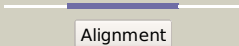
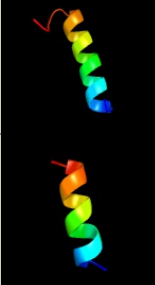


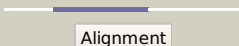

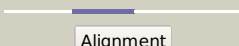
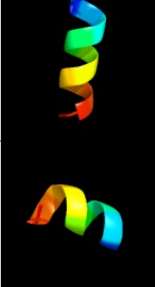
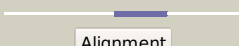
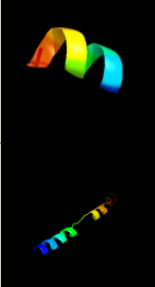
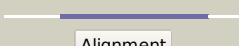
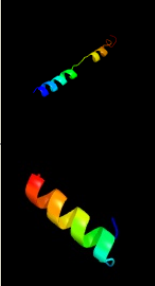
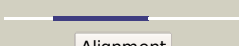
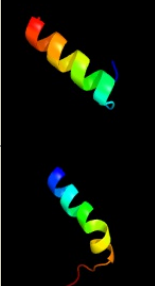

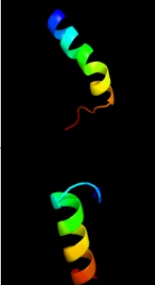

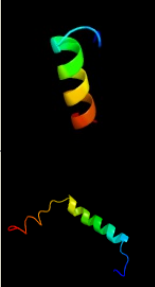

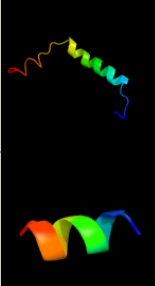

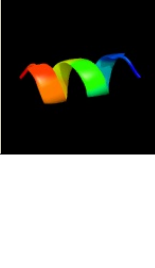
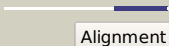

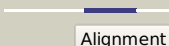

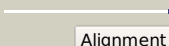



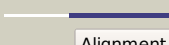

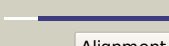



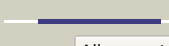



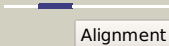
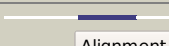
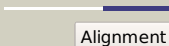

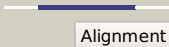


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0749A (- )_841740_841877
Date	Fri Jul 26 01:50:32 BST 2019
Unique Job ID	27c924d13b61e132

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pg6D_</a>	 Alignment		19.1	27	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase dtx3l; <b>PDBTitle:</b> the carboxyl terminal domain of human deltex 3-like
2	<a href="#">c5wlpA_</a>	 Alignment		18.9	36	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> autophagy-related protein 32; <b>PDBTitle:</b> solution structure of the pseudo-receiver domain of atg32
3	<a href="#">d1u7ka_</a>	 Alignment		15.0	26	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
4	<a href="#">c5z7iC_</a>	 Alignment		11.8	31	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
5	<a href="#">d2pofa1</a>	 Alignment		11.5	18	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> CDH-like
6	<a href="#">c1z23A_</a>	 Alignment		10.7	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> crk-associated substrate; <b>PDBTitle:</b> the serine-rich domain from crk-associated substrate2 (p130cas)
7	<a href="#">c6hwyB_</a>	 Alignment		7.8	26	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative gag polyprotein; <b>PDBTitle:</b> mature mlv capsid pentamer structure in intact virus particles
8	<a href="#">d1h3na1</a>	 Alignment		7.7	18	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
9	<a href="#">c6hwwA_</a>	 Alignment		7.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative gag polyprotein; <b>PDBTitle:</b> immature mlv capsid hexamer structure in intact virus particles
10	<a href="#">c3cwzB_</a>	 Alignment		7.5	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> rab6-interacting protein 1; <b>PDBTitle:</b> structure of rab6(gtp)-rip1 complex
11	<a href="#">c2wj0B_</a>	 Alignment		7.1	50	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal hjc; <b>PDBTitle:</b> crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate

12	<a href="#">c2mqbA_</a>	 Alignment		6.9	45	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable beta-lactamase; <b>PDBTitle:</b> nmr structure of putative beta-lactamase (np_372339.1) from2 staphylococcus aureus mu50
13	<a href="#">c2qxB_</a>	 Alignment		6.4	55	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> enhancer of zeste homolog 2; <b>PDBTitle:</b> structural basis of ezh2 recognition by eed
14	<a href="#">c1icIA_</a>	 Alignment		6.2	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> th1ox; <b>PDBTitle:</b> solution structure of designed beta-sheet mini-protein th1ox
15	<a href="#">c1yybA_</a>	 Alignment		6.1	56	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 5; <b>PDBTitle:</b> solution structure of 1-26 fragment of human programmed2 cell death 5 protein
16	<a href="#">c5graA_</a>	 Alignment		6.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (cytidine/uridine-2'-o-)-methyltransferase trmj; <b>PDBTitle:</b> crystal structure of trmj from z. mobilis zm4
17	<a href="#">c1e40A_</a>	 Alignment		6.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
18	<a href="#">c6bk4A_</a>	 Alignment		6.0	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> caprin homolog; <b>PDBTitle:</b> crystal structure of the hr-1 domain of drosophila caprin in the2 p212121 space group
19	<a href="#">d1jr9a2</a>	 Alignment		5.9	23	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
20	<a href="#">d1smpi_</a>	 Alignment		5.9	43	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> beta-Barrel protease inhibitors <b>Family:</b> Metalloprotease inhibitor
21	<a href="#">d2e1za1</a>	 Alignment	not modelled	5.8	57	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
22	<a href="#">c3iz6T_</a>	 Alignment	not modelled	5.6	33	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s21 (s21e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
23	<a href="#">c2h9aA_</a>	 Alignment	not modelled	5.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoid/iron-sulfur <b>PDBTitle:</b> corrinoid iron-sulfur protein
24	<a href="#">d1g99a1</a>	 Alignment	not modelled	5.1	71	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
25	<a href="#">c5mduA_</a>	 Alignment	not modelled	5.0	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rp7-binding protein seb1; <b>PDBTitle:</b> structure of the rna recognition motif (rrm) of seb1 from s. pombe.