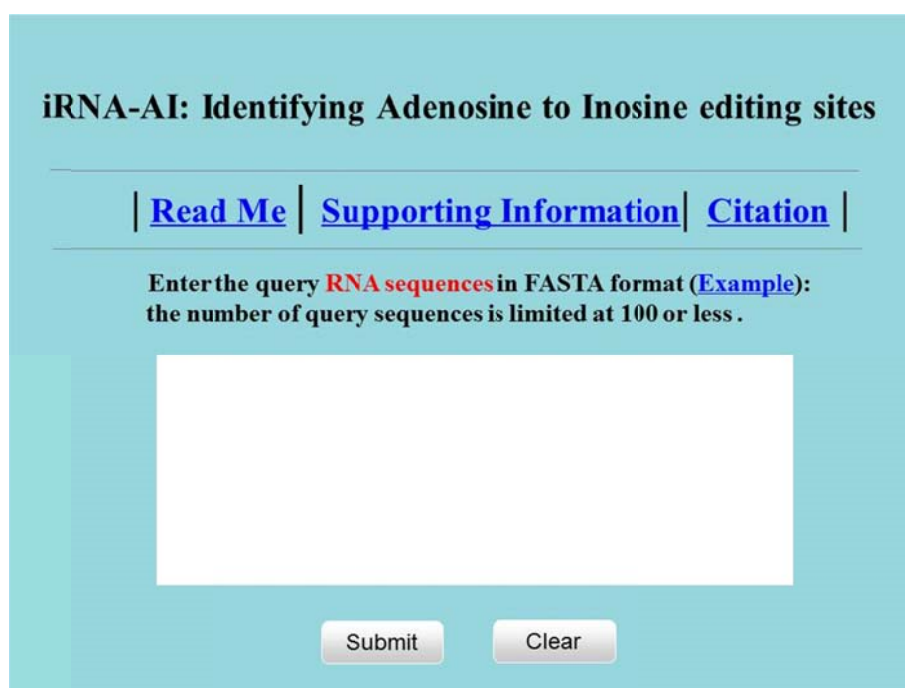


Supporting Information S3. User Guide for the Web-Server iRNA-AI

To maximize the users' convenience, a step-by-step guide has been provided below for how to use **iRNA-AI**.

Step 1. Open the web server at <http://lin.uestc.edu.cn/server/iRNA-AI/> and you will see the top page of the **iRNA-AI** predictor on your computer screen, as shown in figure bellow. Click on the [Read Me](#) button to see a brief introduction about the predictor and the caveat when using it.



iRNA-AI: Identifying Adenosine to Inosine editing sites

| [Read Me](#) | [Supporting Information](#) | [Citation](#) |

Enter the query **RNA sequences** in FASTA format ([Example](#)):
the number of query sequences is limited at 100 or less .

Submit Clear

Step 2. Either type or copy/paste the query RNA sequences into the input box at the center of **Fig.S1**. The input sequence should be in FASTA format. For the example of RNA sequences in FASTA format, click the [Example](#) button right above the input box.

Step 3. Click on the [Submit](#) button to see the predicted result. If you use the two query RNA sequences in the [Example](#) window as the input, you will see the following shown on the screen of your computer: the **1st** query sequence is 102-nt long with **25** A (adenosine) residues of which the ones at position **26, 65, 69, 73, and 77** can be edited to I (inosine), while all the other cannot; the **2nd** query sequence is 197-nt long with **15A** (adenosine) residues of which the ones at position **49 and 90** can be edited to I (inosine), while all the other cannot.

Step 4. Click on the [Data](#) button to download the datasets used to train and test the model.

Step 5. Click on the [Citation](#) button to find the relevant publications that document the detailed development and algorithm of **iRNA-AI**.