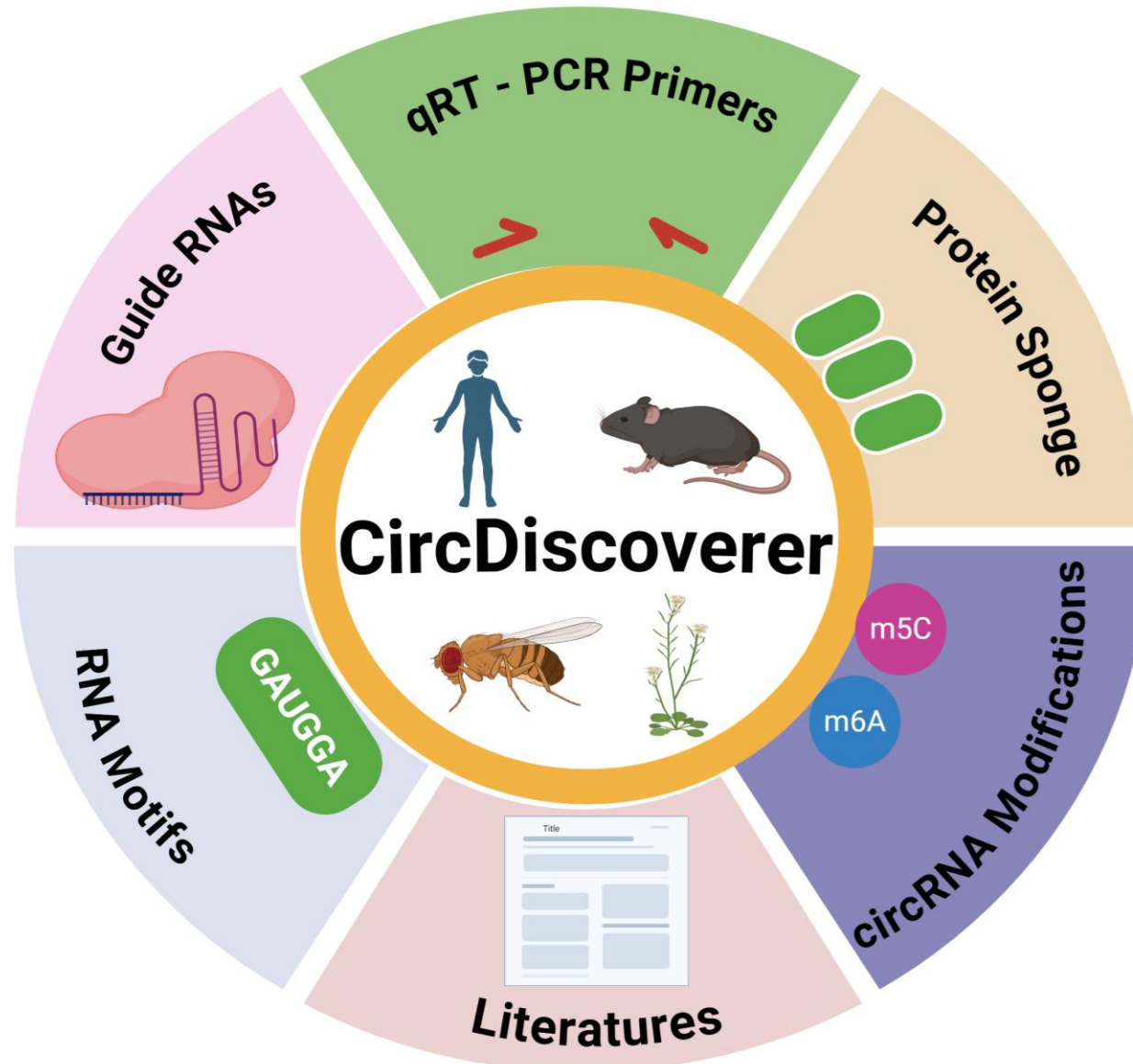


Welcome To CircDiscoverer



Literature Section

Explore the circRNA-Protein Interaction reported in the literatures

Enter the name of protein to get the following details (Page 2-5) :

E.g. Search by Protein, i.e. **LIN28B** in this case

CircDiscoverer

A Resource for Enabling Discovery in Circular RNA Biology

[Home](#)[Literature Section](#)[Predicted Section](#)[Explore circRNA Section](#)[Help](#)[Download](#)

