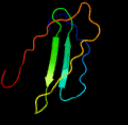
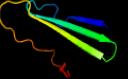
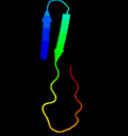
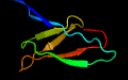
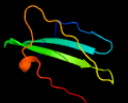
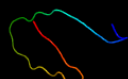


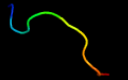


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1906c (- )_2152432_2152902
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	68ce3d99453974d3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5az4A_</a>	Alignment		21.6	44	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook subunit protein; <b>PDBTitle:</b> crystal structure of a 79kda fragment of flge, the hook protein from2 campylobacter jejuni
2	<a href="#">c4kh9B_</a>	Alignment		16.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4785 family protein (lpg0956) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 2.003 a resolution
3	<a href="#">d2e74f1</a>	Alignment		16.5	47	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetM subunit of the cytochrome b6f complex <b>Family:</b> PetM subunit of the cytochrome b6f complex
4	<a href="#">d1j0ha2</a>	Alignment		15.4	11	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
5	<a href="#">c5npyA_</a>	Alignment		13.9	22	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar basal body protein; <b>PDBTitle:</b> crystal structure of helicobacter pylori flagellar hook protein flge2
6	<a href="#">c2zt9F_</a>	Alignment		12.2	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
7	<a href="#">c4h44F_</a>	Alignment		12.2	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
8	<a href="#">c4ogqF_</a>	Alignment		12.2	50	<b>PDB header:</b> electron transport <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
9	<a href="#">d1ht6a1</a>	Alignment		11.5	24	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
10	<a href="#">d1z0na1</a>	Alignment		10.4	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
11	<a href="#">c2ymvA_</a>	Alignment		10.3	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acg nitroreductase; <b>PDBTitle:</b> structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg

12	<a href="#">c6iujA</a>	Alignment		10.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gh30 xylanase b; <b>PDBTitle:</b> crystal structure of gh30 xylanase b from taralomycetes cellulolyticus
13	<a href="#">d1m53a1</a>	Alignment		9.4	17	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
14	<a href="#">d1wzla2</a>	Alignment		8.9	12	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
15	<a href="#">d1ji1a2</a>	Alignment		8.0	11	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
16	<a href="#">c1nofA</a>	Alignment		7.9	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> xylanase; <b>PDBTitle:</b> the first crystallographic structure of a xylanase from glycosyl2 hydrolase family 5: implications for catalysis
17	<a href="#">c3bcwB</a>	Alignment		7.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
18	<a href="#">c2e61A</a>	Alignment		7.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> zinc finger cw-type pwwp domain protein 1; <b>PDBTitle:</b> solution structure of the zf-cw domain in zinc finger cw-type pwwp2 domain protein 1
19	<a href="#">d2j9ua1</a>	Alignment		6.8	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> VPS28 C-terminal domain-like <b>Family:</b> VPS28 C-terminal domain-like
20	<a href="#">d1zdxal</a>	Alignment		6.7	42	<b>Fold:</b> FimD N-terminal domain-like <b>Superfamily:</b> FimD N-terminal domain-like <b>Family:</b> Usher N-domain
21	<a href="#">c4wgkB</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> neutral ceramidase; <b>PDBTitle:</b> crystal structure of human neutral ceramidase with zn-bound phosphate
22	<a href="#">d1zdva1</a>	Alignment	not modelled	6.6	42	<b>Fold:</b> FimD N-terminal domain-like <b>Superfamily:</b> FimD N-terminal domain-like <b>Family:</b> Usher N-domain
23	<a href="#">c2j9wB</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> vps28-prov protein; <b>PDBTitle:</b> structural insight into the escrt-i-ii link and its role in mvb2 trafficking
24	<a href="#">c3be3A</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
25	<a href="#">c2xtiB</a>	Alignment	not modelled	6.2	21	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structure of the major pilus backbone protein from streptococcus2 agalactiae
26	<a href="#">d1uoka1</a>	Alignment	not modelled	6.0	10	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
27	<a href="#">d2f15a1</a>	Alignment	not modelled	5.6	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
28	<a href="#">d1ikpa2</a>	Alignment	not modelled	5.5	43	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> ADP-ribosylating toxins
						<b>PDB header:</b> de novo protein

29	<a href="#">c5kwoA_</a>	Alignment	not modelled	5.5	60	<b>Chain: A: PDB Molecule:</b> designed peptide nc_ehe_d1; <b>PDBTitle:</b> nmr solution structure of designed peptide nc_ehe_d1
30	<a href="#">c2qg3B_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> unknown function <b>Chain: B: PDB Molecule:</b> upf0130 protein af_2059; <b>PDBTitle:</b> crystal structure of a tyw3 methyltransferase-like protein (af_2059)2 from archaeoglobus fulgidus dsm 4304 at 1.95 a resolution
31	<a href="#">c1tjA_</a>	Alignment	not modelled	5.1	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain: A: PDB Molecule:</b> hypothetical upf0130 protein sso0622; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function2 sso0622 from sulfobolus solfataricus