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Review Article

Showcase to Illustrate how the Web-Server Ipreny-Pseaac is working

Running Title: Showcase for iPreny-PseAAC

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Received date: February 03, 2020; Accepted date: April 17, 2020; Published date: May 11, 2020
Citation: Kuo-Chen Chou. Showcase to illustrate how the web-server iPreny-PseAAC is working, Clinical Research Notes, 1(2); DOI:10.31579/2690-8816/008

In 2017 a very powerful web-server predictor has been established for predicting C-terminal cysteine prenylation sites in proteins [1], which is one of the most important modifications in proteins. To see how the web-server is working, please do the following.

Step 1. Open the web server at http://app.aporc.org/iPreny-PseAAC/and you will see the top page of the predictor on your computer screen, as shown in **Figure 1**. Click on the Read Me button to see a brief introduction about **iPreny-PseAAC** predictor and the caveat when using it.

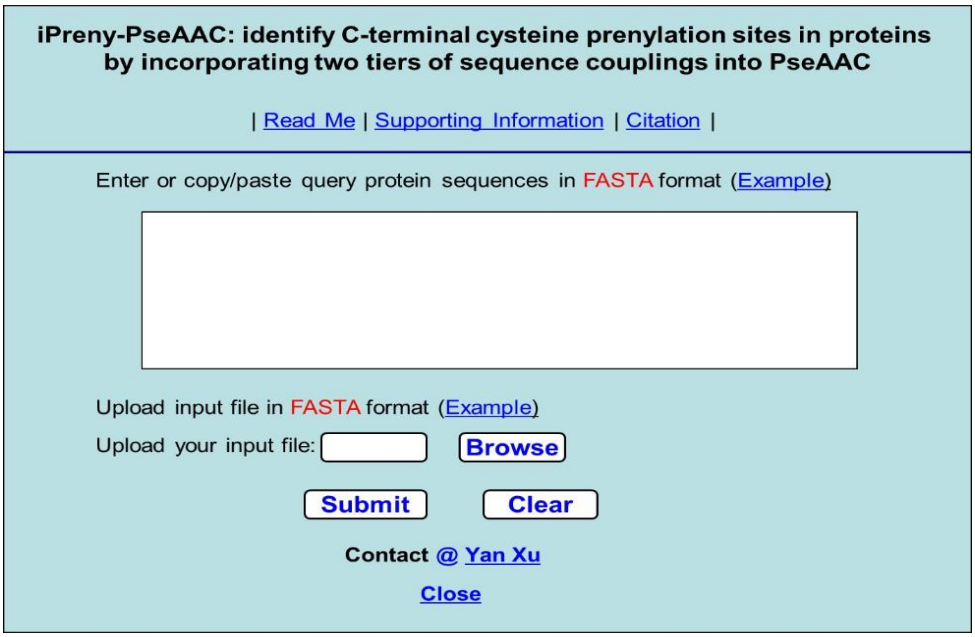

Figure 1. A semi-screenshot to show the top page of the iPreny-PseAAC server.

Its website address is at http://app.aporc.org/iPreny-PseAAC/.
(Adapted from [1] {with permission).

Step 2. Either type or copy/paste the sequences of query proteins into the input box shown at the center of **Figure 1**. The input sequence should be in the FASTA format. Example sequences in FASTA format can be seen by clicking on the Example button right above the open box.

Step 3. Click on the Submit button to see the predicted result. For example, if you use the query protein sequences in the Example window as the input, after clicking the Submit button, you will see on your screen the corresponding predicted results, which are fully consistent with the experimentally verified results.

Step 4. As shown on the lower panel of Figure 1, you may also submit your query proteins in an input file (with FASTA format) via the "Browse" button. To see the sample of input file, click on the Example button right under the input box.

Step 5. Click on the Data button to download the benchmark dataset used to train and test the iNitro-Tyr predictor.

It is anticipated that the Web-Server will be very useful because the vast majority of biological scientists can easily get their desired results without the need to go through the complicated equations in {Xu, 2014 #2988} that were presented just for the integrity in developing the predictor.

Also, note that the web-server predictor 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]): (**1**) crystal clear in logic development, (**2**) completely transparent in operation, (**3**) easily to repeat the reported

results by other investigators, (**4**) with high potential in stimulating other sequence-analyzing methods, and (**5**) very convenient to be used by the majority of experimental scientists.

It has not escaped our notice that during the development of iNitro-Tyr web-server, the approach of general pseudo amino acid components [33] or PseAAC [34] had been utilized and hence its accuracy would be much higher than its counterparts, as concurred by many investigators [1-6, 8-11, 13, 18, 26, 30, 32-300].

For the wonderful and awesome roles of the "5-steps rule" in driving proteome, genome analyses and drug development, see a series of recent papers [31, 32, 291, 301-310] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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