Explore Literatures of circRNA–Protein Interaction

circRNAs binding to LIN28B

Search by Protein

Search by Disease

circBase ID	circAtlas ID	Gene	Disease/Physiology	Function	Drugs	Modification	DOI
hsa_circ_0058058	hsa-ATIC_0018	ATIC	Bladder Cancer	Promote	Cisplatin	-	DOI
hsa_circ_0049658	hsa-NFIX_0005	NFIX	Ovarian Cancer	Promote	-	-	DOI

Figure 1

Details of the Literature Section

- hg19 : The ***circBase*** ID of the binding circRNA.
- hg38 : The ***circAtlas 3.0*** ID of the binding circRNA.
- Gene : The gene from which the circRNA is derived.
- Disease : The disease in which this circRNA-Protein Interaction is reported.
- Function : Function of this circRNA-Protein interaction in the respective disease, whether the circRNA-Protein interaction either promotes or inhibits the respective disease. Clicking this will open a pop up, describing the mechanism of the CPI in the respective disease.
- Drugs : The drugs, whose response is affected in the disease by this circRNA-Protein Interaction.
- Modifications : The modifications found in the interacting circRNA.
- DOI of the literature.

Literature Section Continued

Enter the name of a diseases to get the following details (Page 4-5) :

E.g. Search by Protein, i.e. **Ovarian Cancer** in this case.

CircDiscoverer							
A Resource for Enabling Discovery in Circular RNA Biology							
Home Literature Section Predicted Section Explore circRNA Section Help Download							
Explore Literatures of circRNA–Protein Interaction							
Results for Ovarian Cancer							
Search by Protein		LIN28B		Search by Disease		Ovarian Cancer	
Protein	circBase ID	circAtlas ID	Gene	Function	Drugs	Modification	DOI
MST1	-	hsa-ARHGEF28_0041	ARHGEF28	Promote	Cisplatin	-	DOI
MST2	-	hsa-ARHGEF28_0041	ARHGEF28	Promote	Cisplatin	-	DOI
UBE2T	hsa_circ_0002077	hsa-NUP50_0001	NUP50	Promote	Cisplatin	-	DOI
LIN28B	hsa_circ_0049658	hsa-NFIX_0005	NFIX	Promote	-	-	DOI

Literature Section Continued

- Protein : List of Proteins interacting with the circRNAs, involved in the disease.
- hg19 : The ***circBase*** ID of the binding circRNA.
- hg38 : The ***circAtlas 3.0*** ID of the binding circRNA.
- Gene : The gene from which the circRNA is derived.
- Function : Function of this circRNA-Protein interaction in the respective disease, whether the circRNA-Protein interaction either promotes or inhibits the respective disease. Clicking this will open a pop up, describing the mechanism of the CPI in the respective disease.
- Drugs : The drugs, whose response is affected in the disease by this circRNA-Protein Interaction.
- Modifications : The modifications found in the interacting circRNA.
- DOI of the literature.

Predicted Section

Get possible circRNA's binding to the proteins

The screenshot shows the CircDiscoverer web interface. The header includes the logo 'CircDiscoverer' and the tagline 'A Resource for Enabling Discovery in Circular RNA Biology'. The navigation bar has links for 'Home', 'Literature Section', 'Predicted Section', 'Explore circRNA Section' (highlighted with a yellow box), 'Help', and 'Download'. Below the navigation bar, the main heading is 'Get circRNA's Binding to your Protein'. There are two input fields: 'Select Organism:' with 'Homo sapiens' and 'Select Protein:' with 'FXR1' (highlighted with a red box). Below these fields, the section is titled 'circRNAs binding to FXR1'. A table is displayed with the following data:

circRNA	Sample Count	Sample Score	circRNA Score	Evidence Type	Tools
hsa-RMRP_0001	5	0.833	1	CLIP-Seq	CIRCEplorer2
hsa-SH2B3_0001	3	0.5	0.6	CLIP-Seq	CIRCEplorer2, CIRI2
hsa-DOCK1_0035	2	0.333	0.4	CLIP-Seq	CIRCEplorer2, CIRI2
hsa-MSANTD3-TMEFF1_0004	2	0.333	0.4	CLIP-Seq	CIRCEplorer2, CIRI2

