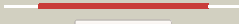
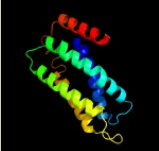

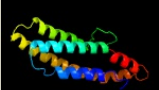
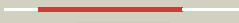


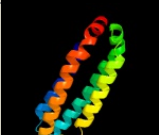

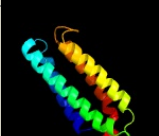





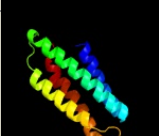

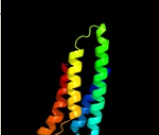

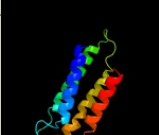




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2633c (- )_2959345_2959830
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	dbb85f5ca6ee0f18

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2p0nA_</a>	 Alignment		99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein nmb1532; <b>PDBTitle:</b> nmb1532 protein from neisseria meningitidis, unknown function
2	<a href="#">c3v5yC_</a>	 Alignment		99.8	16	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> f-box/lrr-repeat protein 5; <b>PDBTitle:</b> structure of fbx15 hemerythrin domain, p2(1) cell
3	<a href="#">c5fnpB_</a>	 Alignment		99.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> iron-sulfur cluster repair protein ytf6; <b>PDBTitle:</b> high resolution zn containing iron sulfur cluster repair2 protein ytf6
4	<a href="#">c2awyB_</a>	 Alignment		97.8	15	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> B: <b>PDB Molecule:</b> hemerythrin-like domain protein dcrh; <b>PDBTitle:</b> met-dcrh-hr
5	<a href="#">c4xpyA_</a>	 Alignment		97.5	18	<b>PDB header:</b> oxygen binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriohemerythrin; <b>PDBTitle:</b> crystal structure of hemerythrin : I114y mutant
6	<a href="#">c3caxA_</a>	 Alignment		97.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0695; <b>PDBTitle:</b> crystal structure of uncharacterized protein pf0695
7	<a href="#">d1i4ya_</a>	 Alignment		92.7	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
8	<a href="#">d2mhra_</a>	 Alignment		92.7	12	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
9	<a href="#">d2hmza_</a>	 Alignment		92.0	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
10	<a href="#">d1hrba_</a>	 Alignment		80.3	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
11	<a href="#">c4rd8B_</a>	 Alignment		52.6	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein from legionella pneumophila subsp. pneumophila str. philadelphia 1

12	<a href="#">c3qzcA_</a>	Alignment		19.1	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic protein cpxp; <b>PDBTitle:</b> structure of the periplasmic stress response protein cpxp
13	<a href="#">d1dd4d_</a>	Alignment		11.2	28	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
14	<a href="#">c2gaaA_</a>	Alignment		11.1	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 39.9 kda protein; <b>PDBTitle:</b> crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
15	<a href="#">d1jhga_</a>	Alignment		10.9	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
16	<a href="#">c3j47O_</a>	Alignment		10.0	54	<b>PDB header:</b> protein binding <b>Chain:</b> O: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn9; <b>PDBTitle:</b> formation of an intricate helical bundle dictates the assembly of the 26s proteasome lid
17	<a href="#">c5hypB_</a>	Alignment		9.8	26	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> m28 protein; <b>PDBTitle:</b> structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein
18	<a href="#">c5wxmV_</a>	Alignment		9.5	20	<b>PDB header:</b> ribosomal protein <b>Chain:</b> V: <b>PDB Molecule:</b> u3 small nucleolar rna-associated protein mpp10; <b>PDBTitle:</b> crystal structure of the imp3 and mpp10 complex
19	<a href="#">d1trra_</a>	Alignment		7.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
20	<a href="#">c3itfA_</a>	Alignment		7.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic adaptor protein cpxp; <b>PDBTitle:</b> structural basis for the inhibitory function of the cpxp adaptor2 protein
21	<a href="#">d1ifwa_</a>	Alignment	not modelled	6.3	18	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> PABC (PABP) domain <b>Family:</b> PABC (PABP) domain
22	<a href="#">c5xlnB_</a>	Alignment	not modelled	6.1	36	<b>PDB header:</b> rna binding protein/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of the trs_une-t and 4ehp complex
23	<a href="#">c5gwmA_</a>	Alignment	not modelled	5.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> metabotropic gaba-b receptor subtype 1; <b>PDBTitle:</b> solution structure of heterodimeric coiled-coil domain of drosophila2 gabab receptor 1 and 3
24	<a href="#">c2ogfD_</a>	Alignment	not modelled	5.4	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein mj0408; <b>PDBTitle:</b> crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
25	<a href="#">c3korD_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus