


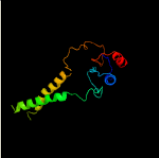
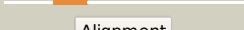




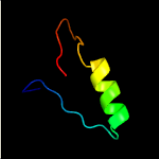

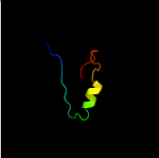

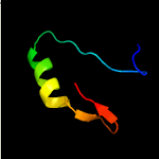

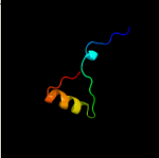
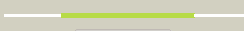


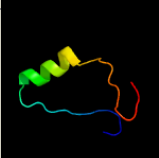

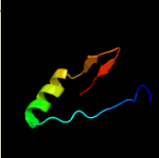
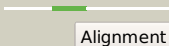

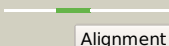

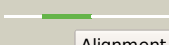
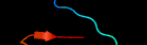
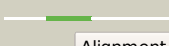

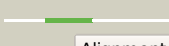


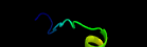


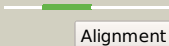
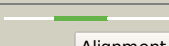

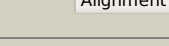
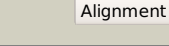
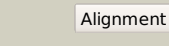
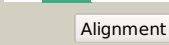


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1234_(-)_1376982_1377509
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	5adacdc59696199d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6btmD_</a>	 Alignment		97.8	8	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> alternative complex iii subunit d; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
2	<a href="#">c6f0kD_</a>	 Alignment		96.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> actd; <b>PDBTitle:</b> alternative complex iii
3	<a href="#">c1x60A_</a>	 Alignment		83.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation-specific n-acetylmuramoyl-l-alanine <b>PDBTitle:</b> solution structure of the peptidoglycan binding domain of 2 b. subtilis cell wall lytic enzyme cwlc
4	<a href="#">dlutaa_</a>	 Alignment		76.2	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Sporulation related repeat <b>Family:</b> Sporulation related repeat
5	<a href="#">d1wi6a1</a>	 Alignment		67.6	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
6	<a href="#">c2kxnB_</a>	 Alignment		64.9	8	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> transformer-2 protein homolog beta; <b>PDBTitle:</b> nmr structure of human tra2beta1 rrm in complex with aagaac rna
7	<a href="#">c2jvrA_</a>	 Alignment		61.1	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolar protein 3; <b>PDBTitle:</b> segmental isotope labeling of npl3p
8	<a href="#">c3ffjA_</a>	 Alignment		60.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase (family 31); <b>PDBTitle:</b> the crystal structure of the glycosyl hydrolase (family 31) from 2 ruminococcus obeum atcc 29174
9	<a href="#">c6iu3A_</a>	 Alignment		60.2	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
10	<a href="#">c3begB_</a>	 Alignment		59.9	17	<b>PDB header:</b> transferase/splicing <b>Chain:</b> B: <b>PDB Molecule:</b> splicing factor, arginine/serine-rich 1; <b>PDBTitle:</b> crystal structure of sr protein kinase 1 complexed to its substrate2 asf/sf2
11	<a href="#">c2dgxA_</a>	 Alignment		59.8	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0430 protein; <b>PDBTitle:</b> solution structure of the rna recognition motif in kiaa04302 protein