Figure 2

Clicking on any of these circRNA's, for e.g. hsa-RMRP_0001, will directly land in the circAtlas database(Page 5)

circAtlas 3.0 Results Page

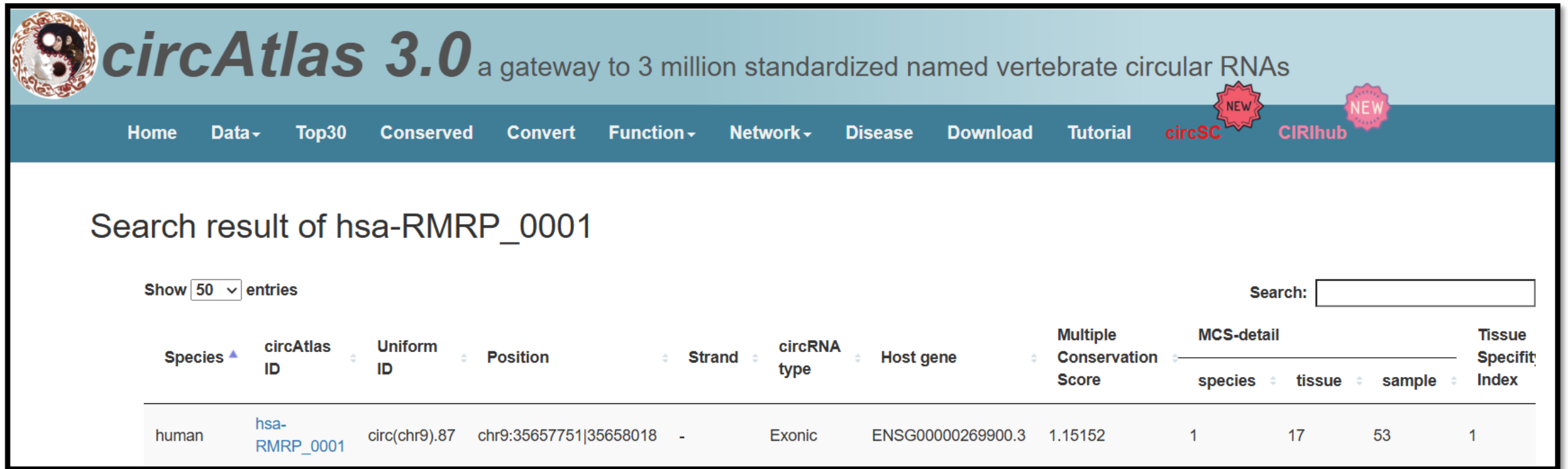


Figure 3

Details of the Predicted Section

- **circRNA** : List of circRNAs binding to the protein of interest.
- **Sample Count** : Its the total number of samples in which a particular circRNA is found. On clicking the numbers in the sample count, a pop up will open, detailing in brief about the samples and the details of the circRNAs in those samples.
- **Sample Score** : A metric used to measure the abundance of a circRNA. It tells in how many samples out of the total samples analysed the circRNA is found.
- **circRNA Score** : A metric for ranking a circRNA, relative to the circRNA present in highest sample count for a given protein.
- **Evidence Type** : Represents what type of evidences were used to infer the circRNA-Protein Interactions(CPIs).
- **Tools**: The respective tools used to analyse the CPIs across all the samples overall.

Explore circRNA Section

This section allows users to explore a given circRNA of the selected organism in detail, as shown below, this section consists of four tabs, i.e. ***Get Proteins***, ***Get Guide RNA***, ***Get Modifications*** and ***Get Primers***.

CircDiscoverer
A Resource for Enabling Discovery in Circular RNA Biology

[Home](#) [Literature Section](#) [Predicted Section](#) **[Explore circRNA Section](#)** [Help](#) [Download](#)

Explore circRNA

Select Organism:

Select circRNA:

[Get Proteins](#) [Get Guide RNAs](#) [Get Modifications](#) [Get Primers](#)

Explore circRNA Section

Select the organism and circRNA of interest, followed by clicking on the respective tabs, as shown below, for getting information for the respective section, for e.g., Get Proteins.

