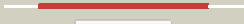



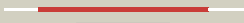














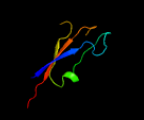
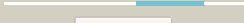
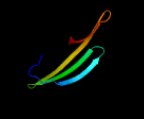



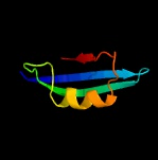
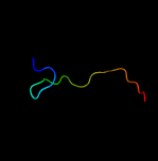

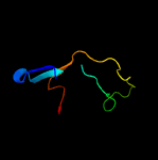
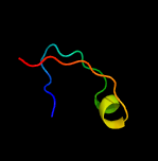
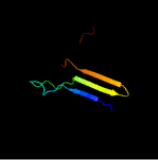


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1890c (- )_2139083_2139694
Date	Fri Aug 2 13:30:50 BST 2019
Unique Job ID	9b30c07fed4cdf92

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1y0ga_</a>	 Alignment		100.0	14	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Ycel-like <b>Family:</b> Ycel-like
2	<a href="#">d1wuba_</a>	 Alignment		100.0	23	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Ycel-like <b>Family:</b> Ycel-like
3	<a href="#">c5ixhB_</a>	 Alignment		100.0	25	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ycei-like domain protein; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia bcna
4	<a href="#">c5ixgD_</a>	 Alignment		100.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> ycei; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia bcnb
5	<a href="#">c2fgsA_</a>	 Alignment		100.0	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of campylobacter jejuni ycei protein,2 structural genomics
6	<a href="#">c3hpeB_</a>	 Alignment		100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> crystal structure of ycei (hp1286) from helicobacter pylori
7	<a href="#">c2x34A_</a>	 Alignment		100.0	14	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose-binding protein, x158; <b>PDBTitle:</b> structure of a polyisoprenoid binding domain from saccharophagus2 degradans implicated in plant cell wall breakdown
8	<a href="#">c3q34A_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ycei-like family protein; <b>PDBTitle:</b> the crystal structure of ycei-like family protein from pseudomonas2 syringae
9	<a href="#">c5vtgB_</a>	 Alignment		58.7	14	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> translocation and assembly module subunit tamb; <b>PDBTitle:</b> the structure of tamb963-1138 from escherichia coli reveals a novel2 hydrophobic beta-taco fold
10	<a href="#">c5e6wA_</a>	 Alignment		53.3	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> re-refinement of the crystal structure of the plexin-semaphorin-2 integrin domain/hybrid domain/i-egf1 segment from the human integrin3 b2 subunit
11	<a href="#">c4r80A_</a>	 Alignment		38.8	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or486; <b>PDBTitle:</b> crystal structure of a de novo designed beta sheet protein, cystatin2 fold, northeast structural genomics consortium (nesg) target or486

12	<a href="#">d1n4ka2</a>	Alignment		29.2	19	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> MIR domain <b>Family:</b> MIR domain
13	<a href="#">c6fzvA</a>	Alignment		20.5	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of the metalloproteinase enhancer pcpe-1 bound to2 the procollagen c propeptide trimer (short)
14	<a href="#">c5k31E</a>	Alignment		19.5	13	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen alpha-1(i) chain; <b>PDBTitle:</b> crystal structure of human fibrillar procollagen type i c-propeptide2 homo-trimer
15	<a href="#">d2gqfa2</a>	Alignment		17.4	15	<b>Fold:</b> HI0933 insert domain-like <b>Superfamily:</b> HI0933 insert domain-like <b>Family:</b> HI0933 insert domain-like
16	<a href="#">d1pbya4</a>	Alignment		13.0	27	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
17	<a href="#">c4aejA</a>	Alignment		12.7	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of human fibrillar procollagen type iii c-2 propeptide trimer
18	<a href="#">c2vxeA</a>	Alignment		10.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cg10686-pa; <b>PDBTitle:</b> solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch)
19	<a href="#">c1zeqX</a>	Alignment		9.8	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> cation efflux system protein cusf; <b>PDBTitle:</b> 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
20	<a href="#">c4qa8A</a>	Alignment		8.8	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein lprf; <b>PDBTitle:</b> crystal structure of lprf from mycobacterium bovis
21	<a href="#">d2vxfA1</a>	Alignment	not modelled	8.8	16	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> LSM14 N-terminal domain-like
22	<a href="#">c3uc0B</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
23	<a href="#">c5ulsA</a>	Alignment	not modelled	7.5	53	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of grp94 in the active conformation
24	<a href="#">c5tvzA</a>	Alignment	not modelled	7.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin pom152; <b>PDBTitle:</b> solution nmr structure of saccharomyces cerevisiae pom152 ig-like2 repeat, residues 718-820
25	<a href="#">c1y96C</a>	Alignment	not modelled	7.3	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> gem-associated protein 6; <b>PDBTitle:</b> crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
26	<a href="#">c5hsbA</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase; <b>PDBTitle:</b> andes virus endonuclease
27	<a href="#">c5thA</a>	Alignment	not modelled	6.7	59	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal spycatcher fusion of wildtype zebrafish tnf <b>PDBTitle:</b> heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
28	<a href="#">c4ipeA</a>	Alignment	not modelled	6.6	59	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated protein 1; <b>PDBTitle:</b> crystal structure of mitochondrial hsp90 (trap1) with

					amppnp
29	<a href="#">c2l55A_</a>	Alignment	not modelled	6.4	24 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> silb,silver efflux protein, mfp component of the three <b>PDBTitle:</b> solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
30	<a href="#">d2icha1</a>	Alignment	not modelled	6.2	11 <b>Fold:</b> AttH-like <b>Superfamily:</b> AttH-like <b>Family:</b> AttH-like
31	<a href="#">c3d8mA_</a>	Alignment	not modelled	6.2	23 <b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate protein, receptor binding protein; <b>PDBTitle:</b> crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
32	<a href="#">d1u7ba2</a>	Alignment	not modelled	5.9	13 <b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
33	<a href="#">c3da0C_</a>	Alignment	not modelled	5.6	23 <b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> cleaved chimeric receptor binding protein from <b>PDBTitle:</b> crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
34	<a href="#">d1rwza2</a>	Alignment	not modelled	5.4	12 <b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
35	<a href="#">c2qazC_</a>	Alignment	not modelled	5.3	16 <b>PDB header:</b> hydrolase activator <b>Chain:</b> C: <b>PDB Molecule:</b> sspb protein; <b>PDBTitle:</b> structure of c. crescentus sspb ortholog
36	<a href="#">d1ud9a2</a>	Alignment	not modelled	5.0	31 <b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
37	<a href="#">d2nysa1</a>	Alignment	not modelled	5.0	19 <b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> AGR C 3712p-like