
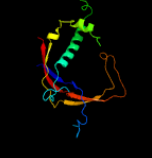

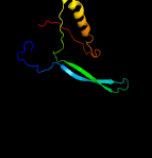

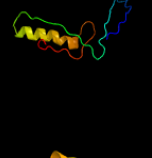


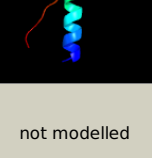


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2821c (- )_3128263_3128973
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	c2c7a2364a11a425

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ifnF_</a>	 Alignment		100.0	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> F; <b>PDB Molecule:</b> type iii-a crispr-associated ramp protein csm3; <b>PDBTitle:</b> crystal structure of type iii-a crispr csm complex
2	<a href="#">c4n0lB_</a>	 Alignment		100.0	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> predicted component of a thermophile-specific dna repair <b>PDBTitle:</b> methanopyrus kandleri csm3 crystal structure
3	<a href="#">c6musK_</a>	 Alignment		100.0	40	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> K; <b>PDB Molecule:</b> uncharacterized protein csm3; <b>PDBTitle:</b> cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
4	<a href="#">c5yjdB_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> csm3; <b>PDBTitle:</b> structural insights into the crispr-cas-associated ribonuclease2 activity of staphylococcus epidermidis csm3
5	<a href="#">c4qtsC_</a>	 Alignment		100.0	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> crispr type iii-associated ramp protein csm3; <b>PDBTitle:</b> crystal structure of csm3-csm4 subcomplex in the type iii-a crispr-cas2 interference complex
6	<a href="#">c6ae2B_</a>	 Alignment		100.0	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> csm3; <b>PDBTitle:</b> crystal structure of csm3 of the type iii-a crispr-cas effector2 complex
7	<a href="#">c4w8vA_</a>	 Alignment		100.0	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> crispr system cmr subunit cmr6; <b>PDBTitle:</b> crystal structure of cmr6 from pyrococcus furiosus
8	<a href="#">c3x1lE_</a>	 Alignment		100.0	27	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> E; <b>PDB Molecule:</b> cmr4; <b>PDBTitle:</b> crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
9	<a href="#">c4w8wB_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> crispr system cmr subunit cmr4; <b>PDBTitle:</b> crystal structure of oligomeric cmr4 from pyrococcus furiosus
10	<a href="#">c3x1lH_</a>	 Alignment		99.9	24	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> H; <b>PDB Molecule:</b> cmr6; <b>PDBTitle:</b> crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
11	<a href="#">c6ig0H_</a>	 Alignment		99.7	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> H; <b>PDB Molecule:</b> type iii-a crispr-associated ramp protein csm5; <b>PDBTitle:</b> type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound

12	<a href="#">c4w8xA</a>	Alignment		99.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr1-1; <b>PDBTitle:</b> crystal structure of cmr1 from pyrococcus furiosus bound to a2 nucleotide
13	<a href="#">c6musF</a>	Alignment		99.5	26	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein csm5; <b>PDBTitle:</b> cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
14	<a href="#">c4l6uB</a>	Alignment		99.5	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
15	<a href="#">c6muuE</a>	Alignment		98.4	19	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein csm4; <b>PDBTitle:</b> cryo-em structure of csm-crrna binary complex in type iii-a crispr-cas2 system
16	<a href="#">c6ig0B</a>	Alignment		97.9	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> type iii-a crispr-associated ramp protein csm4; <b>PDBTitle:</b> type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound
17	<a href="#">c4qtsB</a>	Alignment		97.7	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> crispr type iii-associated ramp protein csm4; <b>PDBTitle:</b> crystal structure of csm3-csm4 subcomplex in the type iii-a crispr-cas2 interference complex
18	<a href="#">c6fjwA</a>	Alignment		94.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cas6 protein; <b>PDBTitle:</b> streptococcus thermophilus cas6
19	<a href="#">c4c97B</a>	Alignment		92.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cas6a; <b>PDBTitle:</b> cas6 (ttha0078) h37a mutant
20	<a href="#">c4ilmH</a>	Alignment		92.1	16	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas6 2; <b>PDBTitle:</b> crispr rna processing endoribonuclease
21	<a href="#">c6njyB</a>	Alignment	not modelled	87.1	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> type iv crispr associated cas6 rna endonuclease; <b>PDBTitle:</b> type iv crispr associated rna endonuclease cas6 - apo form
22	<a href="#">c3i4hX</a>	Alignment	not modelled	79.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> endoribonuclease; <b>PDBTitle:</b> crystal structure of cas6 in pyrococcus furiosus
23	<a href="#">c3qjjB</a>	Alignment	not modelled	77.3	19	<b>PDB header:</b> immune system/rna <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0350; <b>PDBTitle:</b> one ramp protein binding different rna substrates
24	<a href="#">c4txdA</a>	Alignment	not modelled	76.7	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> csc2; <b>PDBTitle:</b> crystal structure of thermofilum pendens csc2
25	<a href="#">c4c9dA</a>	Alignment	not modelled	74.1	23	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> cas6b; <b>PDBTitle:</b> cas6 (tthb231) product complex
26	<a href="#">c1ajnA</a>	Alignment	not modelled	74.0	17	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin amidohydrolase; <b>PDBTitle:</b> penicillin acylase complexed with p-nitrophenylacetic acid
27	<a href="#">c5yi6A</a>	Alignment	not modelled	72.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas6 1; <b>PDBTitle:</b> crispr associated protein cas6
28	<a href="#">c1cp9A</a>	Alignment	not modelled	71.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin g amidase; <b>PDBTitle:</b> crystal structure of penicillin g acylase from the bro1 mutant strain2 of providencia rettgeri

29	<a href="#">c4z7B_</a>	Alignment	not modelled	71.0	33	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> cas6b; <b>PDBTitle:</b> crystal structure of cas6b
30	<a href="#">c1gk9A_</a>	Alignment	not modelled	71.0	17	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin g acylase alpha subunit; <b>PDBTitle:</b> crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
31	<a href="#">c1e3aA_</a>	Alignment	not modelled	68.7	17	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin amidase alpha subunit; <b>PDBTitle:</b> a slow processing precursor penicillin acylase from escherichia coli
32	<a href="#">c4yfbD_</a>	Alignment	not modelled	65.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein related to penicillin acylase; <b>PDBTitle:</b> structure of n-acylhomoserine lactone acylase macq in complex with2 phenylacetic acid
33	<a href="#">c6nvyC_</a>	Alignment	not modelled	57.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> penicillin g acylase; <b>PDBTitle:</b> crystal structure of penicillin g acylase from bacillus thermotolerans
34	<a href="#">c2ae3A_</a>	Alignment	not modelled	53.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl 7-aminocephalosporanic acid acylase; <b>PDBTitle:</b> glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
35	<a href="#">c2wybA_</a>	Alignment	not modelled	50.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-homoserine lactone acylase pvdq subunit <b>PDBTitle:</b> the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
36	<a href="#">c3k3wA_</a>	Alignment	not modelled	49.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin g acylase; <b>PDBTitle:</b> thermostable penicillin g acylase from alcaligenes faecalis in2 orthorhombic form
37	<a href="#">c4hsrA_</a>	Alignment	not modelled	49.5	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl-7-aminocephalosporanic acid acylase alpha chain; <b>PDBTitle:</b> crystal structure of a class iii engineered cephalosporin acylase
38	<a href="#">c1oqzB_</a>	Alignment	not modelled	39.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaryl acylase; <b>PDBTitle:</b> crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 insight into autoproteolytic activation
39	<a href="#">c6dd5B_</a>	Alignment	not modelled	22.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mmb-1 cas6 fused to maltose binding protein,crispr- <b>PDBTitle:</b> crystal structure of the cas6 domain of marinomonas mediterranea mmb-12 cas6-rt-cas1 fusion protein
40	<a href="#">c5il5A_</a>	Alignment	not modelled	15.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mlnd; <b>PDBTitle:</b> crystal structure of the dehydratase domain of mlnd from bacillus2 amyloliquefaciens
41	<a href="#">c4u3vA_</a>	Alignment	not modelled	15.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pksr; <b>PDBTitle:</b> crystal structure of the trans-acyltransferase polyketide synthase2 enoyl-isomerase
42	<a href="#">c4uedB_</a>	Alignment	not modelled	15.1	47	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation factor 4e-binding protein 1; <b>PDBTitle:</b> complex of human eif4e with the 4e binding protein 4e-bp1
43	<a href="#">c6h9iB_</a>	Alignment	not modelled	14.4	45	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> csf5; <b>PDBTitle:</b> csf5, crispr-cas type iv cas6 crrna endonuclease
44	<a href="#">d1qr0a1</a>	Alignment	not modelled	13.4	25	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> 4'-Phosphopantetheinyl transferase SFP
45	<a href="#">c5hu7B_</a>	Alignment	not modelled	12.2	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide synthase; <b>PDBTitle:</b> crystal structure of the trans-at pks dehydratase domain of c0zgg42 from brevibacillus brevis
46	<a href="#">c3um0B_</a>	Alignment	not modelled	10.6	50	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
47	<a href="#">d2qamr1</a>	Alignment	not modelled	10.4	28	<b>Fold:</b> L21p-like <b>Superfamily:</b> L21p-like <b>Family:</b> Ribosomal protein L21p
48	<a href="#">c3ga2A_</a>	Alignment	not modelled	9.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624
49	<a href="#">c3c26A_</a>	Alignment	not modelled	9.3	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase ta0821; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
50	<a href="#">c4xpuA_</a>	Alignment	not modelled	9.1	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> the crystal structure of endov from e.coli
51	<a href="#">d1cixa_</a>	Alignment	not modelled	8.6	54	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
52	<a href="#">c1cixA_</a>	Alignment	not modelled	8.6	54	<b>PDB header:</b> antimicrobial peptide <b>Chain:</b> A: <b>PDB Molecule:</b> protein (tachystatin a); <b>PDBTitle:</b> three-dimensional structure of antimicrobial peptide2 tachystatin a isolated from horseshoe crab
53	<a href="#">c4nspA_</a>	Alignment	not modelled	8.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of human endov

54	<a href="#">c3keyA_</a>	Alignment	not modelled	8.4	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein stn1; <b>PDBTitle:</b> crystal structure of s. cerevisiae stn1 c-terminal
55	<a href="#">c6gnyD_</a>	Alignment	not modelled	7.7	83	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex
56	<a href="#">c2w36B_</a>	Alignment	not modelled	7.7	67	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
57	<a href="#">c6gnxB_</a>	Alignment	not modelled	7.7	83	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex -2 selenomethionine derivative
58	<a href="#">d1r5ba3</a>	Alignment	not modelled	7.6	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
59	<a href="#">c3gocB_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
60	<a href="#">c2lycA_</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 1 homolog; <b>PDBTitle:</b> structure of c-terminal domain of ska1
61	<a href="#">c6qsrA_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
62	<a href="#">c5mlcT_</a>	Alignment	not modelled	6.8	10	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 50s ribosomal protein l21, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
63	<a href="#">c3bboT_</a>	Alignment	not modelled	6.3	10	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> ribosomal protein l21; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
64	<a href="#">d2ix0a3</a>	Alignment	not modelled	6.2	43	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
65	<a href="#">c4regA_</a>	Alignment	not modelled	6.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure analysis of pf0642
66	<a href="#">c5mmiS_</a>	Alignment	not modelled	6.0	10	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 50s ribosomal protein l21, chloroplastic; <b>PDBTitle:</b> structure of the large subunit of the chloroplast ribosome
67	<a href="#">c4byrP_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
68	<a href="#">c5bp2A_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mycocerosic acid synthase-like polyketide synthase; <b>PDBTitle:</b> dehydratase domain (dh) of a mycocerosic acid synthase-like (mas-like)2 pks, crystal form 1