a>	 Alignment		40.2	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Atu0297-like
4	<a href="#">c3lo3E_</a>	 Alignment		40.2	35	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
5	<a href="#">d1jcb1</a>	 Alignment		32.1	17	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
6	<a href="#">c2l14B_</a>	 Alignment		30.1	32	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
7	<a href="#">c5uz5C_</a>	 Alignment		27.6	25	<b>PDB header:</b> nuclear protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein a,tap tag; <b>PDBTitle:</b> s. cerevisiae u1 snrnp
8	<a href="#">c3i08D_</a>	 Alignment		23.6	24	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
9	<a href="#">c2ly4B_</a>	 Alignment		21.9	25	<b>PDB header:</b> nuclear protein/antitumour protein <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> hmgb1-facilitated p53 dna binding occurs via hmgb1/p532 transactivation domain interaction and is regulated by the acidic3 tail
10	<a href="#">c3dcaC_</a>	 Alignment		19.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodospseudomonas palustris- a structural3 genomics target
11	<a href="#">c2mzdB_</a>	 Alignment		11.1	29	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> characterization of the p300 taz2-p53 tad2 complex and comparison with2 the p300 taz2-p53 tad1 complex

12	<a href="#">c6ehil_</a>	 Alignment		9.7	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> nuclease nuct; <b>PDBTitle:</b> nuct from helicobacter pylori
13	<a href="#">c2jp3A_</a>	 Alignment		9.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
14	<a href="#">c2n8fA_</a>	 Alignment		9.1	38	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> spider toxin pi-hexatoxin-hi1a; <b>PDBTitle:</b> chemical shift assignments and structure calculation of spider toxin2 pi-hexatoxin-hi1a
15	<a href="#">c2ahmG_</a>	 Alignment		8.0	25	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
16	<a href="#">c2jo1A_</a>	 Alignment		7.5	16	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
17	<a href="#">c2mkvA_</a>	 Alignment		7.1	37	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
18	<a href="#">c2dmwA_</a>	 Alignment		7.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptobrevin-like 1 variant; <b>PDBTitle:</b> solution structure of the longin domain of synaptobrevin-2 like protein 1
19	<a href="#">c2zxeG_</a>	 Alignment		6.5	37	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
20	<a href="#">c1xkmD_</a>	 Alignment		6.0	13	<b>PDB header:</b> antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> distinctin chain b; <b>PDBTitle:</b> nmr structure of antimicrobial peptide distinctin in water
21	<a href="#">c1xkmB_</a>	 Alignment	not modelled	6.0	13	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> distinctin chain b; <b>PDBTitle:</b> nmr structure of antimicrobial peptide distinctin in water
22	<a href="#">c2pxgA_</a>	 Alignment	not modelled	5.9	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein; <b>PDBTitle:</b> nmr solution structure of om1a
23	<a href="#">c1gshA_</a>	 Alignment	not modelled	5.4	15	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
24	<a href="#">d1g94a1</a>	 Alignment	not modelled	5.3	29	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain