

Research Article

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Showcase to Illustrate How the Web-Server Idna6ma-Pseknc is Working

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In 2017 a very powerful web-server predictor has been established for identifying N6-methyladenosine (m6A), which is one of the most important modifications in RNA [1]. To see how the web-server is working, please do the following.

Click the link at <http://lin-group.cn/server/iDNA-6mA-PseKNC> and you'll see the web-server's top-page as shown in Figure.1

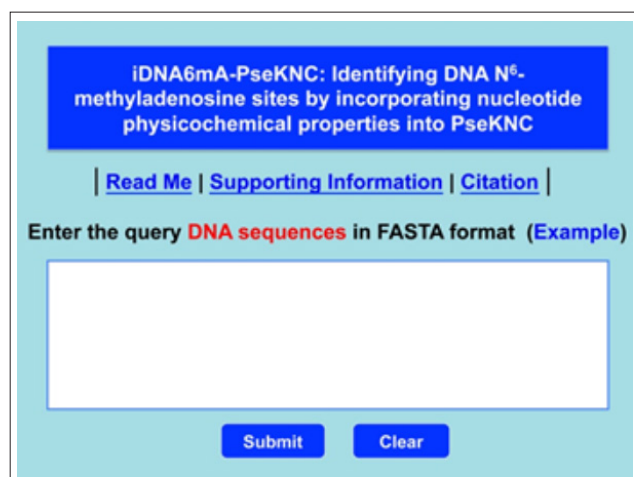


Figure 1: A semi-screenshot for the top-page of the iDNA6mA-PseKNC web-server at <http://lin-group.cn/server/iDNA6mA-PseKNC> (Adapted from [1] with permission).

Either type or copy/paste the sequences of query DNA 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 Ex-ample button right above the input box.

Click on the Submit button to see the predicted result. For instance, if you use the two DNA sequences in the Example window as the input, after a few seconds, you will see the following on the screen of your computer. (i) Seq 1 contains 17 A (adenine) nucleotides, and only the ones in the positions 35, 41, 62, and 71 may be of 6mA

modification. (ii) Seq 2 contains 14 A nucleotides, and only the ones in the positions 38, 62, and 71 may be of 6mA modification.

Click the Supporting Information button to download the Supporting Information's mentioned in this paper. Click on the Citation button to find the papers that have played the key roles in developing the current predictor of iDNA6mA-PseKNC. It is instructive to point out 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.

Moreover, it has not escaped our notice that during the development of iDNA6mA-PseKNC 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 [2-6, 8-11, 13, 18, 26, 30, 32-301].

It is anticipated that iDNA6mA-PseKNC may become a very 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, 292, 302-310]. Where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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