

# How the Artificial Intelligence Tool iRNA-PseU is Working in Predicting the RNA Pseudouridine Sites?

**Kuo Chen Chou\***

Gordon Life Science Institute, United States of America

\*Corresponding author: Kuo Chen Chou, Gordon Life Science Institute, Boston, Massachusetts 02478, United States of America



## ARTICLE INFO

**Received:** 📅 December 20, 2019

**Published:** 📅 January 06, 2020

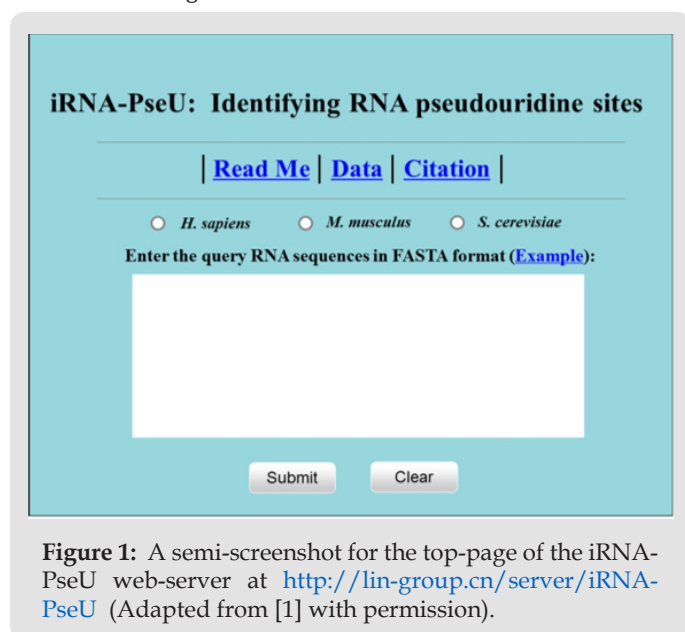
## ABSTRACT

**Citation:** Kuo Chen Chou. How the Artificial Intelligence Tool iRNA-PseU is Working in Predicting the RNA Pseudouridine Sites?. Biomed J Sci & Tech Res 24(2)-2020. BJSTR. MS.ID.004016.

## Short Communication

In 2016 a very powerful AI (artificial intelligence) tool has been established for identifying RNA pseudouridine sites, which is one of the important post modifications in RNA [1]. To see how the webserver is working, please do the following.

**Step 1.** Open the web server at <http://lin-group.cn/server/iRNA-PseU> and you will see the top page of the iRNA-PseU predictor on your computer screen, as shown in Figure 1. Click on the Read Me button to see a brief introduction about the predictor and the caveat when using it.



**Figure 1:** A semi-screenshot for the top-page of the iRNA-PseU web-server at <http://lin-group.cn/server/iRNA-PseU> (Adapted from [1] with permission).

**Step 2.** Select the organism or species by checking on the corresponding open circle. Either type or copy/paste the query RNA sequences into the input box at the center of Figure 1. The input sequence should be in FASTA format. For the examples 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. For example, if using the three query RNA sequences from the *H. sapiens* species in the Example window as the input and checking on the *H. sapiens* button, after clicking the Submit button, you will see the following shown on the screen of your computer.

- The 1<sup>st</sup> query sequence includes 5 U (uridine) residues, of which the one at position 11 can be modified to be of pseudouridine ( $\Psi$  site).
- The 2<sup>nd</sup> query sequence includes 3U residues, of which none can be modified to be of pseudouridine.
- The 3<sup>rd</sup> query sequence includes 7 U residues, of which the one at position 21 can be modified to be of pseudouridine. All these results are fully consistent with the experimental observations.

Note: to get the anticipated prediction accuracy, the species button must be consistent with the source of query sequences: if the query sequences are from *H. sapiens*, check on the *H. sapiens*

button; from *M. musculus*, check on the *M. musculus* button; from *S. cerevisiae*, check on the *S. cerevisiae* button.

**Step 4.** Click on the Data button to download the datasets used to train and test the iRNA-PseU predictor.

**Step 5.** Click on the Citation button to find the relevant papers that document the detailed development and algorithm of iRNA-PseU.

It is instructive to point out that the AI tool has been developed by strictly observing the guidelines of “Chou’s 5-steps rule” and hence have the following notable merits (see, e.g., [2-29] and three comprehensive review papers [30-32]):

- a. Crystal clear in logic development,
- b. Completely transparent in operation,
- c. Easily to repeat the reported results by other investigators,
- d. With high potential in stimulating other sequence-analyzing methods, and
- e. Very convenient to be used by most experimental scientists.

Also, it has not escaped our notice that during the development of iRNA-PseU AI tool, the approach of general pseudo amino acid components [33] or PseAAC [34] had been applied and hence its accuracy would be much higher than its counterparts, as concurred by many investigators [30, 33-281]. It is anticipated that iRNA-PseU may become a useful high throughput tool for conducting genome analysis as well as drug development. For the remarkable and awesome roles of the “5-steps rule” in driving proteome, genome analyses and drug development, see a series of recent papers [31, 32, 282-292] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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ISSN: 2574-1241

DOI: 10.26717/BJSTR.2020.24.004016

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