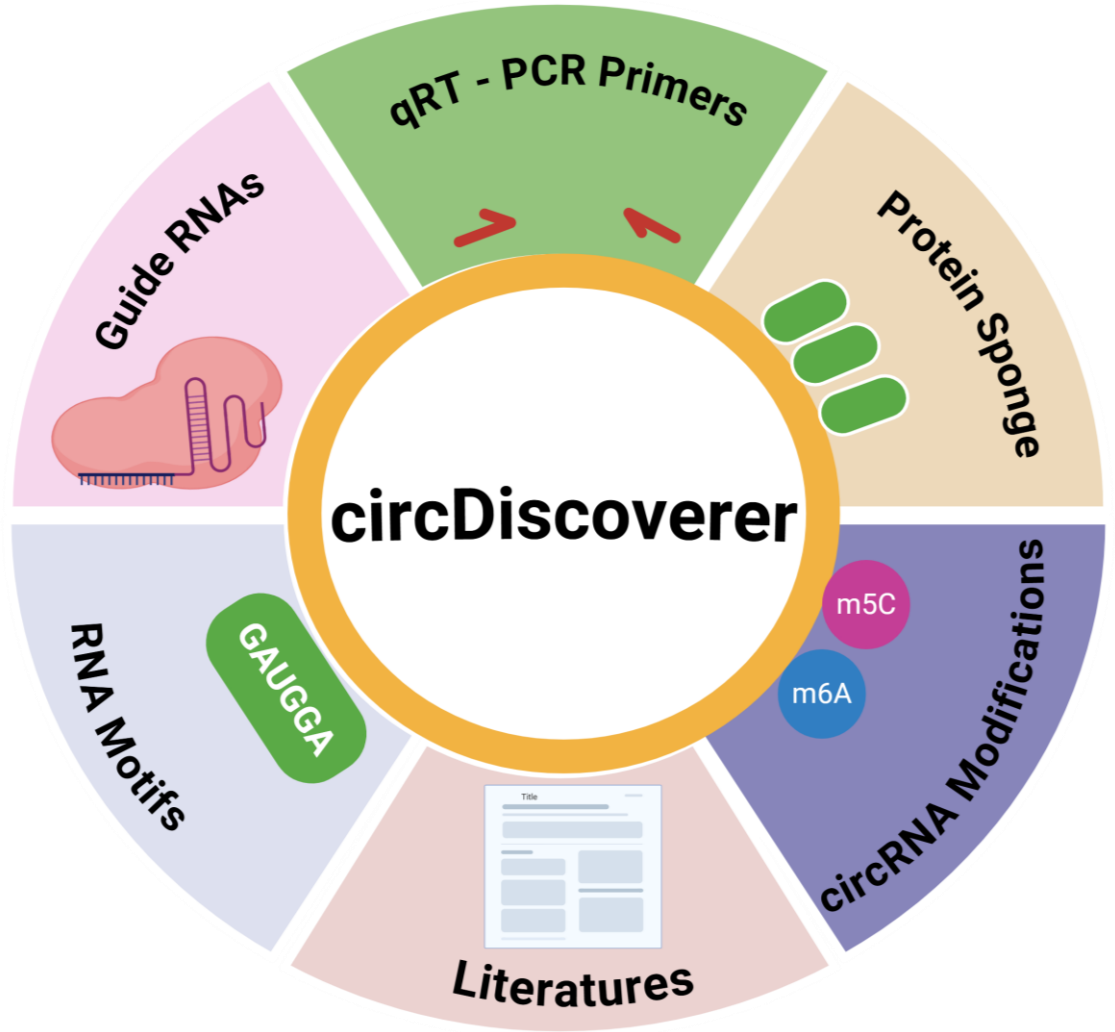
# circDiscoverer Tutorial Page

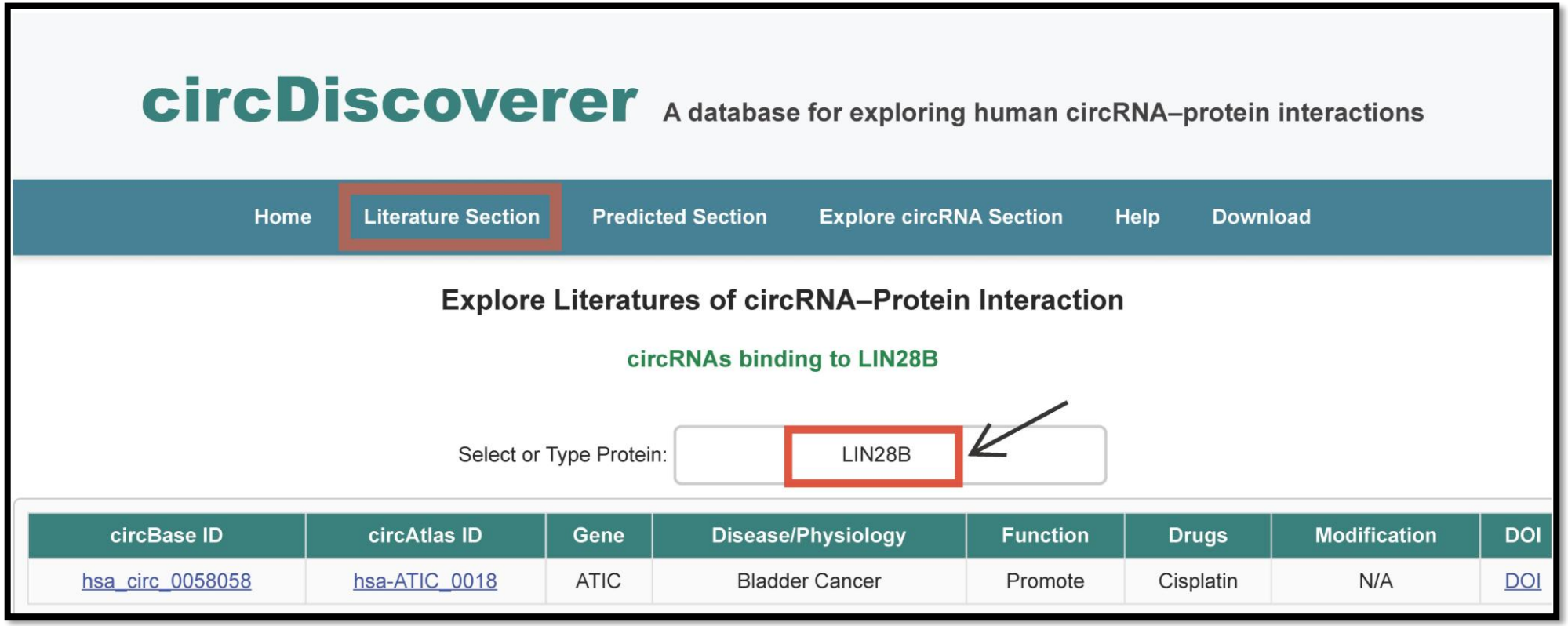


# Literature Section

Explore the circRNA-Protein Interaction reported in the literatures

Enter the name of protein & get the following details (Page 2 & 3) :

E.g. LIN28B in this case




| circBase ID | circAtlas ID | Gene | Disease/Physiology | Function | Drugs | Modification | DOI |
|---|---|---|---|---|---|---|---|
| hsa_circ_0058058 | hsa-ATIC_0018 | ATIC | Bladder Cancer | Promote | Cisplatin | N/A | DOI |

**Figure 1**

# Details of the Literature Section

- hg19 : The circbase ID of the binding circRNA.
- hg38 : The circAtlas 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.
- 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