12	<a href="#">c2mheB_</a>	 Alignment		59.6	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein np_419126.1 from caulobacter crescentus
13	<a href="#">d1ifya_</a>	 Alignment		58.7	12	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
14	<a href="#">d3begb1</a>	 Alignment		58.4	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
15	<a href="#">d1wgl1a_</a>	 Alignment		57.2	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
16	<a href="#">c2osrA_</a>	 Alignment		56.1	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolar protein 3; <b>PDBTitle:</b> nmr structure of rrm-2 of yeast npl3 protein
17	<a href="#">d2ghpa1</a>	 Alignment		56.1	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
18	<a href="#">d1whxa_</a>	 Alignment		55.3	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
19	<a href="#">d1sjqa_</a>	 Alignment		53.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
20	<a href="#">c2dnqA_</a>	 Alignment		53.0	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 4b; <b>PDBTitle:</b> solution structure of rna binding domain 1 in rna-binding2 protein 30
21	<a href="#">c3bs9A_</a>	 Alignment	not modelled	52.9	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolysin tia-1 isoform p40; <b>PDBTitle:</b> x-ray structure of human tia-1 rrm2
22	<a href="#">c2lepA_</a>	 Alignment	not modelled	52.7	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rhomboid protease glpg 1; <b>PDBTitle:</b> solution structure of n-terminal cytosolic domain of rhomboid2 intramembrane protease from escherichia coli
23	<a href="#">c2hvxA_</a>	 Alignment	not modelled	50.5	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor, arginine/serine-rich 7; <b>PDBTitle:</b> solution structure of the rrm domain of sr rich factor 9g8
24	<a href="#">c4b9zA_</a>	 Alignment	not modelled	50.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase, putative, adg31b; <b>PDBTitle:</b> crystal structure of agd31b, alpha-transglucosylase,2 complexed with acarbose
25	<a href="#">d1h6kx_</a>	 Alignment	not modelled	50.0	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
26	<a href="#">c4c7gA_</a>	 Alignment	not modelled	49.8	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding glycine-rich protein; <b>PDBTitle:</b> solution structure of the nt. gr-rbp1 rrm domain
27	<a href="#">c6druB_</a>	 Alignment	not modelled	49.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolases family 31 family protein; <b>PDBTitle:</b> xylosidase from aspergillus niger
28	<a href="#">c3ns5B_</a>	 Alignment	not modelled	49.2	9	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b; <b>PDBTitle:</b> crystal structure of the rna recognition motif of yeast eif3b residues2 76-161

29	<a href="#">c2rvjA_</a>	Alignment	not modelled	48.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> epithelial splicing regulatory protein 1; <b>PDBTitle:</b> nmr structure of epithelial splicing regulatory protein 1
30	<a href="#">c2e44A_</a>	Alignment	not modelled	48.0	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> insulin-like growth factor 2 mrna binding <b>PDBTitle:</b> solution structure of rna binding domain in insulin-like2 growth factor 2 mrna binding protein 3
31	<a href="#">c1ciiA_</a>	Alignment	not modelled	47.9	16	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
32	<a href="#">d1no8a_</a>	Alignment	not modelled	47.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
33	<a href="#">c1no8A_</a>	Alignment	not modelled	47.7	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> aly; <b>PDBTitle:</b> solution structure of the nuclear factor aly rbd domain
34	<a href="#">c2dgtA_</a>	Alignment	not modelled	47.1	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna-binding protein 30; <b>PDBTitle:</b> solution structure of the second rna binding domain in rna-2 binding protein 30
35	<a href="#">d1fxla2</a>	Alignment	not modelled	46.9	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
36	<a href="#">c2ku7A_</a>	Alignment	not modelled	46.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> mll1 phd3-cyp33 rrm chimeric protein; <b>PDBTitle:</b> solution structure of mll1 phd3-cyp33 rrm chimeric protein
37	<a href="#">c2nlwA_</a>	Alignment	not modelled	46.4	21	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 <b>PDBTitle:</b> solution structure of the rrm domain of human eukaryotic2 initiation factor 3b
38	<a href="#">c5m8iA_</a>	Alignment	not modelled	46.3	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cugbp elav-like family member 2; <b>PDBTitle:</b> solution structure of cug-bp2 rrm3 in complex with 5'-uuuaa-3' rna
39	<a href="#">d2cqpa1</a>	Alignment	not modelled	46.3	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
40	<a href="#">d1x4ea1</a>	Alignment	not modelled	46.1	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
41	<a href="#">c3ex7B_</a>	Alignment	not modelled	45.8	33	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> B; <b>PDB Molecule:</b> rna-binding protein 8a; <b>PDBTitle:</b> the crystal structure of ejc in its transition state
42	<a href="#">d1b7fa2</a>	Alignment	not modelled	45.6	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
43	<a href="#">c5x3kA_</a>	Alignment	not modelled	45.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycoside hydrolase family 31; <b>PDBTitle:</b> kfla1895 d451a mutant in complex with isomaltose
44	<a href="#">c6e4pF_</a>	Alignment	not modelled	44.8	21	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> F; <b>PDB Molecule:</b> rna-binding protein, putative; <b>PDBTitle:</b> structure of the t. brucei rrm domain in complex with rna
45	<a href="#">d2pjuA1</a>	Alignment	not modelled	44.7	23	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> PrpR receptor domain-like <b>Family:</b> PrpR receptor domain-like
46	<a href="#">d2cpea1</a>	Alignment	not modelled	44.6	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
47	<a href="#">d2disa1</a>	Alignment	not modelled	44.3	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
48	<a href="#">c4a8xA_</a>	Alignment	not modelled	44.3	24	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> rna-binding protein with serine-rich domain 1; <b>PDBTitle:</b> structure of the core asap complex
49	<a href="#">c2e5jA_</a>	Alignment	not modelled	43.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> methenyltetrahydrofolate synthetase domain <b>PDBTitle:</b> solution structure of rna binding domain in2 methenyltetrahydrofolate synthetase domain containing
50	<a href="#">c5jouA_</a>	Alignment	not modelled	43.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-xylosidase bogh31a; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh31
51	<a href="#">c3tl8K_</a>	Alignment	not modelled	43.9	24	<b>PDB header:</b> transferase/ligase <b>Chain:</b> K; <b>PDB Molecule:</b> effector protein hopab2; <b>PDBTitle:</b> the avrptob-bak1 complex reveals two structurally similar2 kinaseinteracting domains in a single type iii effector
52	<a href="#">c2g3nA_</a>	Alignment	not modelled	43.8	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
53	<a href="#">d1x4da1</a>	Alignment	not modelled	43.8	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
54	<a href="#">d1fxla1</a>	Alignment	not modelled	43.8	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
55	<a href="#">c2d9oA_</a>	Alignment	not modelled	43.3	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dnaj (hsp40) homolog, subfamily c, member 17;

