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Short Communication

Showcase to Illustrate How the Web-server iPTM-mLys is working

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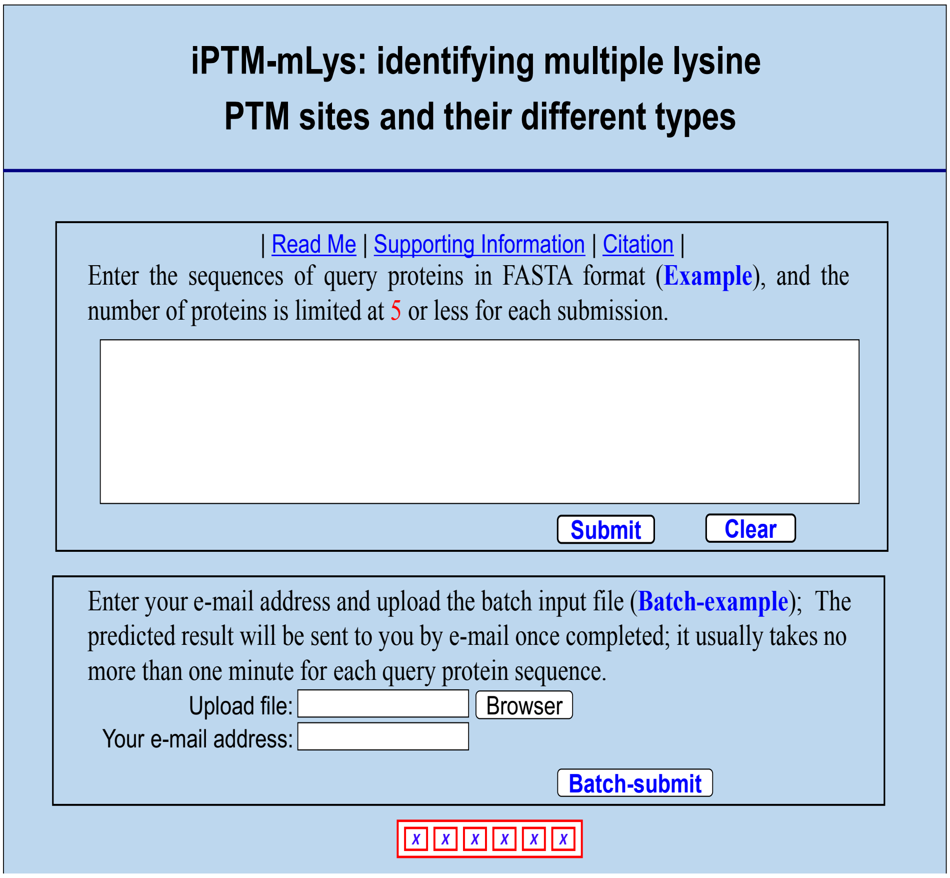
In 2016 a very powerful web-server predictor has been established for predicting multiple lysine PTM sites and their different types [1].

To see how the web-server is working, please do the following.

Step 1: Opening the web-server at http://www.jci-bioinfo.cn/iPTM-mLys, you will see the top page of **iPTM-mLys** on your computer screen, as shown in **figure1**. Click on the Read Me button to see a brief introduction about the predictor.



iPTM-mLys: identifying multiple lysine PTM sites and their different types

| Read Me | Supporting Information | Citation |

Enter the sequences of query proteins in FASTA format (**Example**), and the number of proteins is limited at 5 or less for each submission.

Enter your e-mail address and upload the batch input file (**Batch-example**); The predicted result will be sent to you by e-mail once completed; it usually takes no more than one minute for each query protein sequence.

Upload file:

Your e-mail address:

Figure 1. A semi-screenshot for the top page of the web server iPTM-mLys at http://www.jci-bioinfo.cn/iPTM-mLys. (Adapted from {Qiu, 2016 #3249} with permission).

Step 2: Either type or copy/paste your query protein sequences into the input box at the center of **Fig.1**. The input sequence should be in the FASTA format. For the examples of sequences in FASTA format, click the Example button right above the input box.

Step 3: Click the Submit button to get the predicted result. For example, if you use the Example window as the input, the corresponding predicted results are quite consistent with experimental observations.

Step 4: As shown on the lower panel of **Fig.1**, you may also choose the batch prediction by entering your e-mail address and your desired batch input file (in FASTA format of course) via the Browse button. To see the sample of batch input file, click on the button Batch-example.

Step 5: Click the Supporting Information button to download the benchmark dataset used in this study.

Step 6: Click the Citation button to find the relevant papers that document the detailed development and algorithm of **iPTM-mLys**.

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 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 iRNA-2methyl 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 [33–73][2–6, 8–11, 13, 18, 26, 30, 32, 74–301]

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, 292, 302–311] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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