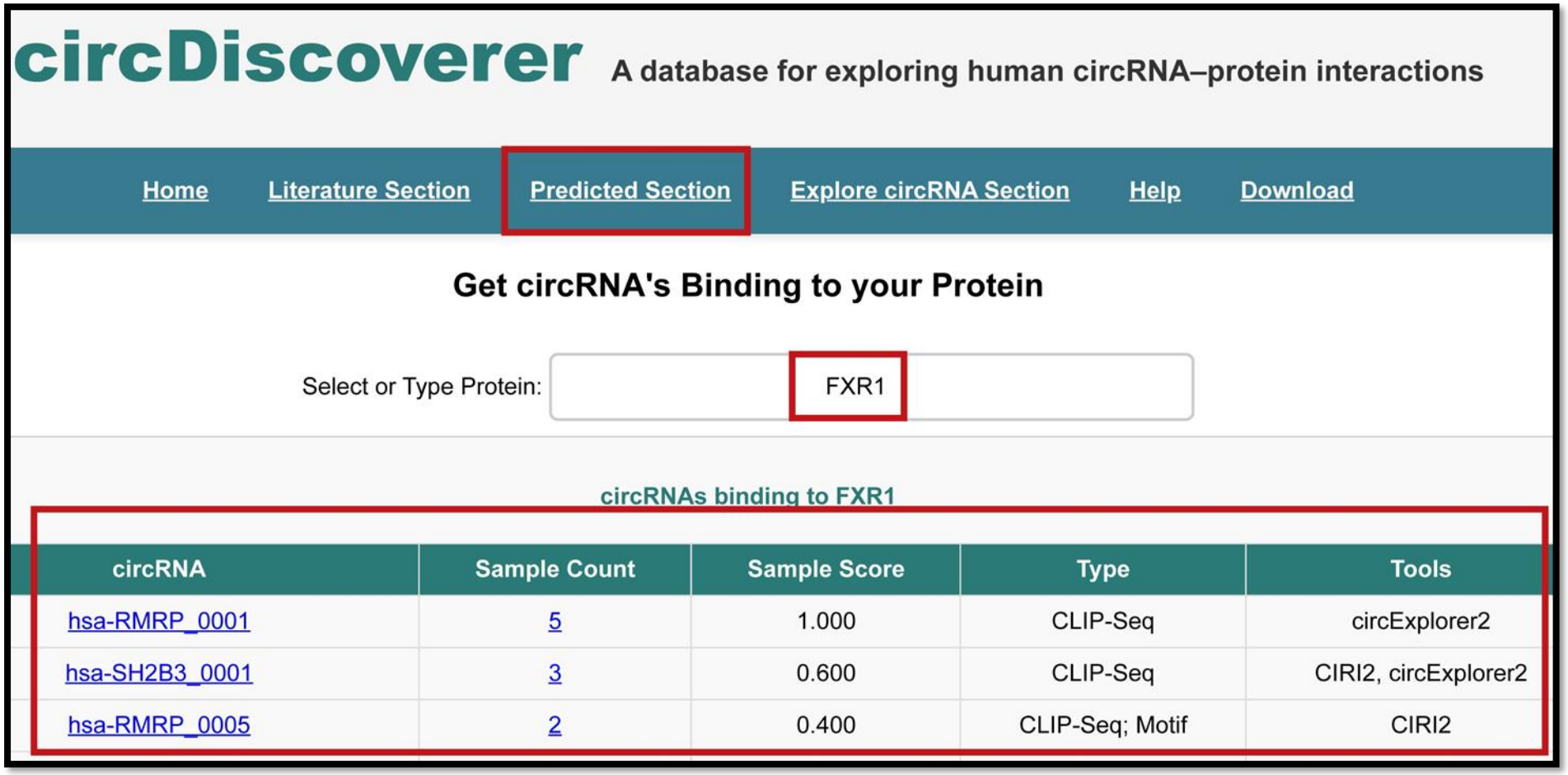



**Figure 2**

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

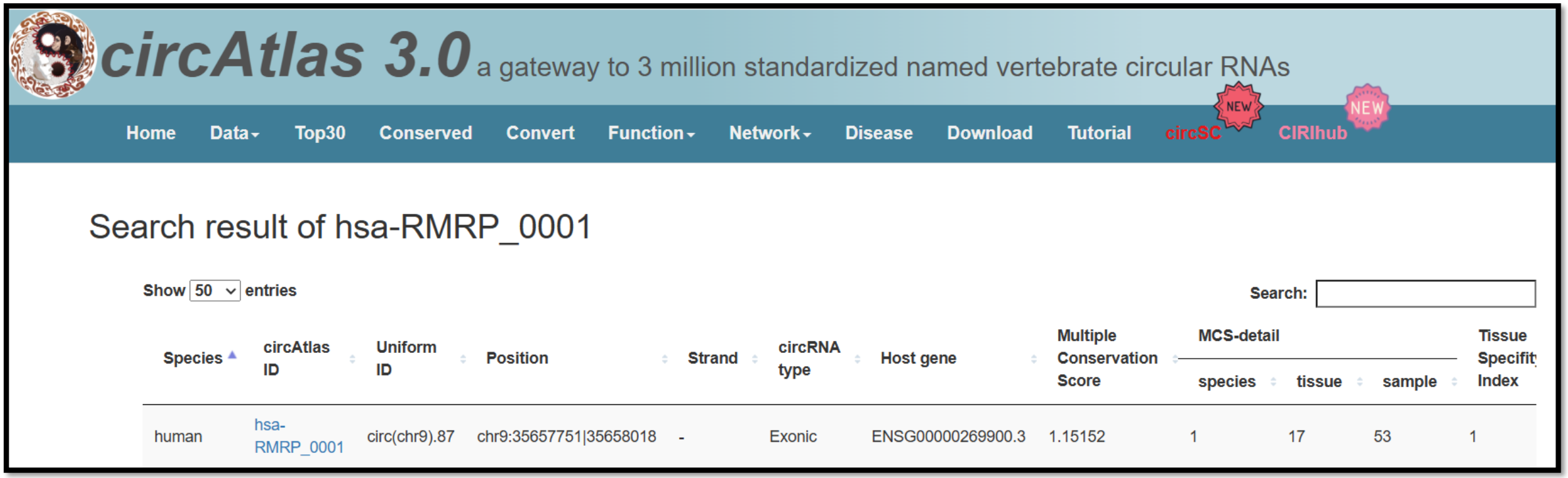



**Figure 3**

# 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.

- **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

Just paste the circRNA ID and then click on the respective 4 tabs, as shown above, and then clicking on these respective tabs will give information for the respective section, for e.g., Get Proteins.

