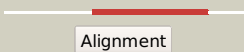

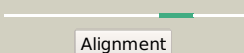

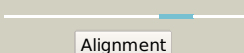


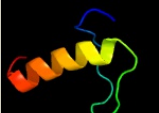
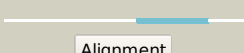

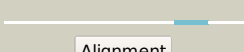
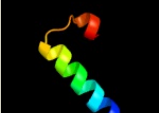


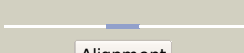
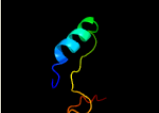






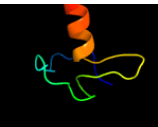
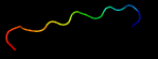



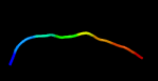
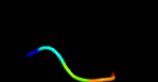
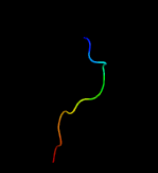



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0029 (-) _32057_33154
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	79238f393a7e8187

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5imuA_	 Alignment		100.0	34	PDB header: signaling protein Chain: A; PDB Molecule: tat (twin-arginine translocation) pathway signal sequence PDBTitle: a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis
2	c5ganC_	 Alignment		42.5	24	PDB header: transcription Chain: C; PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrrp at2 3.7 angstrom
3	c3jb9B_	 Alignment		37.3	27	PDB header: rna binding protein/rna Chain: B; PDB Molecule: pre-mrna-splicing factor cwf10; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
4	c5mqfB_	 Alignment		35.5	35	PDB header: splicing Chain: B; PDB Molecule: 116 kda u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
5	d1afra_	 Alignment		35.1	20	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
6	c6cknA_	 Alignment		35.0	20	PDB header: dna binding protein Chain: A; PDB Molecule: protein af-10; PDBTitle: crystal structure of an af10 fragment
7	c5lj3C_	 Alignment		32.1	24	PDB header: splicing Chain: C; PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
8	c3en0A_	 Alignment		24.5	18	PDB header: hydrolase Chain: A; PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
9	d1bola_	 Alignment		23.8	50	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
10	c3t0oA_	 Alignment		22.2	63	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease t2; PDBTitle: crystal structure analysis of human rnase t2
11	d1iooa_	 Alignment		21.0	63	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like

12	c5z58C_	Alignment		20.3	36	PDB header: splicing Chain: C: PDB Molecule: 116 kda u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
13	c1nchA_	Alignment		19.7	40	PDB header: cell adhesion protein Chain: A: PDB Molecule: n-cadherin; PDBTitle: structural basis of cell-cell adhesion by cadherins
14	d1iqqa_	Alignment		19.6	24	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
15	d2fc6a1	Alignment		19.0	46	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
16	d1ucda_	Alignment		19.0	63	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
17	d1sgla_	Alignment		18.5	50	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
18	d1d0gr3	Alignment		17.6	60	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
19	d1jy5a_	Alignment		17.5	50	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
20	c2mv3A_	Alignment		16.6	23	PDB header: nucleotide binding protein Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: the n-domain of the aaa metalloproteinase yme1 from saccharomyces2 cerevisiae
21	d1d4va3	Alignment	not modelled	16.4	60	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
22	c2fc6A_	Alignment	not modelled	16.2	46	PDB header: transcription Chain: A: PDB Molecule: target of egr1, member 1; PDBTitle: solution structure of the zf-ccch domain of target of egr1,2 member 1 (nuclear)
23	c5ancK_	Alignment	not modelled	15.1	12	PDB header: translation Chain: K: PDB Molecule: elongation factor tu gtp-binding domain-containing protein PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
24	d1dixa_	Alignment	not modelled	15.1	31	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
25	d2p0ta1	Alignment	not modelled	14.6	28	Fold: PSPTO4464-like Superfamily: PSPTO4464-like Family: PSPTO4464-like
26	c2p0tA_	Alignment	not modelled	14.6	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0307 protein pspto_4464; PDBTitle: structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
27	c4k59A_	Alignment	not modelled	14.1	36	PDB header: rna binding protein Chain: A: PDB Molecule: rna binding protein rsmf; PDBTitle: crystal structure of pseudomonas aeruginosa rsmf
28	c2pqxA_	Alignment	not modelled	14.0	50	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease i; PDBTitle: e. coli rnase 1 (in vivo folded)
						PDB header: cell adhesion/immune system

