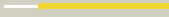
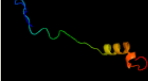
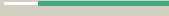


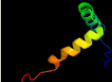





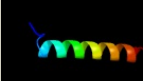

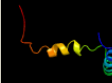



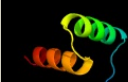

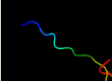




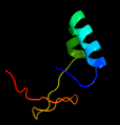








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0959A (RVBD0959A)_1073331_1073552
 Date Fri Jul 26 01:50:55 BST 2019
 Unique Job ID 2e2a914914184e78

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87D_	 Alignment		74.5	43	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	d2bsqe1	 Alignment		49.6	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
3	c2h1oH_	 Alignment		47.0	20	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
4	c2ki2A_	 Alignment		34.1	19	PDB header: rna binding protein/ss-dna binding prote Chain: A: PDB Molecule: ss-dna binding protein 12rnp2; PDBTitle: solution structure of ss-dna binding protein 12rnp22 precursor, hp0827(o25501_helpy) form helicobacter pylori
5	d2cqha1	 Alignment		32.5	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
6	d1s4ka_	 Alignment		30.5	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdIL-like
7	c2k5jB_	 Alignment		21.7	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
8	c1ea4K_	 Alignment		20.5	27	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
9	d2cpga_	 Alignment		20.5	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	c5bjrA_	 Alignment		18.7	31	PDB header: splicing Chain: A: PDB Molecule: mec-8 protein; PDBTitle: crystal structure of the n-terminal rrm domain from mec-8
11	c6ez7A_	 Alignment		18.3	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein pes4; PDBTitle: pes4 rrm3 structure

12	c2lkzA_	Alignment		15.7	40	PDB header: rna binding protein Chain: A; PDB Molecule: rna-binding protein 5; PDBTitle: solution structure of the second rrm domain of rbm5
13	c6n0wA_	Alignment		15.2	25	PDB header: ligase Chain: A; PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
14	c4rgwB_	Alignment		15.0	22	PDB header: transferase/transcription Chain: B; PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid
15	c2rkjM_	Alignment		15.0	38	PDB header: ligase/rna Chain: M; PDB Molecule: tyrosyl-trna synthetase; PDBTitle: cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
16	c5l8xA_	Alignment		13.9	47	PDB header: transferase Chain: A; PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of apo methanocaldococcus jannaschii methyltransferase2 subunit a at 1.85 angstrom
17	c5laaB_	Alignment		13.9	33	PDB header: transferase Chain: B; PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of the methyltransferase subunit a from methanothermus2 fervidus in complex with cobalamin
18	d2up1a2	Alignment		13.7	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
19	c5x3zA_	Alignment		13.5	13	PDB header: rna binding protein/rna Chain: A; PDB Molecule: rna-binding protein musashi homolog 1; PDBTitle: solution structure of musashi1 rbd2 in complex with rna
20	d1sjqa_	Alignment		13.2	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
21	c3a9rA_	Alignment	not modelled	12.9	52	PDB header: isomerase Chain: A; PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
22	d2cpda1	Alignment	not modelled	12.7	32	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
23	d2ad9a1	Alignment	not modelled	12.1	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
24	c3l4gC_	Alignment	not modelled	11.9	30	PDB header: ligase Chain: C; PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
25	d1jmsa1	Alignment	not modelled	11.4	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
26	d1bwva1	Alignment	not modelled	10.7	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
27	c5ijxA_	Alignment	not modelled	10.6	38	PDB header: ligase Chain: A; PDB Molecule: tyrosine--trna ligase, mitochondrial; PDBTitle: crystal structure of a c-terminally truncated coccidioides posadasii2 mitochondrial tyrosyl-trna synthetase
28	c3fk4A_	Alignment	not modelled	10.5	21	PDB header: isomerase Chain: A; PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
						PDB header: protein binding

