

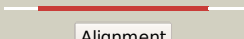

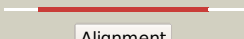






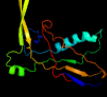





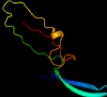

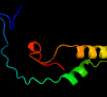

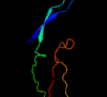
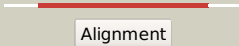

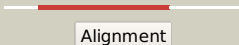


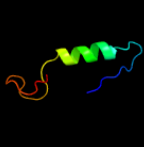


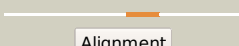



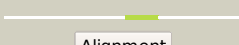
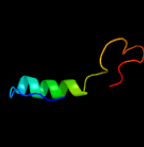
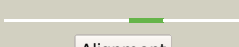
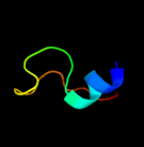

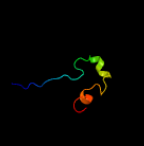


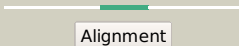
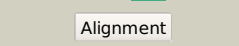

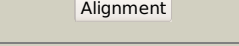
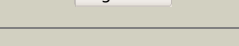



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2820c_(-)_3127374_3128282
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	d6a4de4a30c99cc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ig0B_</a>	 Alignment		100.0	38	<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
2	<a href="#">c6muuE_</a>	 Alignment		100.0	23	<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
3	<a href="#">c4qtsB_</a>	 Alignment		100.0	21	<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
4	<a href="#">c4n0lB_</a>	 Alignment		98.6	14	<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
5	<a href="#">c6ae2B_</a>	 Alignment		98.6	22	<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
6	<a href="#">c6ifnF_</a>	 Alignment		98.5	16	<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
7	<a href="#">c4w8wB_</a>	 Alignment		98.5	18	<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
8	<a href="#">c5yjdB_</a>	 Alignment		98.2	15	<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
9	<a href="#">c6musK_</a>	 Alignment		98.1	15	<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
10	<a href="#">c4w8vA_</a>	 Alignment		97.4	13	<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
11	<a href="#">c3x1lE_</a>	 Alignment		97.3	19	<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

12	<a href="#">c4h4kA</a>	 Alignment		97.3	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr3; <b>PDBTitle:</b> structure of the cmr2-cmr3 subcomplex of the cmr rna-silencing complex
13	<a href="#">c4qtsC</a>	 Alignment		97.1	16	<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
14	<a href="#">c3x1lH</a>	 Alignment		96.1	16	<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
15	<a href="#">c4ilmH</a>	 Alignment		92.8	19	<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
16	<a href="#">c6fjwA</a>	 Alignment		84.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cas6 protein; <b>PDBTitle:</b> streptococcus thermophilus cas6
17	<a href="#">c4c97B</a>	 Alignment		67.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cas6a; <b>PDBTitle:</b> cas6 (ttha0078) h37a mutant
18	<a href="#">c4c9dA</a>	 Alignment		62.5	21	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> cas6b; <b>PDBTitle:</b> cas6 (tthb231) product complex
19	<a href="#">c3i4hX</a>	 Alignment		59.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> endoribonuclease; <b>PDBTitle:</b> crystal structure of cas6 in pyrococcus furiosus
20	<a href="#">d1q0qa3</a>	 Alignment		51.8	19	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
21	<a href="#">c5kqaA</a>	 Alignment	not modelled	48.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
22	<a href="#">c6dd5B</a>	 Alignment	not modelled	47.9	23	<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
23	<a href="#">c2h5xA</a>	 Alignment	not modelled	47.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruva; <b>PDBTitle:</b> ruva from mycobacterium tuberculosis
24	<a href="#">c5yi6A</a>	 Alignment	not modelled	46.7	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
25	<a href="#">c2qtpA</a>	 Alignment	not modelled	42.2	36	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf1185 family protein (spo0826) from2 silicibacter pomeroyi dss-3 at 2.10 a resolution
26	<a href="#">d2qtpa1</a>	 Alignment	not modelled	42.2	36	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> BB2672-like <b>Family:</b> BB2672-like
27	<a href="#">d3byqa1</a>	 Alignment	not modelled	40.9	19	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> BB2672-like <b>Family:</b> BB2672-like
28	<a href="#">c3au9A</a>	 Alignment	not modelled	40.8	17	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase;