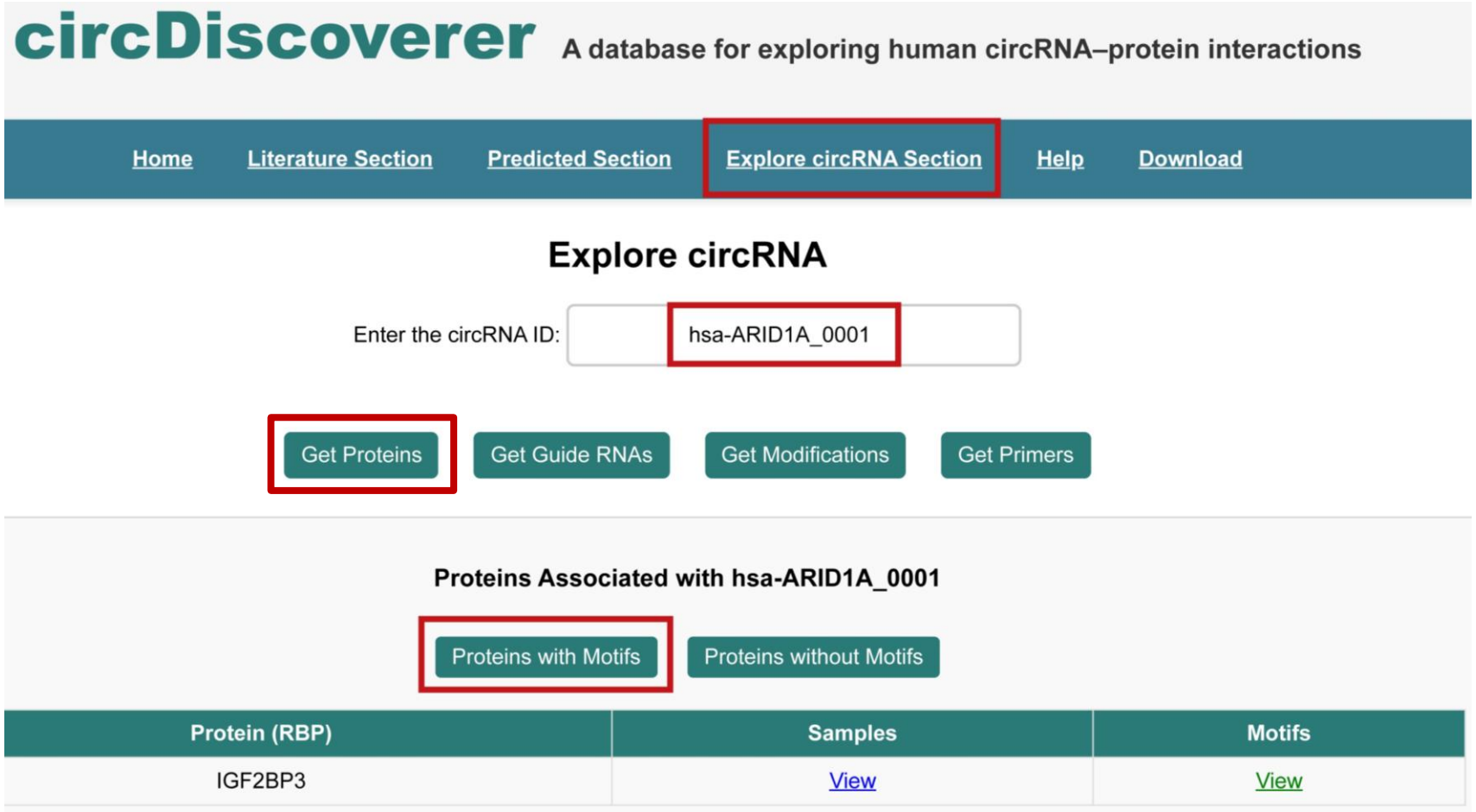



**Figure 4**

# 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.

**View** : Clicking on this opens a pop up, that displays the sample in which the circRNA-RBP interaction were found.

**Motifs** : Clicking on this opens a pop up, that displays details of the known RNA binding motifs of a protein in that circRNA.

