
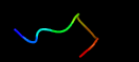

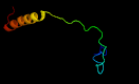

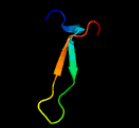

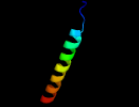

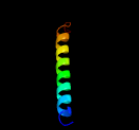

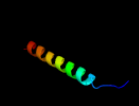
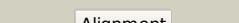


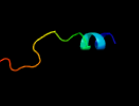

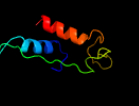


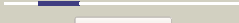
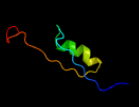


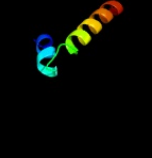



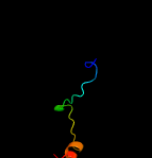

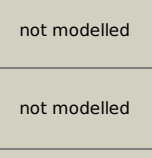


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2473 (-) _2775578_2776294
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	5cc38457c5649852

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1jmtB_</a>	 Alignment		48.4	67	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> splicing factor u2af 65 kda subunit; <b>PDBTitle:</b> x-ray structure of a core u2af65/u2af35 heterodimer
2	<a href="#">c6hwhX_</a>	 Alignment		27.8	17	<b>PDB header:</b> electron transport <b>Chain:</b> X; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from <i>Mycobacterium smegmatis</i>
3	<a href="#">c4ng2E_</a>	 Alignment		26.5	35	<b>PDB header:</b> transcription regulator <b>Chain:</b> E; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lasr lbd-qlsa complex from <i>Pseudomonas aeruginosa</i>
4	<a href="#">c2y69Q_</a>	 Alignment		18.9	20	<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
5	<a href="#">c6hu9e_</a>	 Alignment		18.1	17	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from <i>S. cerevisiae</i>
6	<a href="#">d1v54d_</a>	 Alignment		16.4	20	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
7	<a href="#">c4dlpB_</a>	 Alignment		14.0	36	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> aminoacyl-trna synthetase, class I; aminoacyl-trna <b>PDBTitle:</b> crystal structure of methionyl-trna synthetase from <i>Brucella melitensis</i> bound to selenomethionine
8	<a href="#">c1w8xP_</a>	 Alignment		13.6	23	<b>PDB header:</b> virus <b>Chain:</b> P; <b>PDB Molecule:</b> protein p16; <b>PDBTitle:</b> structural analysis of prd1
9	<a href="#">d2fiqa1</a>	 Alignment		11.4	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> GatZ-like
10	<a href="#">c1zzaA_</a>	 Alignment		9.8	32	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
11	<a href="#">c4e6nB_</a>	 Alignment		8.5	20	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure of bacterial pnpk-c/hen1-n heterodimer

12	<a href="#">c4ardA_</a>	Alignment		8.4	70	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein p27; <b>PDBTitle:</b> structure of the immature retroviral capsid at 8a resolution by cryo-2 electron microscopy
13	<a href="#">d1mp9a1</a>	Alignment		8.2	24	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
14	<a href="#">c6c48E_</a>	Alignment		7.9	38	<b>PDB header:</b> cell cycle/dna binding <b>Chain:</b> E: <b>PDB Molecule:</b> protein lin-52 homolog; <b>PDBTitle:</b> crystal structure of b-myb-lin9-lin52 complex
15	<a href="#">d1aisa1</a>	Alignment		7.4	29	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
16	<a href="#">c2jmvA_</a>	Alignment		7.2	55	<b>PDB header:</b> antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> scytovirin; <b>PDBTitle:</b> solution structure of scytovirin refined against residual2 dipolar couplings
17	<a href="#">c2ky8A_</a>	Alignment		6.6	38	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 2; <b>PDBTitle:</b> solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
18	<a href="#">c5v8kA_</a>	Alignment		6.6	36	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> p800 reaction center core protein; <b>PDBTitle:</b> homodimeric reaction center of h. modesticaldum
19	<a href="#">c6humI_</a>	Alignment		6.3	24	<b>PDB header:</b> proton transport <b>Chain:</b> I: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit i; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
20	<a href="#">c3ajbB_</a>	Alignment		6.3	100	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 19; <b>PDBTitle:</b> crystal structure of human pex3p in complex with n-terminal pex19p2 peptide
21	<a href="#">c1qytG_</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> e. coli aminopeptidase a (pepa)
22	<a href="#">c6h1bA_</a>	Alignment	not modelled	5.9	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid coa ligase; <b>PDBTitle:</b> structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
23	<a href="#">d2d6ya2</a>	Alignment	not modelled	5.4	9	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
24	<a href="#">c4gr5B_</a>	Alignment	not modelled	5.4	34	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of slgn1deltaasub in complex with ampcpp
25	<a href="#">c5x3xq_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> transport protein <b>Chain:</b> Q: <b>PDB Molecule:</b> uncharacterized protein cbiq; <b>PDBTitle:</b> 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
26	<a href="#">c3iymA_</a>	Alignment	not modelled	5.1	44	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> backbone trace of the capsid protein dimer of a fungal partitivirus2 from electron cryomicroscopy and homology modeling