29	c3r27A_	Alignment	not modelled	10.4	33	Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein l; PDBTitle: crystal structure of the first rrm domain of heterogeneous nuclear2 ribonucleoprotein l (hnrrnp l)
30	c2m9kA_	Alignment	not modelled	10.3	33	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein with multiple splicing 2; PDBTitle: rbpms2-nter
31	d2od0a1	Alignment	not modelled	10.3	32	Fold: Secretion chaperone-like Superfamily: YgaC/TfoX-N like Family: TfoX N-terminal domain-like
32	c5d78A_	Alignment	not modelled	10.1	40	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein mip6; PDBTitle: structure of rrm3 domain of mip6 at 1.25 a resolution
33	c5ihxB_	Alignment	not modelled	9.0	38	PDB header: ligase Chain: B: PDB Molecule: tyrosine--trna ligase, mitochondrial; PDBTitle: crystal structure of a c-terminally truncated aspergillus nidulans2 mitochondrial tyrosyl-trna synthetase
34	d2adca2	Alignment	not modelled	9.0	50	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
35	c4oudA_	Alignment	not modelled	8.9	25	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
36	d1svda1	Alignment	not modelled	8.8	29	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
37	c5j73A_	Alignment	not modelled	8.8	45	PDB header: de novo protein Chain: A: PDB Molecule: protein design 2l4hc2_9; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
38	c9rubB_	Alignment	not modelled	8.4	28	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
39	c5ehbA_	Alignment	not modelled	8.3	57	PDB header: de novo protein Chain: A: PDB Molecule: phiosyi; PDBTitle: a de novo designed hexameric coiled-coil peptide with iodotyrosine
40	c5ehbB_	Alignment	not modelled	8.3	57	PDB header: de novo protein Chain: B: PDB Molecule: phiosyi; PDBTitle: a de novo designed hexameric coiled-coil peptide with iodotyrosine
41	d2ghpa1	Alignment	not modelled	8.2	36	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
42	c6otjA_	Alignment	not modelled	8.1	19	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
43	d2b0ga1	Alignment	not modelled	8.1	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
44	d2bcqa1	Alignment	not modelled	8.1	25	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
45	d2csba4	Alignment	not modelled	8.0	73	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
46	d1a9nb_	Alignment	not modelled	8.0	27	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
47	c5uz5C_	Alignment	not modelled	8.0	50	PDB header: nuclear protein/rna Chain: C: PDB Molecule: u1 small nuclear ribonucleoprotein a,tap tag; PDBTitle: s. cerevisiae u1 snrnp
48	c2e5gA_	Alignment	not modelled	7.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: u6 snrna-specific terminal uridylyltransferase 1; PDBTitle: solution structure of rna binding domain in rna binding2 motif protein 21
49	c2a3jA_	Alignment	not modelled	7.8	14	PDB header: rna binding protein Chain: A: PDB Molecule: u1 small nuclear ribonucleoprotein a; PDBTitle: structure of urndesign, a complete computational redesign2 of human u1a protein
50	c2janD_	Alignment	not modelled	7.5	38	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
51	c3l4gl_	Alignment	not modelled	7.4	30	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
52	d1whxa_	Alignment	not modelled	7.4	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
53	d2cqda1	Alignment	not modelled	7.3	6	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
54	d5ruba1	Alignment	not modelled	7.3	28	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
						PDB header: ligase

55	c4oudB	Alignment	not modelled	7.2	25	Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
56	c2n3oA	Alignment	not modelled	7.2	33	PDB header: rna binding protein/rna Chain: A: PDB Molecule: polypyrimidine tract-binding protein 1; PDBTitle: structure of ptb rrm1(41-163) bound to an rna stemloop containing a2 structured loop derived from viral internal ribosomal entry site rna
57	c3jb9k	Alignment	not modelled	6.9	45	PDB header: rna binding protein/rna Chain: K: PDB Molecule: pre-mrna-splicing factor prp5; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
58	c2zviB	Alignment	not modelled	6.7	45	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
59	d1l3ka2	Alignment	not modelled	6.6	20	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
60	c2mqIA	Alignment	not modelled	6.6	33	PDB header: rna binding protein Chain: A: PDB Molecule: protein hnrnpI; PDBTitle: structural investigation of hnrnp I
61	c4hv0B	Alignment	not modelled	6.4	40	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
62	d2k3ka1	Alignment	not modelled	6.3	25	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
63	d1h6kx	Alignment	not modelled	6.2	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
64	c5x1eF	Alignment	not modelled	6.1	25	PDB header: protein transport Chain: F: PDB Molecule: icmo (dotI); PDBTitle: structure of dotI(656-783)-icms-icmw derived from legionella2 pneumophila
65	d1l3ka1	Alignment	not modelled	6.0	6	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
66	d1sr2a	Alignment	not modelled	6.0	22	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Sensor-like histidine kinase YojN, C-terminal domain
67	d2cq1a1	Alignment	not modelled	6.0	33	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
68	c1h3eA	Alignment	not modelled	5.9	38	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
69	c4kh8A	Alignment	not modelled	5.9	73	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a lipocalin-like protein (ef0376) from2 enterococcus faecalis v583 at 1.60 a resolution
70	c6h5hA	Alignment	not modelled	5.8	20	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
71	d1wexa	Alignment	not modelled	5.8	27	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
72	c2dh9A	Alignment	not modelled	5.6	27	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
73	c2dguA	Alignment	not modelled	5.5	38	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein q; PDBTitle: solution structure of the rna binding domain in2 heterogeneous nuclear ribonucleoprotein q
74	d1fnxh1	Alignment	not modelled	5.5	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
75	c2e5jA	Alignment	not modelled	5.5	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: methenyltetrahydrofolate synthetase domain PDBTitle: solution structure of rna binding domain in2 methenyltetrahydrofolate synthetase domain containing
76	c2mzsA	Alignment	not modelled	5.4	20	PDB header: rna binding protein Chain: A: PDB Molecule: protein hrb1; PDBTitle: nmr structure of the rrm2 domain of hrb1
77	d1p1ta	Alignment	not modelled	5.4	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
78	d8ruca1	Alignment	not modelled	5.3	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
79	c2qygC	Alignment	not modelled	5.3	43	PDB header: unknown function Chain: C: PDB Molecule: ribulose biphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
80	c5e2aD	Alignment	not modelled	5.3	10	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco;

80	c3c2gd_	Alignment	not modelled	5.3	19	PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
81	d1geha1	Alignment	not modelled	5.2	26	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
82	c5lj3Y_	Alignment	not modelled	5.2	27	PDB header: splicing Chain: Y; PDB Molecule: u2 small nuclear ribonucleoprotein b"; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
83	c2do4A_	Alignment	not modelled	5.2	13	PDB header: immune system Chain: A; PDB Molecule: squamous cell carcinoma antigen recognized by t- PDBTitle: solution structure of the rna binding domain of squamous2 cell carcinoma antigen recognized by t cells 3
84	d1bxna1	Alignment	not modelled	5.1	33	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain