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How the artificial intelligence tool iPGK-PseAAC is working in predicting lysine phosphoglycerylation sites in proteins

Short Communication

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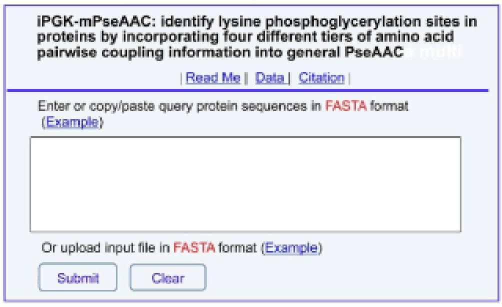
In 2017 a very powerful AI (artificial intelligence) tool has been established for predicting lysine phosphoglycerylation sites in proteins, one of the most important post modifications in proteins [1].

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

Step 1: Opening the web-server at http://app.aporc.org/iPGK-PseAAC/, you will see the top page of iPGK-PseAAC on your computer screen, as shown in Figure 1. Click on the Read Me button to see a brief introduction about this predictor.



iPGK-mPseAAC: identify lysine phosphoglycerylation sites in proteins by incorporating four different tiers of amino acid pairwise coupling information into general PseAAC

Enter or copy/paste query protein sequences in FASTA format (Example)

Or upload input file in FASTA format (Example)

Figure 1: A semi-screenshot for the top-page of the iPGK-PseAAC web-server at http://app.aporc.org/iPGK-PseAAC/. (Adapted from [1] with permission).

Step 2: Either type or copy/paste your query protein sequences into the inputbox at the center of Figure 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 **iPGK-PseAAC**.

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., [2-4] and three comprehensive review papers [5-7]): (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 iDNA6mA-PseKNC web-server, the approach of general pseudo amino acid components [8] or PseAAC [9] had been utilized and hence its accuracy would be much higher than its counterparts, as concurred by many investigators (see, e.g., [10-12]).

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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 [13-34] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

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