# Protein without Motifs

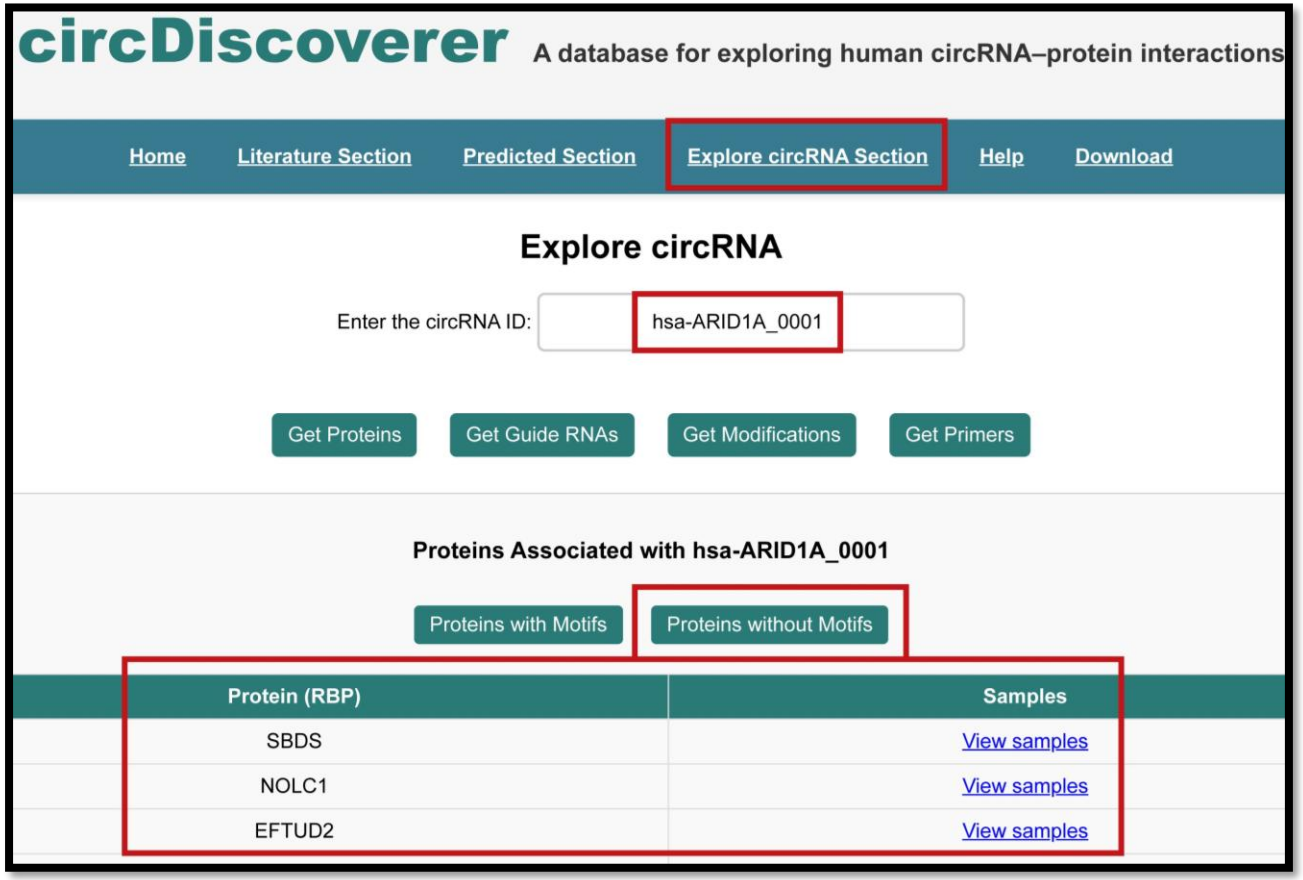



**Figure 5**

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

**View Samples** : Clicking on this opens a pop up, that displays the sample in which the circRNA-RBP interaction were found.