						<b>PDBTitle:</b> solution structure of rna binding domain in hypothetical2 protein flj10634
56	<a href="#">c1rkjA</a>	Alignment	not modelled	42.5	14	<b>PDB header:</b> transcription/rna <b>Chain:</b> A; <b>PDB Molecule:</b> nucleolin; <b>PDBTitle:</b> solution structure of the complex formed by the two n-2 terminal rna-binding domains of nucleolin and a pre-rna3 target
57	<a href="#">d1hl6a</a>	Alignment	not modelled	42.4	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
58	<a href="#">c6r5kH</a>	Alignment	not modelled	41.4	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> H; <b>PDB Molecule:</b> polyadenylate-binding protein, cytoplasmic and nuclear; <b>PDBTitle:</b> cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
59	<a href="#">c5iegA</a>	Alignment	not modelled	41.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> neutral alpha-glucosidase ab; <b>PDBTitle:</b> murine endoplasmic reticulum alpha-glucosidase ii with n-9'-2 methoxynonyl-1-deoxynojirimycin
60	<a href="#">d1fnxh1</a>	Alignment	not modelled	41.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
61	<a href="#">c3md3A</a>	Alignment	not modelled	41.0	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> nuclear and cytoplasmic polyadenylated rna-binding protein <b>PDBTitle:</b> crystal structure of the first two rrm domains of yeast poly(u)2 binding protein (pub1)
62	<a href="#">c2lmiA</a>	Alignment	not modelled	41.0	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> g-rich sequence factor 1; <b>PDBTitle:</b> nmr structure of the protein bc040485 from homo sapiens
63	<a href="#">c3cw18</a>	Alignment	not modelled	40.9	14	<b>PDB header:</b> splicing <b>Chain:</b> 8; <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein 70 kda; <b>PDB Fragment:</b> nucleotides 57-82 absent, replaced with kissing loop; <b>PDBTitle:</b> crystal structure of human spliceosomal u1 snrnp
64	<a href="#">d1x4aa1</a>	Alignment	not modelled	40.7	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
65	<a href="#">c2lf3A</a>	Alignment	not modelled	40.3	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> effector protein hopab3; <b>PDBTitle:</b> solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. e54326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
66	<a href="#">c2n3oA</a>	Alignment	not modelled	40.3	18	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> polypyrimidine tract-binding protein 1; <b>PDBTitle:</b> structure of ptb rrm1(41-163) bound to an rna stemloop containing a2 structured loop derived from viral internal ribosomal entry site rna
67	<a href="#">c2do0A</a>	Alignment	not modelled	40.1	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein m; <b>PDBTitle:</b> solution structure of the rna binding domain of2 heterogeneous nuclear ribonucleoprotein m
68	<a href="#">d2bz2a1</a>	Alignment	not modelled	39.8	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
69	<a href="#">c4awaA</a>	Alignment	not modelled	39.8	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> legumain; <b>PDBTitle:</b> crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
70	<a href="#">c2lfvA</a>	Alignment	not modelled	39.7	30	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> protein damx; <b>PDBTitle:</b> solution structure of the spor domain from e. coli damx
71	<a href="#">c2dnmA</a>	Alignment	not modelled	39.6	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> srp46 splicing factor; <b>PDBTitle:</b> solution structure of rna binding domain in srp46 splicing2 factor
72	<a href="#">c5f7cC</a>	Alignment	not modelled	39.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of family 31 alpha-glucosidase (bt_0339) from2 bacteroides thetaiotaomicron
73	<a href="#">c2adcA</a>	Alignment	not modelled	39.3	11	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> polypyrimidine tract-binding protein 1; <b>PDBTitle:</b> solution structure of polypyrimidine tract binding protein2 rbd34 complexed with cucucu rna
74	<a href="#">c3h2uD</a>	Alignment	not modelled	39.2	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> raver-1; <b>PDBTitle:</b> human raver1 rrm1, rrm2, and rrm3 domains in complex with2 human vinculin tail domain vt
75	<a href="#">d2cqia1</a>	Alignment	not modelled	39.1	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
76	<a href="#">c5uscB</a>	Alignment	not modelled	39.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
77	<a href="#">c6aztA</a>	Alignment	not modelled	39.1	17	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> asparaginyl endopeptidase 1; <b>PDBTitle:</b> asparaginyl endopeptidase 1 bound to aan peptide, a tetrahedral2 intermediate
78	<a href="#">c2go9A</a>	Alignment	not modelled	39.0	8	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> u4/u6 snrna-associated splicing factor prp24; <b>PDBTitle:</b> rrm domains 1 and 2 of prp24 from s. cerevisiae
79	<a href="#">d1b7fa1</a>	Alignment	not modelled	38.9	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
						<b>Fold:</b> Ferredoxin-like

80	<a href="#">d1x5sa1</a>	Alignment	not modelled	38.9	11	<b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
81	<a href="#">c2pjuD</a>	Alignment	not modelled	38.8	23	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
82	<a href="#">c1b7fA</a>	Alignment	not modelled	38.7	25	<b>PDB header:</b> rna-binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sxl-lethal protein); <b>PDBTitle:</b> sxl-lethal protein/rna complex
83	<a href="#">c2q5cA</a>	Alignment	not modelled	38.7	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator; <b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
84	<a href="#">c2i38A</a>	Alignment	not modelled	38.6	18	<b>PDB header:</b> rna binding protein/chimera <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein consists of immunoglobulin g-binding protein <b>PDBTitle:</b> solution structure of the rrm of srp20
85	<a href="#">c2qmjA</a>	Alignment	not modelled	38.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltase-glucoamylase, intestinal; <b>PDBTitle:</b> crystal structure of the n-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
86	<a href="#">d2u2fa</a>	Alignment	not modelled	38.2	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
87	<a href="#">c2mzsA</a>	Alignment	not modelled	38.2	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein hrb1; <b>PDBTitle:</b> nmr structure of the rrm2 domain of hrb1
88	<a href="#">c2dnnA</a>	Alignment	not modelled	38.1	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 12; <b>PDBTitle:</b> solution structure of rna binding domain in rna-binding2 protein 12
89	<a href="#">d1whwa</a>	Alignment	not modelled	37.9	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
90	<a href="#">d1fjeb2</a>	Alignment	not modelled	37.9	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
91	<a href="#">d1gccA</a>	Alignment	not modelled	37.8	31	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> GCC-box binding domain
92	<a href="#">c2jrsA</a>	Alignment	not modelled	37.8	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 39; <b>PDBTitle:</b> solution nmr structure of caper rrm2 domain. northeast2 structural genomics target hr4730a
93	<a href="#">c5f7sA</a>	Alignment	not modelled	37.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 31; <b>PDBTitle:</b> cycloalternan-degrading enzyme from trueperella pyogenes
94	<a href="#">c5zwoX</a>	Alignment	not modelled	37.6	19	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> u2 snrnp component ist3; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
95	<a href="#">c3md1B</a>	Alignment	not modelled	37.5	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear and cytoplasmic polyadenylated rna-binding protein <b>PDBTitle:</b> crystal structure of the second rrm domain of yeast poly(u)-binding2 protein (pub1)
96	<a href="#">d2cqca1</a>	Alignment	not modelled	37.1	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
97	<a href="#">c2f3jA</a>	Alignment	not modelled	37.1	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna and export factor binding protein 2; <b>PDBTitle:</b> the solution structure of the ref2-i mrna export factor2 (residues 1-155).
98	<a href="#">c3topA</a>	Alignment	not modelled	37.1	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltase-glucoamylase, intestinal; <b>PDBTitle:</b> crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
99	<a href="#">c6g6sA</a>	Alignment	not modelled	37.0	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> apoptotic chromatin condensation inducer in the nucleus; <b>PDBTitle:</b> crystal structure of human acinus rna recognition motif domain
100	<a href="#">c2m9kA</a>	Alignment	not modelled	36.9	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein with multiple splicing 2; <b>PDBTitle:</b> rbpms2-nter
101	<a href="#">c5x7rB</a>	Alignment	not modelled	36.8	16	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 31 alpha-glucosidase; <b>PDBTitle:</b> crystal structure of paenibacillus sp. 598k alpha-1,6-2 glucosyltransferase complexed with isomaltohexaose
102	<a href="#">c2f06B</a>	Alignment	not modelled	36.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron
103	<a href="#">c2mzqA</a>	Alignment	not modelled	36.8	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand telomeric dna-binding protein gbp2; <b>PDBTitle:</b> nmr structure of the rrm3 domain of gbp2
104	<a href="#">d2cpda1</a>	Alignment	not modelled	36.8	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
105	<a href="#">c2dguA</a>	Alignment	not modelled	36.7	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein q;