						<b>PDBTitle:</b> crystal structure of the quaternary complex-1 of an isomerase
29	<a href="#">c6ig0H_</a>	Alignment	not modelled	40.6	11	<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
30	<a href="#">c2eghA_</a>	Alignment	not modelled	39.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
31	<a href="#">c3qjB_</a>	Alignment	not modelled	37.9	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
32	<a href="#">d2b9da1</a>	Alignment	not modelled	30.3	18	<b>Fold:</b> E7 C-terminal domain-like <b>Superfamily:</b> E7 C-terminal domain-like <b>Family:</b> E7 C-terminal domain-like
33	<a href="#">c6musF_</a>	Alignment	not modelled	29.2	15	<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
34	<a href="#">c6njyB_</a>	Alignment	not modelled	25.7	17	<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
35	<a href="#">c2jcyA_</a>	Alignment	not modelled	24.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis
36	<a href="#">c1d8A_</a>	Alignment	not modelled	23.4	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> protein (holliday junction dna helicase ruva); <b>PDBTitle:</b> e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
37	<a href="#">c5yzcB_</a>	Alignment	not modelled	23.3	22	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycoprotein f1,measles virus fusion protein; <b>PDBTitle:</b> crystal structure of the prefusion form of measles virus fusion2 protein in complex with a fusion inhibitor compound (as-48)
38	<a href="#">d2ewla1</a>	Alignment	not modelled	23.0	14	<b>Fold:</b> E7 C-terminal domain-like <b>Superfamily:</b> E7 C-terminal domain-like <b>Family:</b> E7 C-terminal domain-like
39	<a href="#">c1ixrB_</a>	Alignment	not modelled	20.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
40	<a href="#">c3j6vJ_</a>	Alignment	not modelled	18.7	16	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 28s ribosomal protein s10, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
41	<a href="#">c2v3mF_</a>	Alignment	not modelled	18.7	29	<b>PDB header:</b> ribosomal protein <b>Chain:</b> F: <b>PDB Molecule:</b> naf1; <b>PDBTitle:</b> structure of the gar1 domain of naf1
42	<a href="#">c4ql6A_</a>	Alignment	not modelled	18.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxy-terminal processing protease; <b>PDBTitle:</b> structure of c. trachomatis ct441
43	<a href="#">c4z7lB_</a>	Alignment	not modelled	17.6	29	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> cas6b; <b>PDBTitle:</b> crystal structure of cas6b
44	<a href="#">c4w8xA_</a>	Alignment	not modelled	15.8	14	<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
45	<a href="#">d2aw2a1</a>	Alignment	not modelled	14.6	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
46	<a href="#">c3a14B_</a>	Alignment	not modelled	12.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of dxr from thermotoga maritima, in complex with2 nadph
47	<a href="#">c1hjpA_</a>	Alignment	not modelled	12.4	11	<b>PDB header:</b> dna recombination <b>Chain:</b> A: <b>PDB Molecule:</b> ruva; <b>PDBTitle:</b> holliday junction binding protein ruva from e. coli
48	<a href="#">c3mgjA_</a>	Alignment	not modelled	12.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1480; <b>PDBTitle:</b> crystal structure of the saccharop_dh_n domain of mj1480 protein from2 methanococcus jannaschii. northeast structural genomics consortium3 target mjr83a.
49	<a href="#">d1xaau_</a>	Alignment	not modelled	11.8	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
50	<a href="#">c1k5hB_</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose-5-phosphate reductoisomerase
51	<a href="#">c2ovsB_</a>	Alignment	not modelled	9.3	14	<b>PDB header:</b> gene regulation, ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> i0044; <b>PDBTitle:</b> crystal structure of a type three secretion system protein
52	<a href="#">c5hkd_</a>	Alignment	not modelled	8.9	16	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> I: <b>PDB Molecule:</b> cdii immunity protein;

52	<a href="#">c3tkqL_</a>	Alignment	not modelled	8.9	10	<b>PDBTitle:</b> crystal structure of cdi complex from escherichia coli stec_o31
53	<a href="#">d2gycf2</a>	Alignment	not modelled	8.9	39	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> L9 N-domain-like <b>Family:</b> Ribosomal protein L9 N-domain
54	<a href="#">d1cqua_</a>	Alignment	not modelled	8.4	39	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> L9 N-domain-like <b>Family:</b> Ribosomal protein L9 N-domain
55	<a href="#">d1f06a2</a>	Alignment	not modelled	7.1	28	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
56	<a href="#">c3gqqD_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> splicing <b>Chain:</b> D: <b>PDB Molecule:</b> protein unc-119 homolog a; <b>PDBTitle:</b> crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
57	<a href="#">c1ixrA_</a>	Alignment	not modelled	6.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
58	<a href="#">c6iqsD_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> crystal structure of prc with I245a and I340g mutations in complex2 with nlpi
59	<a href="#">c1v1cA_</a>	Alignment	not modelled	6.5	47	<b>PDB header:</b> sh3-domain <b>Chain:</b> A: <b>PDB Molecule:</b> obscurin; <b>PDBTitle:</b> solution structure of the sh3 domain of obscurin
60	<a href="#">c5mjrA_</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> protein thf1; <b>PDBTitle:</b> structure of psb29 at 1.55a
61	<a href="#">d1k4na_</a>	Alignment	not modelled	6.3	8	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Hypothetical protein YecM (EC4020)
62	<a href="#">c1pnyF_</a>	Alignment	not modelled	6.2	39	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 50s ribosomal protein I9; <b>PDBTitle:</b> crystal structure of the wild type ribosome from e. coli, 50s subunit2 of 70s ribosome. this file, 1pny, contains only molecules of the 50s3 ribosomal subunit. the 30s subunit is in the pdb file 1pnx.
63	<a href="#">c3nvnA_</a>	Alignment	not modelled	6.1	18	<b>PDB header:</b> viral protein/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> evm139; <b>PDBTitle:</b> molecular mechanism of guidance cue recognition
64	<a href="#">d1nf1a_</a>	Alignment	not modelled	5.8	18	<b>Fold:</b> GTPase activation domain, GAP <b>Superfamily:</b> GTPase activation domain, GAP <b>Family:</b> p120GAP domain-like
65	<a href="#">c4oe4A_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate dehydrogenase, <b>PDBTitle:</b> crystal structure of yeast ald4a1 complexed with nad+
66	<a href="#">c5wqlC_</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> protein binding/signaling protein/hydrol <b>Chain:</b> C: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> structure of a pdz-protease bound to a substrate-binding adaptor
67	<a href="#">d1b74a1</a>	Alignment	not modelled	5.2	50	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
68	<a href="#">d1bf4a_</a>	Alignment	not modelled	5.2	11	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> "Histone-like" proteins from archaea
69	<a href="#">c2eqnA_</a>	Alignment	not modelled	5.0	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein loc92345; <b>PDBTitle:</b> solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]