# Get Guide_RNA

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

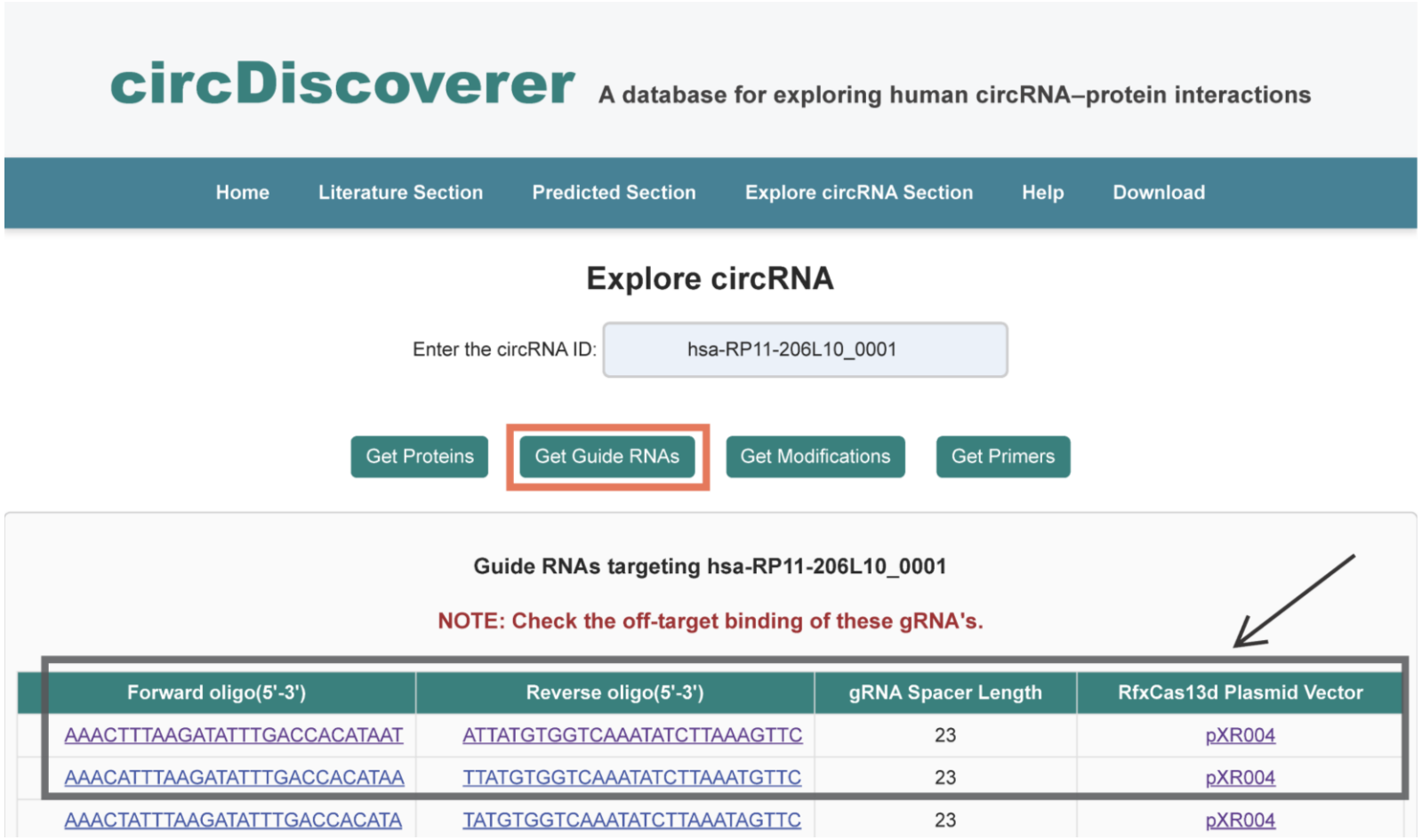



**Figure 6**

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

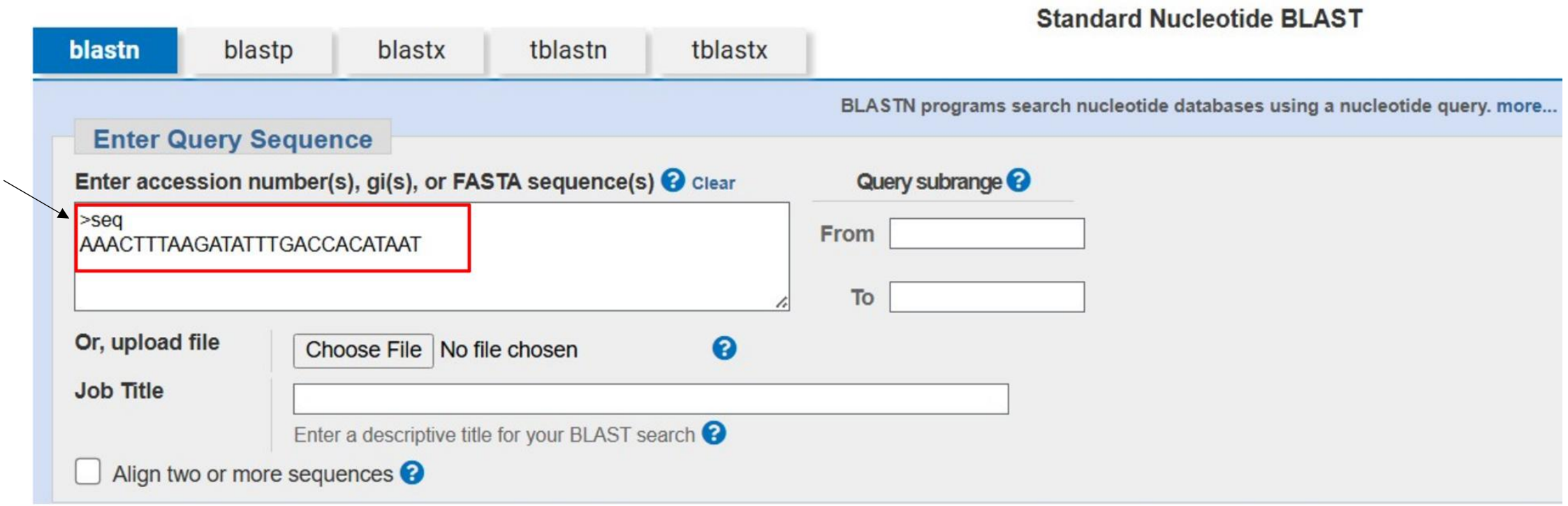



**Figure 7**

# Get Primers

Get primers amplifying the backsplicing junction

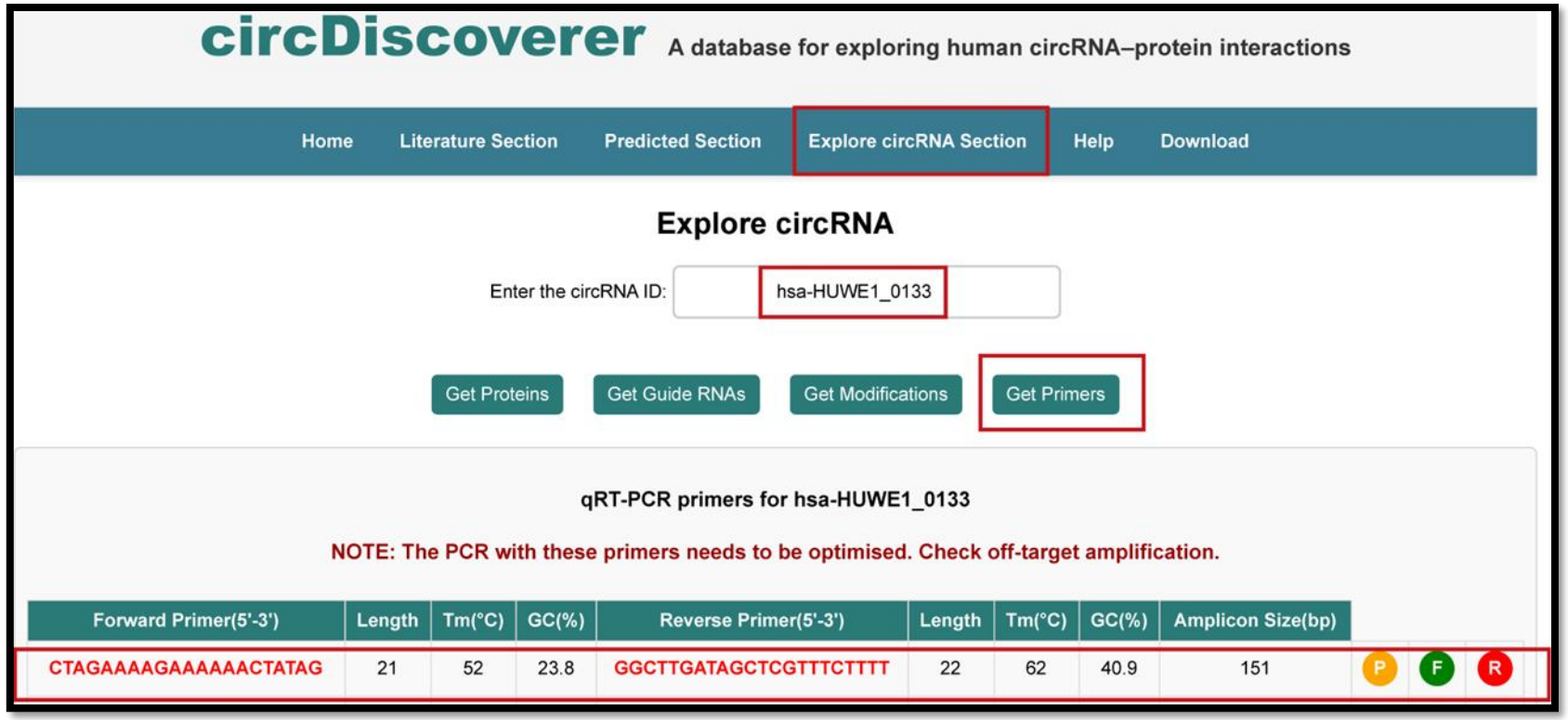
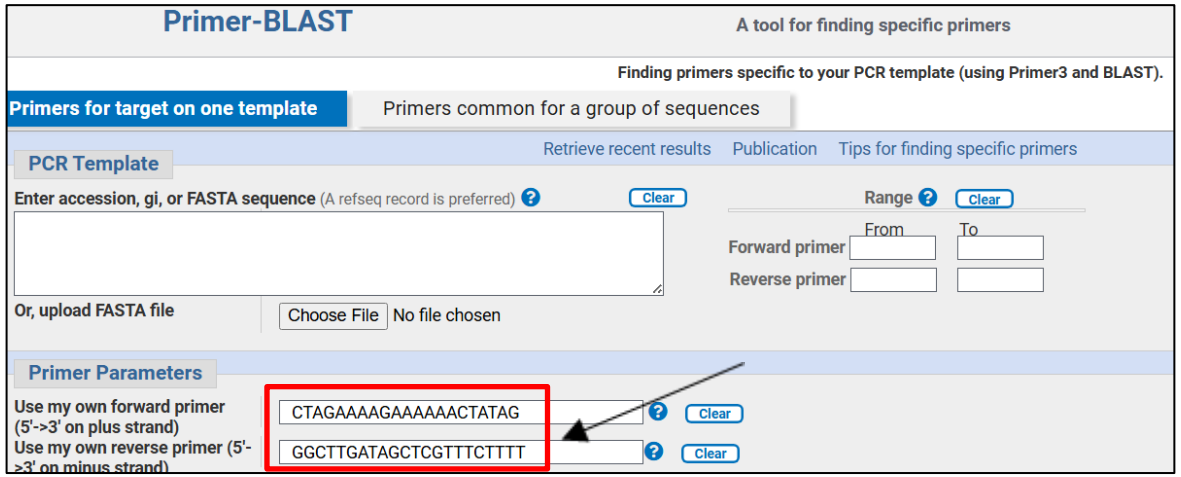



**Figure 8**

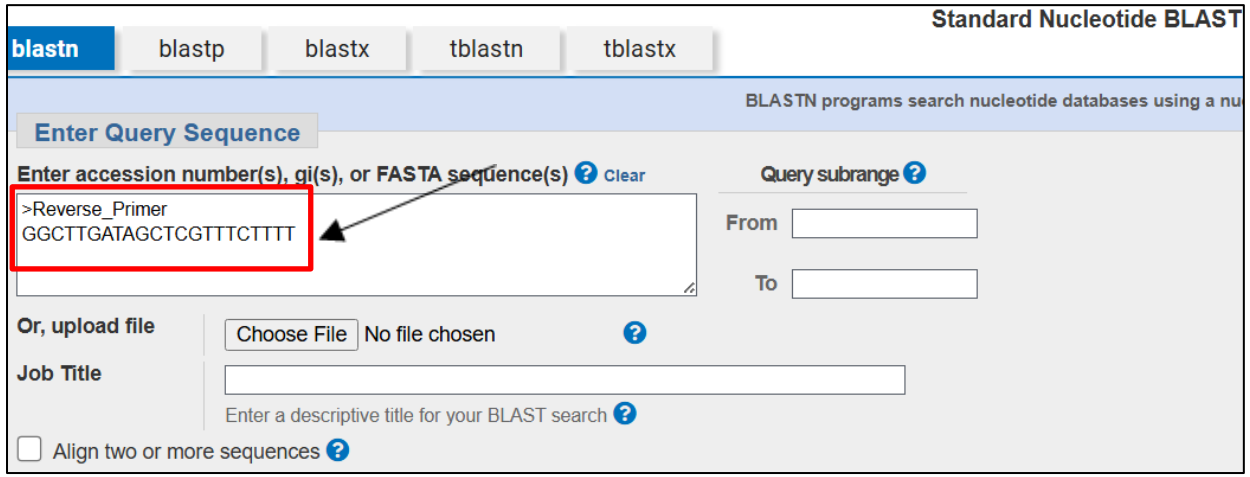
Clicking the buttons, i.e. P(Primer pair), F(Forward primer) ,R(Reverse primer) lands onto the NCBI-primer BLAST page with the primer sequence pasted, where the users can check for the off-targets (Page 11-A,B,C).

# NCBI-Primer BLAST Page

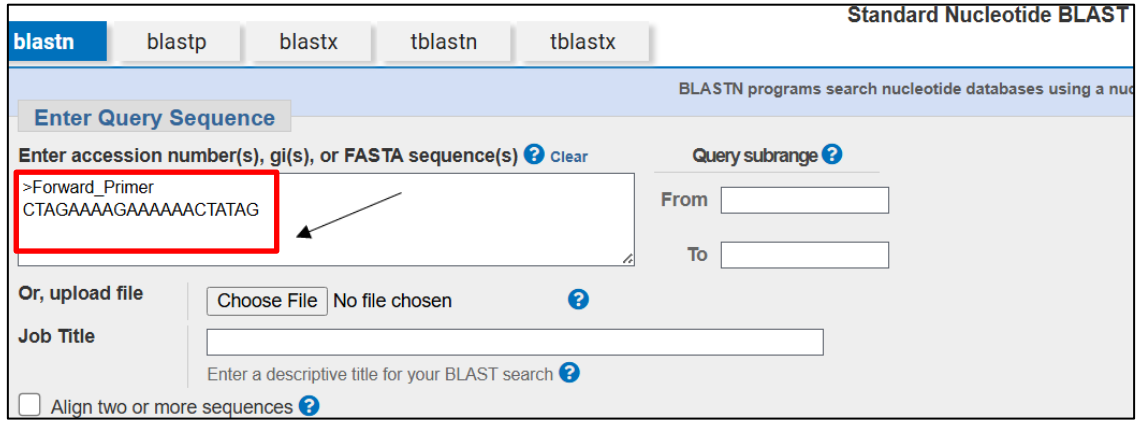
A)




B)

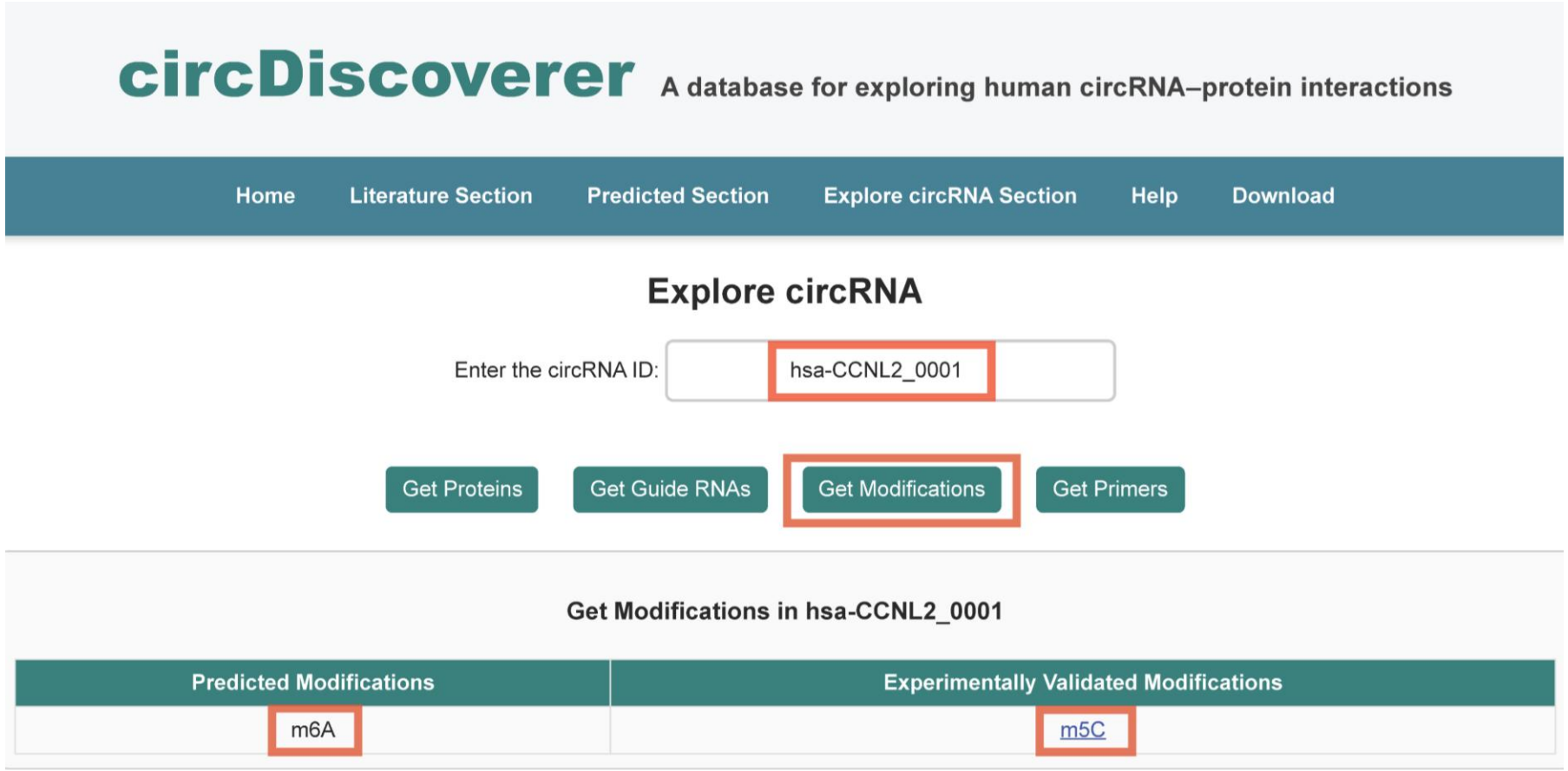



C)