						<b>PDBTitle:</b> solution structure of the rna binding domain in2 heterogeneous nuclear ribonucleoprotein q
106	<a href="#">d2ad9a1</a>	Alignment	not modelled	36.5	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
107	<a href="#">c2n3iA_</a>	Alignment	not modelled	36.3	8	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine/arginine-rich protein 1, pfsr1-rrm1; <b>PDBTitle:</b> solution structure of rna recognition motif-1 of plasmodium falciparum2 serine/arginine-rich protein 1.
108	<a href="#">c2dh9A_</a>	Alignment	not modelled	36.3	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein m; <b>PDBTitle:</b> solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
109	<a href="#">d2cq2a1</a>	Alignment	not modelled	36.3	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
110	<a href="#">c2qvcC_</a>	Alignment	not modelled	36.1	22	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sugar abc transporter, periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic sugar abc transporter from2 thermotoga maritima
111	<a href="#">d2ghpa2</a>	Alignment	not modelled	35.9	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
112	<a href="#">d2dita1</a>	Alignment	not modelled	35.8	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
113	<a href="#">d2b0ga1</a>	Alignment	not modelled	35.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
114	<a href="#">d1jmta_</a>	Alignment	not modelled	35.5	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Splicing factor U2AF subunits
115	<a href="#">c2kviA_</a>	Alignment	not modelled	35.4	6	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear polyadenylated rna-binding protein 3; <b>PDBTitle:</b> structure of nab3 rrm
116	<a href="#">c4n0tA_</a>	Alignment	not modelled	35.3	12	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> u4/u6 snrna-associated-splicing factor prp24; <b>PDBTitle:</b> core structure of the u6 small nuclear ribonucleoprotein at 1.72 angstrom resolution
117	<a href="#">c5mduA_</a>	Alignment	not modelled	35.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpb7-binding protein seb1; <b>PDBTitle:</b> structure of the rna recognition motif (rrm) of seb1 from s. pombe.
118	<a href="#">c2a3iA_</a>	Alignment	not modelled	35.0	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein a; <b>PDBTitle:</b> structure of urndesign, a complete computational redesign2 of human u1a protein
119	<a href="#">c2mjnA_</a>	Alignment	not modelled	34.9	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolysin tia-1 isoform p40; <b>PDBTitle:</b> structure, dynamics and rna binding of the multi-domain splicing2 factor tia-1
120	<a href="#">c3ns6B_</a>	Alignment	not modelled	34.8	8	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b; <b>PDBTitle:</b> crystal structure of hte rna recognition motif of yeast eif3b residues2 76-170