

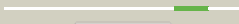




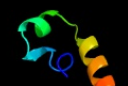

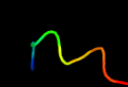

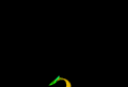

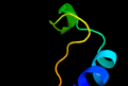

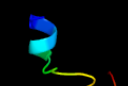

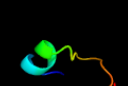










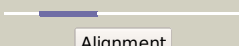

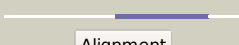

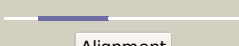
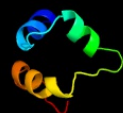
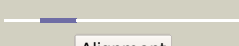


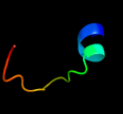



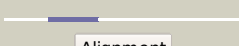

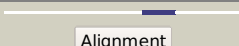


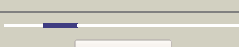


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2239c (-) _2511184_2511660
Date	Mon Aug 5 13:25:37 BST 2019
Unique Job ID	58fa16f85e77ffc4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1rzs_a</a>	 Alignment		67.1	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
2	<a href="#">d1wdia_a</a>	 Alignment		51.7	69	<b>Fold:</b> QueA-like <b>Superfamily:</b> QueA-like <b>Family:</b> QueA-like
3	<a href="#">c2ktr_a</a>	 Alignment		36.9	26	<b>PDB header:</b> signaling protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sequestosome-1; <b>PDBTitle:</b> nmr structure of p62 pb1 dimer determined based on pcs
4	<a href="#">c5loi_a</a>	 Alignment		26.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rad26; <b>PDBTitle:</b> crystal structure of myceliophthora thermophila rad26 (residues 373-2 841)
5	<a href="#">c1yy3_a</a>	 Alignment		24.0	80	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine:trna ribosyltransferase- <b>PDBTitle:</b> structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
6	<a href="#">d1vkya_a</a>	 Alignment		22.8	50	<b>Fold:</b> QueA-like <b>Superfamily:</b> QueA-like <b>Family:</b> QueA-like
7	<a href="#">d1ip9_a</a>	 Alignment		20.3	32	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
8	<a href="#">d2i4sa1</a>	 Alignment		16.6	11	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
9	<a href="#">d1qw2_a</a>	 Alignment		15.3	32	<b>Fold:</b> Hypothetical protein Ta1206 <b>Superfamily:</b> Hypothetical protein Ta1206 <b>Family:</b> Hypothetical protein Ta1206
10	<a href="#">d1lcya1</a>	 Alignment		14.5	22	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> Htra-like serine proteases
11	<a href="#">d2nyga1</a>	 Alignment		14.2	17	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like

12	<a href="#">c3smaD_</a>		Alignment		13.7	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
13	<a href="#">d1v25a_</a>		Alignment		12.8	35	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
14	<a href="#">c6bc3A_</a>		Alignment		12.6	26	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein; <b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via
15	<a href="#">c2zplA_</a>		Alignment		12.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain a
16	<a href="#">c6bwqB_</a>		Alignment		12.0	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel <b>PDBTitle:</b> larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
17	<a href="#">c3bd1B_</a>		Alignment		11.3	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
18	<a href="#">d1qlma_</a>		Alignment		11.1	27	<b>Fold:</b> Methenyltetrahydromethanopterin cyclohydrolase <b>Superfamily:</b> Methenyltetrahydromethanopterin cyclohydrolase <b>Family:</b> Methenyltetrahydromethanopterin cyclohydrolase
19	<a href="#">d2i6va1</a>		Alignment		10.9	11	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
20	<a href="#">c1q0vA_</a>		Alignment		10.5	44	<b>PDB header:</b> transport binding <b>Chain:</b> A: <b>PDB Molecule:</b> hydrophilic protein; has cysteine rich putative <b>PDBTitle:</b> solution structure of tandem uims of vps27
21	<a href="#">c5hj1A_</a>		Alignment	not modelled	10.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase c protein; <b>PDBTitle:</b> crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
22	<a href="#">c5ht0B_</a>		Alignment	not modelled	10.1	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005; <b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
23	<a href="#">c6mb6A_</a>		Alignment	not modelled	10.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein; <b>PDBTitle:</b> aac-iiib binary with coash
24	<a href="#">d2ae0x1</a>		Alignment	not modelled	9.8	25	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> MLTA-like
25	<a href="#">c4fioA_</a>		Alignment	not modelled	9.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methenyltetrahydromethanopterin cyclohydrolase; <b>PDBTitle:</b> crystal structure of methenyltetrahydromethanopterin cyclohydrolase2 from methanobrevibacter ruminantium
26	<a href="#">c6g04B_</a>		Alignment	not modelled	9.2	30	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein s26-a; <b>PDBTitle:</b> nmr solution structure of yeast tsr2(1-152) in complex with s26a(100-2 119)
27	<a href="#">c4qiwH_</a>		Alignment	not modelled	9.2	21	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> dna-directed rna polymerase subunit h; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis <b>PDB header:</b> hydrolase

28	<a href="#">c4gvsA</a>	Alignment	not modelled	9.0	23	<b>Chain:</b> A: <b>PDB Molecule:</b> methenyltetrahydromethanopterin cyclohydrolase; <b>PDBTitle:</b> x-ray structure of the archaeoglobus fulgidus methenyl-2 tetrahydromethanopterin cyclohydrolase in complex with n5-formyl-3 tetrahydromethanopterin
29	<a href="#">d1ky9b2</a>	Alignment	not modelled	9.0	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
30	<a href="#">c2joaA</a>	Alignment	not modelled	9.0	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
31	<a href="#">c4kxbF</a>	Alignment	not modelled	8.6	31	<b>PDB header:</b> transcription/replication <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein pob3n; <b>PDBTitle:</b> structure of the spt16d pob3n heterodimer
32	<a href="#">d1dzfa2</a>	Alignment	not modelled	8.5	29	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
33	<a href="#">d1eika</a>	Alignment	not modelled	8.3	21	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
34	<a href="#">c6mn5A</a>	Alignment	not modelled	8.2	20	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
35	<a href="#">d1hmja</a>	Alignment	not modelled	8.1	7	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
36	<a href="#">c4m4xA</a>	Alignment	not modelled	8.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> aryl hydrocarbon receptor; <b>PDBTitle:</b> structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
37	<a href="#">c6igxC</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> condensin complex subunit 2; <b>PDBTitle:</b> crystal structure of human cap-g in complex with cap-h
38	<a href="#">c2pmzV</a>	Alignment	not modelled	7.7	20	<b>PDB header:</b> translation, transferase <b>Chain:</b> V: <b>PDB Molecule:</b> dna-directed rna polymerase subunit h; <b>PDBTitle:</b> archaeal rna polymerase from sulfolobus solfataricus
39	<a href="#">c2n7pA</a>	Alignment	not modelled	7.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of pdz domain
40	<a href="#">d1ky9a1</a>	Alignment	not modelled	7.5	28	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
41	<a href="#">c3e4fB</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
42	<a href="#">c2p3wB</a>	Alignment	not modelled	7.1	22	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease htra3; <b>PDBTitle:</b> crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgwv)
43	<a href="#">d2g5da1</a>	Alignment	not modelled	6.5	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> MLTA-like
44	<a href="#">c1wypA</a>	Alignment	not modelled	6.5	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> calponin 1; <b>PDBTitle:</b> solution structure of the ch domain of human calponin 1
45	<a href="#">c3n6xA</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutathionylspermidine synthase; <b>PDBTitle:</b> crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
46	<a href="#">c1lcyA</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> htra2 serine protease; <b>PDBTitle:</b> crystal structure of the mitochondrial serine protease htra2
47	<a href="#">c2fvzB</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol monophosphatase 2; <b>PDBTitle:</b> human inositol monophosphatase 2
48	<a href="#">c5t5iL</a>	Alignment	not modelled	6.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdd; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
49	<a href="#">c2gefA</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease vp4; <b>PDBTitle:</b> crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
50	<a href="#">d1ogya1</a>	Alignment	not modelled	5.8	33	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
51	<a href="#">d2jioa1</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
52	<a href="#">c3bn7A</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution
53	<a href="#">c1wa9A</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> circadian rhythm <b>Chain:</b> A: <b>PDB Molecule:</b> period circadian protein; <b>PDBTitle:</b> crystal structure of the pas repeat region of the2

					drosophila clock protein period
54	<a href="#">c2r3yC_</a>	Alignment	not modelled	5.5	33 <b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> C: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of the degs protease in complex with the2 ywf activating peptide
55	<a href="#">c4n81A_</a>	Alignment	not modelled	5.5	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol monophosphatase; <b>PDBTitle:</b> another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis
56	<a href="#">d3c8da1</a>	Alignment	not modelled	5.3	28 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Enterochelin esterase N-terminal domain-like
57	<a href="#">c2egeA_</a>	Alignment	not modelled	5.2	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kiaa1666; <b>PDBTitle:</b> solution structure of the third sh3 domain from human2 kiaa1666 protein
58	<a href="#">d1kqfa1</a>	Alignment	not modelled	5.1	25 <b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
59	<a href="#">c4jj0B_</a>	Alignment	not modelled	5.0	13 <b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> mamp; <b>PDBTitle:</b> crystal structure of mamp