# Get Modifications

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

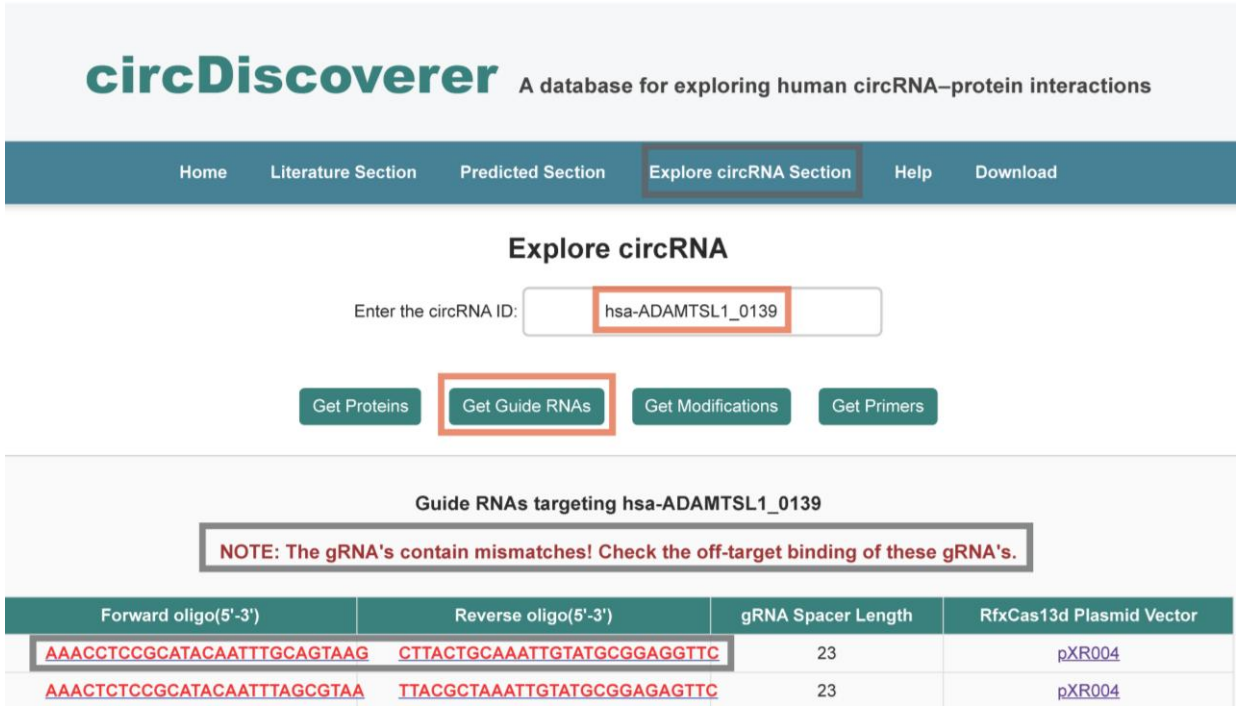



Clicking this hyperlinked Experimentally validated Modification will lead directly to the respective literature, and when clicked on Predicted Modification, a pop will open, detailing possible positions of the modification in circRNA, and the respective cell line where this modification can be found.

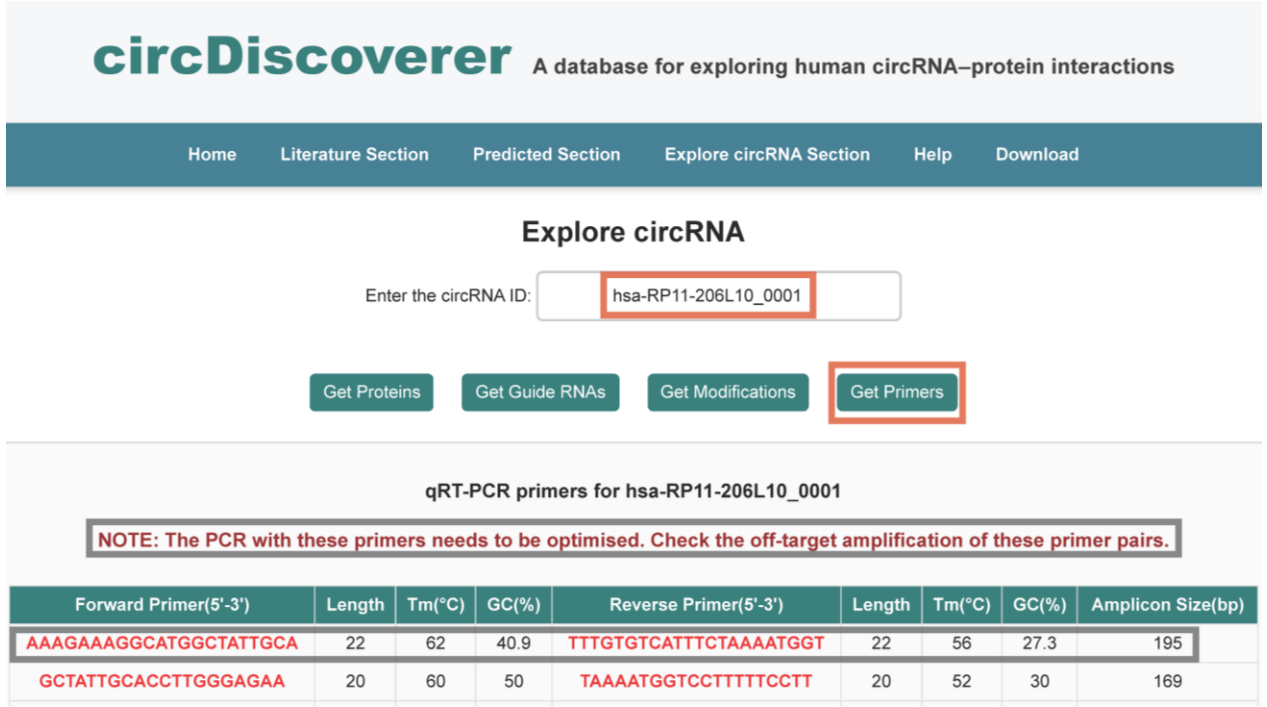
# qRT-PCR primers and gRNAs Designed with Non-Standard Rules

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)




B)



# HELP Page

**circDiscoverer** A database for exploring human circRNA–protein interactions

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**circDiscoverer Tutorial**

Click here to open the Tutorial (PDF)

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