


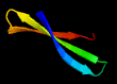

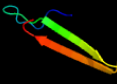



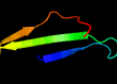

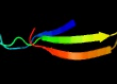



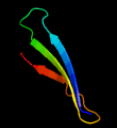

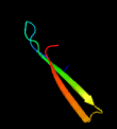

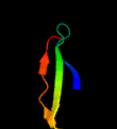




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2576c (-) _2900236_2900700
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	9db04961f0ab82fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lw3A_	 Alignment		95.2	20	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmps4; PDBTitle: solution structure of the soluble domain of mmps4 from mycobacterium2 tuberculosis
2	c1o0wB_	 Alignment		55.2	18	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of ribonuclease iii (tm1102) from thermotoga2 maritima at 2.0 a resolution
3	d2b7va1	 Alignment		54.6	27	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
4	c2n3hA_	 Alignment		51.6	22	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein 4; PDBTitle: solution structure of drb4 dsrbd2 (viz. drb4(81-151))
5	c3adiC_	 Alignment		46.2	18	PDB header: gene regulation/rna Chain: C: PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
6	c2mdrA_	 Alignment		45.7	19	PDB header: hydrolase Chain: A: PDB Molecule: double-stranded rna-specific adenosine deaminase; PDBTitle: solution structure of the third double-stranded rna-binding domain2 (dsrbd3) of human adenosine-deaminase adar1
7	d1qu6a1	 Alignment		44.0	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
8	d1qu6a2	 Alignment		38.5	11	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
9	c5dv7C_	 Alignment		37.4	27	PDB header: rna binding protein Chain: C: PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: crystal structure of nf90 tandem dsrbds with dsrna
10	d1x49a1	 Alignment		37.3	16	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
11	c2khxA_	 Alignment		37.3	13	PDB header: gene regulation,nuclear protein Chain: A: PDB Molecule: ribonuclease 3; PDBTitle: drosha double-stranded rna binding motif

12	d1whqa_	Alignment		37.2	38	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
13	d1x48a1	Alignment		37.1	9	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
14	c3adjA_	Alignment		34.4	13	PDB header: gene regulation Chain: A: PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
15	d1mzya2	Alignment		32.9	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
16	d2dmya1	Alignment		27.3	27	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
17	c4ce4h_	Alignment		26.0	15	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
18	c2l2na_	Alignment		25.8	19	PDB header: rna binding protein, plant protein Chain: A: PDB Molecule: hyponastic leave 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
19	c2n3ga_	Alignment		24.2	22	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein 4; PDBTitle: solution structure of drb4 dsrbd1 (viz. drb4(1-72))
20	c1w8ka_	Alignment		24.0	27	PDB header: antigen Chain: A: PDB Molecule: apical membrane antigen 1; PDBTitle: crystal structure of apical membrane antigen 1 from2 plasmodium vivax
21	c2l33a_	Alignment	not modelled	23.4	27	PDB header: transcription regulator Chain: A: PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
22	c4fusA_	Alignment	not modelled	22.9	21	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
23	c3d6xa_	Alignment	not modelled	22.7	31	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
24	c3c4ta_	Alignment	not modelled	22.6	13	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease dicer; PDBTitle: structure of rnaseiib and dsrna binding domains of mouse dicer
25	d1snra2	Alignment	not modelled	20.8	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
26	c2ljha_	Alignment	not modelled	20.5	30	PDB header: hydrolase Chain: A: PDB Molecule: double-stranded rna-specific editase adar; PDBTitle: nmr structure of double-stranded rna-specific editase adar
27	c2n3fa_	Alignment	not modelled	20.2	22	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein 4; PDBTitle: solution structure of both dsrbds of drb4 along with linker (viz.2 drb4(1-153))
28	c2luwa_	Alianment	not modelled	20.1	8	PDB header: hydrolase Chain: A: PDB Molecule: metalloprotease;