29	c3ff8B_	Alignment	not modelled	13.5	60	Chain: B: PDB Molecule: epithelial cadherin; PDBTitle: structure of nk cell receptor klrp1 bound to e-cadherin
30	d1iyba_	Alignment	not modelled	13.4	29	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
31	c3d3zA_	Alignment	not modelled	12.6	35	PDB header: hydrolase Chain: A: PDB Molecule: actibind; PDBTitle: crystal structure of actibind a t2 rnase
32	c1vd3A_	Alignment	not modelled	12.4	29	PDB header: hydrolase Chain: A: PDB Molecule: rnase ngr3; PDBTitle: ribonuclease nt in complex with 2'-ump
33	c3jcrB_	Alignment	not modelled	12.4	35	PDB header: splicing Chain: B: PDB Molecule: hsnu114; PDBTitle: 3d structure determination of the human* <u>u4/u6.u5*</u> tri-snrnp complex
34	c2r9aA_	Alignment	not modelled	12.0	31	PDB header: protein binding Chain: A: PDB Molecule: non-homologous end-joining factor 1; PDBTitle: crystal structure of human xlf
35	c6fcxA_	Alignment	not modelled	11.9	41	PDB header: oxidoreductase Chain: A: PDB Molecule: methylenetetrahydrofolate reductase; PDBTitle: structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
36	d1ncia_	Alignment	not modelled	11.6	43	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Cadherin
37	c1ncia_	Alignment	not modelled	11.6	43	PDB header: cell adhesion protein Chain: A: PDB Molecule: n-cadherin; PDBTitle: structural basis of cell-cell adhesion by cadherins
38	c5frgA_	Alignment	not modelled	11.5	27	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
39	c4bfhA_	Alignment	not modelled	11.3	50	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: wrightide r1; PDBTitle: crystal structure of alpha-amylase inhibitor wrightide r1 (wr1)2 peptide from wrightia religiosa
40	c2mauA_	Alignment	not modelled	11.0	50	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: wrightide r1; PDBTitle: solution structure of alpha-amylase inhibitor wrightide r1 (wr1)2 peptide from wrightia religiosa
41	d3er7a1	Alignment	not modelled	10.8	58	Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like
42	c5yrzD_	Alignment	not modelled	10.3	100	PDB header: antitoxin/hydrolase Chain: D: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
43	c5yrzB_	Alignment	not modelled	10.3	100	PDB header: antitoxin/hydrolase Chain: B: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
44	c6k6IA_	Alignment	not modelled	10.0	50	PDB header: unknown function Chain: A: PDB Molecule: pseudo deubiquitinase; PDBTitle: ygl082w-catalytic domain
45	c1nchB_	Alignment	not modelled	9.9	55	PDB header: cell adhesion protein Chain: B: PDB Molecule: n-cadherin; PDBTitle: structural basis of cell-cell adhesion by cadherins
46	c3t97A_	Alignment	not modelled	9.4	33	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
47	c3uwsA_	Alignment	not modelled	9.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a clostripain (parmer_00083) from parabacteroides2 merdae atcc 43184 at 1.70 a resolution
48	c5jknA_	Alignment	not modelled	9.4	38	PDB header: hydrolase Chain: A: PDB Molecule: protein fam63a; PDBTitle: crystal structure of deubiquitinase mindy-1
49	c1zvnA_	Alignment	not modelled	9.3	25	PDB header: cell adhesion Chain: A: PDB Molecule: cadherin 1; PDBTitle: crystal structure of chick mn-cadherin ec1
50	d1gv0a2	Alignment	not modelled	9.2	63	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
51	c5gkeB_	Alignment	not modelled	9.1	42	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
52	d2omwb1	Alignment	not modelled	8.9	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Cadherin
53	c6cg7A_	Alignment	not modelled	8.8	27	PDB header: cell adhesion Chain: A: PDB Molecule: cadherin-22; PDBTitle: mouse cadherin-22 ec1-2 adhesive fragment
54	d1kifa1	Alignment	not modelled	8.7	17	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
55	d1guza2	Alignment	not modelled	8.7	50	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
56	c2axcA_	Alignment	not modelled	8.6	20	PDB header: hydrolase Chain: A: PDB Molecule: colicin e7;

