ISSN: 2755-0168

Journal of Biotechnology & Bioinformatics Research

Scientific Research and Community

Research Article

Open Access

How the Artificial Intelligence Tool pSumo-CD is Working for Predicting Sumoylation Sites in Proteins

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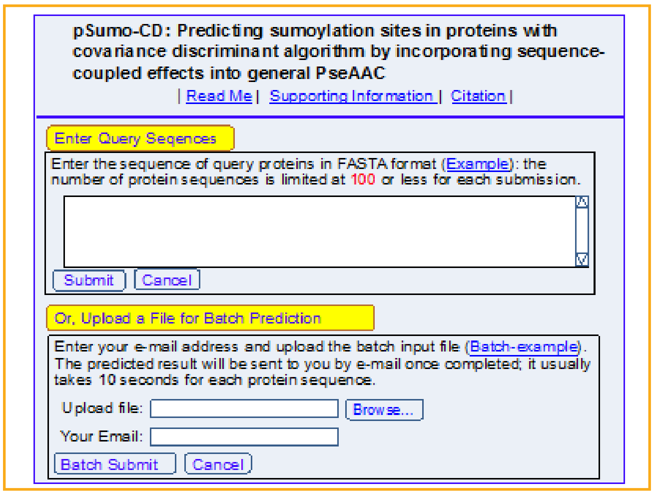
Received: March 16, 2020 ; **Accepted**: March 19, 2020; **Published:** March 22, 2020

Keywords: Artificial intelligence, pSumo-CD, Sumoylation, Proteins

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

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



pSumo-CD: Predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC

Enter the sequence of query proteins in FASTA format (Example): the number of protein sequences is limited at 100 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 10 seconds for each protein sequence.

Figure 1: A semi-screenshot of the top-page for the web-server pSumo-CD at http://www.jci-bioinfo.cn/pSumo-CD. (Adapted from [1] 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 sequences 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 on the Submit button to see the predicted result. For example, if you use the Sequences in the Example window as the input, after a few seconds, you will see the corresponding predicted results, which is fully consistent with experiment observations.

Step 4: Click the Data button to download the benchmark dataset used in this study.

Step 5: Click the Citation button to find the relevant papers that document the detailed development and algorithm for iSuc-PseOpt.

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.

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, 3] and three comprehensive review papers [4-6]): crystal clear in logic development, completely transparent in operation, easily to repeat the reported results by other investigators, with high potential in stimulating other sequence-analyzing methods, and very convenient to be used by the majority of experimental scientists [1-5].

It has not escaped our notice that during the development of iSuc-PseOpt web-server, the approach of general pseudo amino acid components [7] or PseAAC [8] had been utilized and hence its accuracy would be much higher than its counterparts, as concurred by many investigators (see, e.g., [9-10]).

For the marvelous and awesome roles of the "5-steps rule" in driving proteome, genome analyses and drug development, see a series of recent papers [11-32] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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