						PDBTitle: solution structure of vep c-ter 100
29	c2glvA_	Alignment	not modelled	18.9	31	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-acyl carrier protein dehydratase; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
30	c5npgA_	Alignment	not modelled	18.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: loquacious, isoform f; PDBTitle: solution structure of drosophila melanogaster loquacious dsrbd1
31	c1vw45_	Alignment	not modelled	17.1	26	PDB header: ribosome Chain: 5: PDB Molecule: 54s ribosomal protein l3, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
32	d1o0wa2	Alignment	not modelled	16.9	16	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
33	c1rue4_	Alignment	not modelled	15.9	19	PDB header: virus Chain: 4: PDB Molecule: rhinovirus 14; PDBTitle: rhinovirus 14 site directed mutant n1219a complexed with2 antiviral compound win 52035
34	c4wm7D_	Alignment	not modelled	15.5	36	PDB header: virus Chain: D: PDB Molecule: vp4; PDBTitle: crystal structure of human enterovirus d68 in complex with pleconaril
35	d1di2a_	Alignment	not modelled	15.3	24	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
36	c5k0uD_	Alignment	not modelled	15.2	33	PDB header: virus Chain: D: PDB Molecule: capsid protein vp4; PDBTitle: cryoem structure of the full virion of a human rhinovirus c
37	c4v1ah_	Alignment	not modelled	15.0	14	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
38	c5buyA_	Alignment	not modelled	14.3	38	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
39	c3vddD_	Alignment	not modelled	14.3	28	PDB header: virus Chain: D: PDB Molecule: protein vp4; PDBTitle: structure of hrv2 capsid complexed with antiviral compound bta798
40	c1jew4_	Alignment	not modelled	14.3	19	PDB header: virus/receptor Chain: 4: PDB Molecule: coxsackievirus capsid, coat protein vp4; PDB Fragment: residues 21-140; PDBTitle: cryo-em structure of coxsackievirus b3(m strain) with its cellular2 receptor, coxsackievirus and adenovirus receptor (car).
41	c1dgi4_	Alignment	not modelled	14.2	23	PDB header: virus/viral protein, receptor Chain: 4: PDB Molecule: vp4; PDB Fragment: poliovirus fragments vp1,vp2,vp3,vp4; PDBTitle:
42	d1n1ta1	Alignment	not modelled	14.0	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Trypanosoma sialidase, C-terminal domain
43	c5fraD_	Alignment	not modelled	13.7	6	PDB header: sugar binding protein Chain: D: PDB Molecule: sialidase; PDBTitle: cbm40_cpf0721-6'sl
44	c6aksD_	Alignment	not modelled	12.8	15	PDB header: virus Chain: D: PDB Molecule: vp4; PDBTitle: cryo-em structure of cva10 mature virus
45	c5mquD_	Alignment	not modelled	12.8	12	PDB header: virus Chain: D: PDB Molecule: vp4; PDBTitle: crystal structure of bovine enterovirus 2 determined with serial2 femtosecond x-ray crystallography
46	c2lrsA_	Alignment	not modelled	12.2	21	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease dicer homolog 1; PDBTitle: the second dsrbd domain from a. thaliana dicer-like 1
47	c1bev4_	Alignment	not modelled	11.9	22	PDB header: virus Chain: 4: PDB Molecule: bovine enterovirus coat proteins vp1 to vp4; PDBTitle: bovine enterovirus vg-5-27
48	c3muxB_	Alignment	not modelled	11.8	38	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
49	c2lepA_	Alignment	not modelled	11.7	19	PDB header: hydrolase Chain: A: PDB Molecule: rhomboid protease glgp 1; PDBTitle: solution structure of n-terminal cytosolic domain of rhomboid2 intramembrane protease from escherichia coli
50	c3m6yA_	Alignment	not modelled	11.6	38	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
51	c6govN_	Alignment	not modelled	11.5	43	PDB header: transcription Chain: N: PDB Molecule: antitermination protein n; PDBTitle: structure of the rna polymerase lambda-based antitermination complex
52	d2b7ta1	Alignment	not modelled	11.4	27	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
53	d1ihwa_	Alignment	not modelled	11.3	14	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase

54	d1g9ga_	Alignment	not modelled	11.3	24	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
55	d2bw4a2	Alignment	not modelled	10.9	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
56	c6ijjD_	Alignment	not modelled	10.3	19	PDB header: viral protein Chain: D: PDB Molecule: vp4; PDBTitle: cryo-em structure of cv-a10 mature virion
57	c5buxB_	Alignment	not modelled	10.3	31	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of 3-hydroxyacyl- <i>acp</i> dehydratase (fabz) from <i>Yersinia pestis</i> with glycerol bound
58	c6htuA_	Alignment	not modelled	10.0	27	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein stau1 homolog 1; PDBTitle: structure of hstau1 dsrbd3-4 in complex with arf1 rna
59	d1u1za_	Alignment	not modelled	9.9	38	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
60	c4i83A_	Alignment	not modelled	9.5	44	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of (3r)-hydroxymyristoyl- <i>acp</i> dehydratase from <i>Neisseria meningitidis</i> fam18
61	c4h4gG_	Alignment	not modelled	9.5	31	PDB header: lyase Chain: G: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of (3r)-hydroxymyristoyl-[acyl-carrier-protein] ₂ dehydratase from <i>Burkholderia thailandensis</i> e264
62	d1uhza_	Alignment	not modelled	9.2	24	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
63	c1tvtA_	Alignment	not modelled	9.0	36	PDB header: transcription regulator Chain: A: PDB Molecule: transactivator protein; PDBTitle: structure of the equine infectious anemia virus tat protein
64	d2je8a4	Alignment	not modelled	8.9	10	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
65	d1p4da_	Alignment	not modelled	8.9	22	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
66	c4oleD_	Alignment	not modelled	8.8	28	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: next to brca1 gene 1 protein; PDBTitle: crystal structure of a neighbor of brca1 gene 1 (nbr1) from homo2 sapiens at 2.52 a resolution
67	d1x47a1	Alignment	not modelled	8.6	21	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
68	c1kbwA_	Alignment	not modelled	8.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: major outer membrane protein pan 1; PDBTitle: crystal structure of the soluble domain of ania from <i>Neisseria gonorrhoeae</i>
69	c4v1ai_	Alignment	not modelled	8.3	27	PDB header: ribosome Chain: I: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
70	c1yn5B_	Alignment	not modelled	8.3	33	PDB header: unknown function Chain: B: PDB Molecule: eaph2; PDBTitle: crystal structures of eap domains from <i>Staphylococcus aureus</i> reveal an unexpected homology to bacterial superantigens
71	c5npaA_	Alignment	not modelled	8.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: loquacious; PDBTitle: solution structure of <i>Drosophila melanogaster</i> loquacious dsrbd2
72	c2l3jA_	Alignment	not modelled	8.2	27	PDB header: hydrolase/rna Chain: A: PDB Molecule: double-stranded rna-specific editase 1; PDBTitle: the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
73	c3vbhD_	Alignment	not modelled	8.0	8	PDB header: virus Chain: D: PDB Molecule: genome polyprotein, capsid protein vp4; PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group r32)
74	d3btaa1	Alignment	not modelled	8.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: <i>Clostridium</i> neurotoxins, the second last domain
75	c5mqoA_	Alignment	not modelled	7.9	16	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: glycoside hydrolase bt_1003
76	d1stua_	Alignment	not modelled	7.8	20	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
77	c1qu6A_	Alignment	not modelled	7.6	19	PDB header: transferase Chain: A: PDB Molecule: protein kinase pkr; PDBTitle: structure of the double-stranded rna-binding domain of the2 protein kinase pkr reveals the molecular basis of its3 dsrna-mediated activation
78	c3m0zD_	Alignment	not modelled	7.6	50	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from <i>Klebsiella pneumoniae</i> .
79	c3llhB_	Alignment	not modelled	7.3	23	PDB header: rna binding protein Chain: B: PDB Molecule: crisc-loading complex subunit tarbp2; PDBTitle: crystal structure of the first dsrbd of tar rna-binding

						protein 2
80	d1dpta_	Alignment	not modelled	7.1	27	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
81	d1efca2	Alignment	not modelled	7.1	13	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
82	c4zw0A_	Alignment	not modelled	7.1	31	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from candidatus asiaticum
83	c5b16A_	Alignment	not modelled	6.8	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease 3,drosha,ribonuclease 3,drosha,ribonuclease 3; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
84	c1yn4A_	Alignment	not modelled	6.8	50	PDB header: unknown function Chain: A: PDB Molecule: eaph1; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
85	c1yn3A_	Alignment	not modelled	6.5	56	PDB header: toxin, protein binding Chain: A: PDB Molecule: truncated cell surface protein map-w; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
86	d2g3ra1	Alignment	not modelled	6.4	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
87	d1k0ia2	Alignment	not modelled	6.3	15	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: PHBH-like
88	c4kmaA_	Alignment	not modelled	6.1	22	PDB header: protein binding Chain: A: PDB Molecule: gm14141p; PDBTitle: crystal structure of drosophila suppressor of fused
89	d1c6vx_	Alignment	not modelled	6.1	7	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
90	c1c6vX_	Alignment	not modelled	6.1	7	PDB header: dna binding protein Chain: X: PDB Molecule: protein (siu89134); PDBTitle: siv integrase (catalytic domain + dna binding domain comprising2 residues 50-293) mutant with phe 185 replaced by his (f185h)
91	d1nds2	Alignment	not modelled	6.0	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
92	c3fhkF_	Alignment	not modelled	5.8	30	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
93	c1yywB_	Alignment	not modelled	5.8	17	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnaase iii from aquifex aeolicus2 complexed with double stranded rna at 2.8-angstrom3 resolution
94	c4f2fA_	Alignment	not modelled	5.7	12	PDB header: metal binding protein Chain: A: PDB Molecule: cation-transporting atpase, e1-e2 family protein; PDBTitle: crystal structure of the metal binding domain (mbd) of the2 streptococcus pneumoniae d39 cu(i) exporting p-type atpase copa with3 cu(i)
95	c6gmaA_	Alignment	not modelled	5.7	14	PDB header: protein binding Chain: A: PDB Molecule: rb1-inducible coiled-coil protein 1; PDBTitle: crystal structure of the fip200 c-terminal region
96	c6qsrB_	Alignment	not modelled	5.6	38	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apeip from xenorhabdus doucetiae
97	d1wna1	Alignment	not modelled	5.5	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
98	c2yt4A_	Alignment	not modelled	5.4	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein dgcr8; PDBTitle: crystal structure of human dgcr8 core
99	c5fceB_	Alignment	not modelled	5.4	44	PDB header: cell adhesion Chain: B: PDB Molecule: lpxtg family cell surface protein fms2; PDBTitle: the crystal structure of the ligand binding region of serine-glutamate2 repeat protein a (sgra) of enterococcus faecium