						PDBTitle: crystal structure of cole7 translocation domain
57	c2lm0A_	Alignment	not modelled	8.3	13	PDB header: nuclear protein Chain: A: PDB Molecule: af4/fmr2 family member 1/protein af-9 chimera; PDBTitle: solution structure of the af4-af9 complex
58	c4ozwA_	Alignment	not modelled	8.1	22	PDB header: lyase Chain: A: PDB Molecule: alginate lyase; PDBTitle: crystal structure of the periplasmic alginate lyase algI h202a mutant
59	c1q67B_	Alignment	not modelled	8.0	21	PDB header: transcription Chain: B: PDB Molecule: decapping protein involved in mrna degradation- PDBTitle: crystal structure of dcp1p
60	d1uxja2	Alignment	not modelled	7.9	50	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
61	c2kwtA_	Alignment	not modelled	7.8	67	PDB header: viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution structure of ns2 [27-59]
62	c4eo1A_	Alignment	not modelled	7.6	43	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of the tola binding domain from the filamentous2 phage ike
63	c2ju0B_	Alignment	not modelled	7.6	41	PDB header: metal binding protein/signaling protein Chain: B: PDB Molecule: phosphatidylinositol 4-kinase pik1; PDBTitle: structure of yeast frequenin bound to ptdtns 4-kinase
64	c4g4mA_	Alignment	not modelled	7.5	50	PDB header: de novo protein Chain: A: PDB Molecule: alpha4f3(6-13); PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
65	c4g4mB_	Alignment	not modelled	7.5	50	PDB header: de novo protein Chain: B: PDB Molecule: alpha4f3(6-13); PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
66	c4o2tB_	Alignment	not modelled	7.5	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4827 family protein (bdi_1692) from2 parabacteroides distasonis atcc 8503 at 2.40 a resolution
67	c1yzxB_	Alignment	not modelled	7.3	16	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase kappa 1; PDBTitle: crystal structure of human kappa class glutathione transferase
68	c2x3mA_	Alignment	not modelled	7.3	29	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein orf239; PDBTitle: crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
69	c3l32B_	Alignment	not modelled	7.2	14	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
70	d2cvea2	Alignment	not modelled	7.2	41	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: YigZ C-terminal domain-like
71	d2cuab_	Alignment	not modelled	7.2	31	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
72	c1yxeA_	Alignment	not modelled	7.1	57	PDB header: immune system Chain: A: PDB Molecule: apical membrane antigen 1; PDBTitle: structure and inter-domain interactions of domain ii from the blood2 stage malarial protein, apical membrane antigen 1
73	c3ejkA_	Alignment	not modelled	6.9	38	PDB header: isomerase Chain: A: PDB Molecule: dt dp sugar isomerase; PDBTitle: crystal structure of dt dp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
74	c2pmpA_	Alignment	not modelled	6.7	18	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
75	c2ke4A_	Alignment	not modelled	6.6	22	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
76	c5wbuR_	Alignment	not modelled	6.4	63	PDB header: transferase Chain: R: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(delta n)-mlst8-pras40(alpha-helix & beta-2 strand) complex
77	c5wbuQ_	Alignment	not modelled	6.4	63	PDB header: transferase Chain: Q: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(delta n)-mlst8-pras40(alpha-helix & beta-2 strand) complex
78	d1ejxb_	Alignment	not modelled	6.3	44	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
79	c3j9tb_	Alignment	not modelled	6.2	71	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase state 1
80	c5fujB_	Alignment	not modelled	6.2	63	PDB header: oxidoreductase Chain: B: PDB Molecule: mroupo; PDBTitle: crystallization of a dimeric heme peroxxygenase from the2 fungus marasmius rotula
81	c3fybA_	Alignment	not modelled	6.1	41	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
						PDB header: transferase

82	c3biyA_	Alignment	not modelled	6.1	20	Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: crystal structure of p300 histone acetyltransferase domain in complex2 with a bisubstrate inhibitor, lys-coa
83	c2kneB_	Alignment	not modelled	6.1	67	PDB header: metal transport Chain: B: PDB Molecule: atpase, ca++ transporting, plasma membrane 4; PDBTitle: calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
84	c2mzyA_	Alignment	not modelled	6.1	56	PDB header: iron binding protein Chain: A: PDB Molecule: probable fe(2+)-trafficking protein; PDBTitle: 1h, 13c, and 15n chemical shift assignments and structure of probable2 fe(2+)-trafficking protein from burkholderia pseudomallei 1710b.
85	c2mitA_	Alignment	not modelled	6.0	86	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: solution structure of oxidized dimeric form of human defensin 5
86	d2omzb1	Alignment	not modelled	5.9	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Cadherin
87	c1cffB_	Alignment	not modelled	5.9	67	PDB header: calmodulin Chain: B: PDB Molecule: calcium pump; PDBTitle: nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
88	d1lmb3_	Alignment	not modelled	5.9	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
89	c4e86H_	Alignment	not modelled	5.9	86	PDB header: antimicrobial protein Chain: H: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
90	c4e86D_	Alignment	not modelled	5.9	86	PDB header: antimicrobial protein Chain: D: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
91	d2qtva2	Alignment	not modelled	5.9	38	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: beta-sandwich domain of Sec23/24 Family: beta-sandwich domain of Sec23/24
92	c4rbxA_	Alignment	not modelled	5.9	86	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (glu21arg mutant)
93	d2eyqa2	Alignment	not modelled	5.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
94	c1zmpA_	Alignment	not modelled	5.8	86	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
95	c2lxzA_	Alignment	not modelled	5.8	86	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: solution structure of the antimicrobial peptide human defensin 5
96	c1zmpB_	Alignment	not modelled	5.8	86	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
97	c4z42B_	Alignment	not modelled	5.8	22	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
98	c1zmpC_	Alignment	not modelled	5.8	86	PDB header: antimicrobial protein Chain: C: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
99	c4e83A_	Alignment	not modelled	5.8	86	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29nle mutant)