

Showcase To Illustrate How the Web-Server iNitro-Tyr Is Working

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1. Abstract

In 2014 a very powerful web-server predictor has been established for predicting nitrotyrosine 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.

2. Step 1

Open the web server at <http://app.aporc.org/iNitro-Tyr/> and you will see the top page of the predictor on your computer screen, as shown in (Figure1). Click on the Read Me button to see a brief introduction about iNitro-Tyr predictor and the caveat when using it.

3. Step 2

Either type or copy/paste the sequences of query proteins into the input box shown at the center of Fig.6. The input sequence should be in the FASTA format. All the input sequences should be in the FASTA format. A sequence in FASTA format consists of a single initial line beginning with the symbol ">" in the first column, followed by lines of sequence data in which amino acids are represented using single-letter codes. Except for the mandatory symbol ">", all the other characters in the single initial line are optional and only used for the purpose of identification and description. The sequence ends if another line starting with the symbol ">" appears; this indicates the start of another sequence. Example sequences in FASTA format can be seen by clicking on the Example button right above the open box. Note that if your input protein sequences should be formed by the 20 native amino acid codes (ACDEFGHIKLMNPQRSTVWY).

4. 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. It takes about a few seconds for the above computation before the predicted results appear on the computer screen. Of course, the more the number of query proteins and the longer of each sequence, the more time it is usually needed.

5. 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.

6. 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 [1] that were presented just for the integrity in developing the predictor.

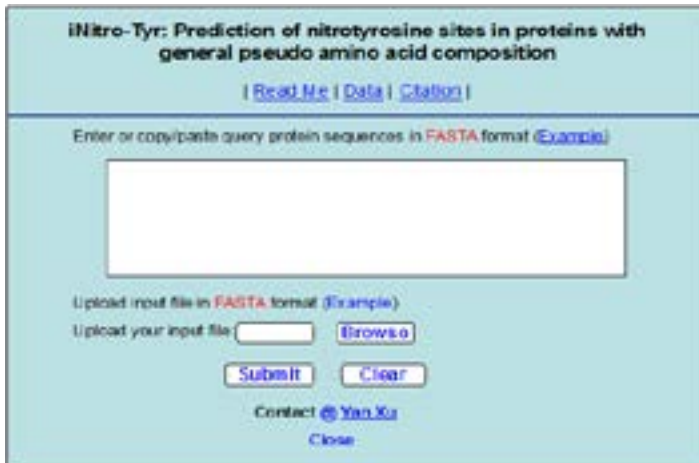


Figure 1: A semi-screenshot to show the top page of the iNitro-Tyr server. Its web-site address is at <http://app.aporc.org/iNitro-Tyr/>. (Adapted from [1] with permission).

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 fantastic 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, 301-309] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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