[Home](#) [Literature Section](#) [Predicted Section](#) **Explore circRNA Section** [Help](#) [Download](#)

Explore circRNA

Select Organism:
Homo sapiens

Select circRNA:
hsa-SMARCA5_0005

Get Proteins

Get Guide RNAs

Get Modifications

Get Primers

Proteins Associated with hsa-SMARCA5_0005

Proteins with Motifs

Proteins without Motifs

Protein	Sample Count	Sample Score	circRNA Score	Binding Sites	Tools
SFPQ	2	1	1	1	CIRI2, circExplorer2
ELAVL1	2	0.667	1	5	CIRI2
HNRNPD	3	0.6	0.6	2	CIRI2, circExplorer2

Figure 4

Explore circRNA Section – Get Proteins Details

Protein with Motifs

Clicking on the “**Protein with Motifs**” gives the list of proteins interacting with the circRNA of interest, having known RNA binding motifs.

Sample Count, Sample Score and circRNA scores are same as for Predicted Section.

Binding Sites : Total number of binding sites for that protein in the given circRNA, clicking which opens a pop up, that displays details of that RNA binding motif.

Protein without Motifs

[Home](#) [Literature Section](#) [Predicted Section](#) [Explore circRNA Section](#) [Help](#) [Download](#)

Explore circRNA

Select Organism:
Homo sapiens

Select circRNA:
hsa-SMARCA5_0005

Get Proteins

Get Guide RNAs

Get Modifications

Get Primers

Proteins Associated with hsa-SMARCA5_0005

Proteins with Motifs

Proteins without Motifs

Protein	Sample Count	Sample Score	circRNA Score	Tools
Beta-Catenin	6	1	1	CIRI2, circExplorer2
HAX1	5	1	1	CIRI2, circExplorer2

Clicking on the “**Protein without Motifs**” gives the list of proteins interacting with the circRNA of interest, but with no RNA binding motifs known.

Sample Count, Sample Score and circRNA scores are same as for Predicted Section.

Get Guide_RNA

Gives list of Forward & the Reverse oligos for cloning the gRNA's in RfxCas13d expressing plasmid vector called pXR004

Explore circRNA

Select Organism: Homo sapiens Select circRNA: hsa-ARID1A_0001 ▼

Get Proteins **Get Guide RNAs** Get Modifications Get Primers

Guide RNAs targeting hsa-ARID1A_0001

NOTE: Check the off-target binding of these gRNA's.

Forward oligo(5'-3')	Reverse oligo(5'-3')	gRNA Spacer Length	RfxCas13d Plasmid Vector
AAACACTGGATGGAGGCAAGCTGGAGG	CTTGCCTCCAGCTTGCCTCCATCCAGT	23	pXR004
AAACGACTGGATGGAGGCAAGCTGGAG	CTTGCTCCAGCTTGCCTCCATCCAGTC	23	pXR004
AAACGGACTGGATGGAGGCAAGCTGGA	CTTGTCCAGCTTGCCTCCATCCAGTCC	23	pXR004

Figure 6

Clicking the guide RNA's will land into the NCBI-BLAST page with the sequence pasted directly, allowing users to check the off-targets in their own settings(Page 9), i.e.

Guide_RNA Results Page

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Query subrange [?](#)

From

To

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Input: `>seq
AAACTTTAAGATATTTGACCACATAAT`

Figure 7

Get Primers

Get primers amplifying the backsplicing junction

Home Literature Section Predicted Section **Explore circRNA Section** Help Download

Explore circRNA

Select Organism: Homo sapiens Select circRNA: hsa-NSMAF_0001

Get Proteins Get Guide RNAs Get Modifications **Get Primers**

qRT-PCR primers for hsa-NSMAF_0001

NOTE: These primers may or may not work as expected. Check off-target amplification.

Forward Primer(5'-3')	Length	Tm(°C)	GC(%)	Reverse Primer(5'-3')	Length	Tm(°C)	GC(%)	Amplicon Size(bp)	P	F	R
AGAGCATCCTGCCTTGACAA	20	63.3	50	GCTGTTCAAAGTAGTACTCC	20	56.8	45	142	P	F	R
AGAGCATCCTGCCTTGACAA	20	63.3	50	GTACTCCTCCAAGTTAAGCA	20	58	45	129	P	F	R
AGAGCATCCTGCCTTGACAA	20	63.3	50	GCAAAATGTGATTGGCTCTAT	21	57.9	38.1	163	P	F	R

Figure 8

Clicking the buttons, i.e. P(Primer pair), F(Forward primer) ,R(Reverse primer) lands onto the NCBI-primer BLAST page with the primer sequence pasted, where the users can check for the off-targets (Page 11-A,B,C).

NCBI-Primer BLAST Page

A)

Primer-BLAST A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template Primers common for a group of sequences

PCR Template Retrieve recent results Publication Tips for finding specific primers

Enter accession, gi, or FASTA sequence (A refseq record is preferred)

Range

Forward primer From To

Reverse primer From To

Or, upload FASTA file No file chosen

Primer Parameters

Use my own forward primer (5'->3' on plus strand)

Use my own reverse primer (5'->3' on minus strand)

B)

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nu

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Query subrange

>Reverse_Primer
GGCTTGATAGCTCGTTTCTTT

From

To

Or, upload file No file chosen

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

C)

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nu

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Query subrange

>Forward_Primer
CTAGAAAAGAAAAACTATAG

From

To

Or, upload file No file chosen

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Get Modifications

Displays the possible modifications in a circRNA, alongwith the experimentally validated modifications.

The screenshot shows a web interface for exploring circRNA modifications. The top navigation bar includes links for Home, Literature Section, Predicted Section, Explore circRNA Section (highlighted with a yellow border), Help, and Download. The main heading is 'Explore circRNA'. Below it, there are two input fields: 'Select Organism:' with 'Homo sapiens' and 'Select circRNA:' with 'hsa-CCSER2_0002'. Both fields are outlined with red boxes. Below these are four buttons: 'Get Proteins', 'Get Guide RNAs', 'Get Modifications' (outlined with a red box), and 'Get Primers'. A section titled 'Get Modifications in hsa-CCSER2_0002' contains a table with two columns: 'Predicted Modifications' and 'Experimentally Validated Modifications'. The 'Predicted Modifications' column lists 'm6A' (hyperlinked in blue), and the 'Experimentally Validated Modifications' column lists 'm5C' (hyperlinked in blue). The entire table area is outlined with a red box.

Predicted Modifications	Experimentally Validated Modifications
m6A	m5C

Clicking this hyperlinked Experimentally validated Modification will lead directly to the respective literature, and when clicked on Predicted Modification, a pop will open, detailing possible positions of the modification in circRNA, and the respective cell line where this modification can be found.

qRT-PCR primers and gRNAs Designed with Non-Standard Rules

Some gRNAs and qRT-PCR Primers have been designed beyond the standard rules, such entries will be reflected with the respective warning as shown below, with the nucleotide sequences highlighted in red:

A)

HomeLiterature SectionPredicted SectionExplore circRNA SectionHelpDownload

Explore circRNA

Select Organism:

Homo sapiens

Select circRNA:

hsa-RP11-206L10_0001

Get Proteins

Get Guide RNAs

Get Modifications

Get Primers

qRT-PCR primers for hsa-RP11-206L10_0001

NOTE: These primers may or may not work as expected. Check off-target amplification.

Forward Primer(5'-3')	Length	Tm(°C)	GC(%)	Reverse Primer(5'-3')	Length	Tm(°C)	GC(%)	Amplicon Size(bp)	P	F	R
AATCGGTTAGACTTCTCAAG	20	55.6	40	TCTCCATCTTCACTATTTAAGAT	23	55.1	30.4	84	P	F	R
AATCGGTTAGACTTCTCAAG	20	55.6	40	GGATGCATATTCATGCTCT	19	56.1	42.1	118	P	F	R

B)

HomeLiterature SectionPredicted SectionExplore circRNA SectionHelpDownload

Explore circRNA

Select Organism:

Homo sapiens

Select circRNA:

hsa-ADAMTSL1_0139

Get Proteins

Get Guide RNAs

Get Modifications

Get Primers

Guide RNAs targeting hsa-ADAMTSL1_0139

NOTE: The gRNA's contain mismatches! Check the off-target binding of these gRNA's.

Forward oligo(5'-3')	Reverse oligo(5'-3')	gRNA Spacer Length	RfxCas13d Plasmid Vector
AAACCTCCGCATACAATTTGCAGTAAG	CTTGCTTACTGCAAATTGTATGCGGAG	23	pXR004
AAACGTCTCCGCATACAATTTGACGTA	CTTGACGTCAAATTGTATGCGGAGAC	23	pXR004