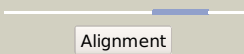
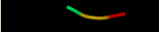
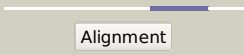
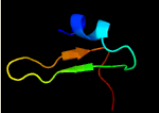
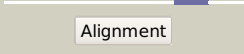


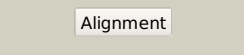

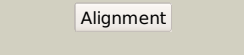

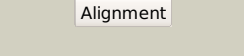

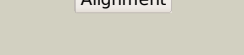

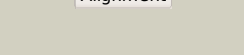

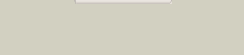
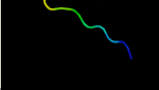




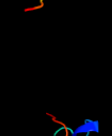
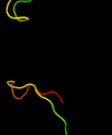
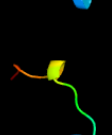


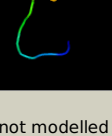
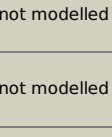


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2288 (- )_2561338_2561715
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	5bec7ef8fdcda418

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1izlM_</a>	 Alignment		25.0	3	<b>PDB header:</b> photosynthesis <b>Chain:</b> M; <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii
2	<a href="#">c2mj6A_</a>	 Alignment		18.9	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative two-component system histidine kinase; <b>PDBTitle:</b> solution structure of the extracellular sensor domain of drak2 histidine kinase
3	<a href="#">c4rrfD_</a>	 Alignment		17.5	63	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> threonine--trna ligase; <b>PDBTitle:</b> editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
4	<a href="#">c1izlC_</a>	 Alignment		16.9	0	<b>PDB header:</b> photosynthesis <b>Chain:</b> C; <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii
5	<a href="#">c2hl2A_</a>	 Alignment		16.5	50	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
6	<a href="#">c4rrcA_</a>	 Alignment		16.1	63	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable threonine--trna ligase 2; <b>PDBTitle:</b> n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3)
7	<a href="#">c2mvaA_</a>	 Alignment		14.6	50	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> rhtx toxin; <b>PDBTitle:</b> solution structure of the toxin, rhtx
8	<a href="#">c5ijlA_</a>	 Alignment		14.1	45	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)
9	<a href="#">c6hmsB_</a>	 Alignment		13.3	45	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> dna polymerase ii large subunit,dna polymerase ii large <b>PDBTitle:</b> cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
10	<a href="#">c5nd1A_</a>	 Alignment		10.1	54	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> viral evolution results in multiple, surface-allocated enzymatic2 activities in a fungal double-stranded rna virus
11	<a href="#">c3ctrA_</a>	 Alignment		8.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of the rrm-domain of the poly(a)-specific2 ribonuclease parn bound to m7gtp

12	<a href="#">d2cs3a1</a>	Alignment		8.3	56	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Variant RING domain
13	<a href="#">c2knxA</a>	Alignment		8.0	64	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> prolow-density lipoprotein receptor-related protein 1; <b>PDBTitle:</b> solution structure of complement repeat cr17 from lrp-1
14	<a href="#">c4gtkB</a>	Alignment		6.5	57	<b>PDB header:</b> transcription/dna <b>Chain:</b> B; <b>PDB Molecule:</b> white-opaque regulator 1; <b>PDBTitle:</b> complex of wopr domain of wor1 in candida albicans with the 17bp dsdna
15	<a href="#">d2nsfa2</a>	Alignment		6.3	41	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Miccothiol-dependent maleylpyruvate isomerase C-terminal domain-like
16	<a href="#">c2xu8B</a>	Alignment		6.1	36	<b>PDB header:</b> structural genomics <b>Chain:</b> B; <b>PDB Molecule:</b> pa1645; <b>PDBTitle:</b> structure of pa1645
17	<a href="#">c5ngnA</a>	Alignment		5.8	50	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> lybatide 2; <b>PDBTitle:</b> lybatide 2, a cystine-rich peptide from lycium barbarum
18	<a href="#">d1k7ba</a>	Alignment		5.8	45	<b>Fold:</b> LDL receptor-like module <b>Superfamily:</b> LDL receptor-like module <b>Family:</b> LDL receptor-like module
19	<a href="#">c2g16A</a>	Alignment		5.8	67	<b>PDB header:</b> luminescent protein <b>Chain:</b> A; <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of s65a y66s gfp variant after backbone2 fragmentation
20	<a href="#">c5ngnB</a>	Alignment		5.4	50	<b>PDB header:</b> plant protein <b>Chain:</b> B; <b>PDB Molecule:</b> lybatide 2; <b>PDBTitle:</b> lybatide 2, a cystine-rich peptide from lycium barbarum
21	<a href="#">d1ajja</a>	Alignment	not modelled	5.4	28	<b>Fold:</b> LDL receptor-like module <b>Superfamily:</b> LDL receptor-like module <b>Family:</b> LDL receptor-like module
22	<a href="#">c5wcoC</a>	Alignment	not modelled	5.4	69	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> ns2; <b>PDBTitle:</b> matrix protein (m1) of infectious salmon anaemia virus
23	<a href="#">d1whva</a>	Alignment	not modelled	5.4	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
24	<a href="#">c4m8bR</a>	Alignment	not modelled	5.3	57	<b>PDB header:</b> transcription/dna <b>Chain:</b> R; <b>PDB Molecule:</b> yhr177w; <b>PDBTitle:</b> fungal protein
25	<a href="#">c4wsiB</a>	Alignment	not modelled	5.2	43	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> maguk p55 subfamily member 5; <b>PDBTitle:</b> crystal structure of pals1/crb complex
26	<a href="#">d1thqa</a>	Alignment	not modelled	5.2	45	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane enzyme PagP
27	<a href="#">c2l3iA</a>	Alignment	not modelled	5.1	71	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> aoxki4a, antimicrobial peptide in spider venom; <b>PDBTitle:</b> ooxki4a, spider derived antimicrobial peptide
28	<a href="#">c2kitA</a>	Alignment	not modelled	5.1	67	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase tor1; <b>PDBTitle:</b> the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k
29	<a href="#">c2jodB</a>	Alignment	not modelled	5.1	83	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> pituitary adenylate cyclase-activating

					<b>PDBTitle:</b> pac1-rshort n-terminal ec domain pacap(6-38) complex
30	<a href="#">d2o4aa1</a>	Alignment	not modelled	5.1	18 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> CUT domain