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The pLoc_bal-mGneg Predictor is a Powerful Web-Server for Identifying the Subcellular Localization of Gram-Negative Bacterial Proteins based on their Sequences Information Alone

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Running Title: Showcase for pLoc_bal-mGneg
Keywords: pLoc_bal-mGneg, Web-Server

Recently a very powerful web-server has been developed for predicting the subcellular localization of Gram-negative bacterial proteins purely according to their sequences information for the multi-label systems [1], in which a same protein may appear or move between two or more location sites and hence its ID (identification) needs two or more labels for distinction, namely the "multi-label mark" [2].

The web-server is called as "pLoc_bal-mGneg", where "bal" means that the predictor has been treated by balancing or quasi-balancing out the training dataset [3-9], and "m" means that the predictor is with the capacity to study the multi-label systems. How the web-server is working can be clearly seen via the showcase below.

Clicking the link at http://www.jci-bioinfo.cn/pLoc_bal-mGneg/, you will see the top page of the pLoc_bal-mGneg web-server prompted on your computer's screen (**Figure 1)**. Then, just simply following the commands given in the Step 2 and Step 3 of [4], you will see **Figure 2** on the screen of your computer**.** For example, if using the query protein sequences in the Example window as the input, after clicking the Submit button, the corresponding detailed prediction results were given in [4]. As you can see from there: nearly all the success rates achieved by the web-server for the Gram-negative bacterial proteins in each of the 8 subcellular locations are within the range of 98-100%, which is far beyond the reach of any of its counterparts.

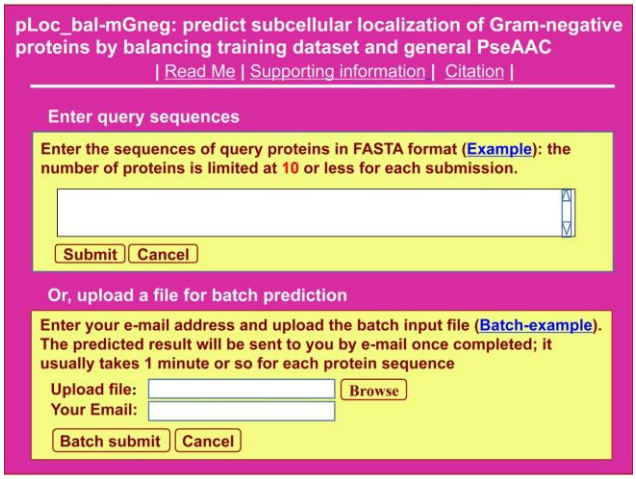

Figure 1. A semi screenshot for the top page of pLoc_bal-mGneg (Adapted from [4] with permission).

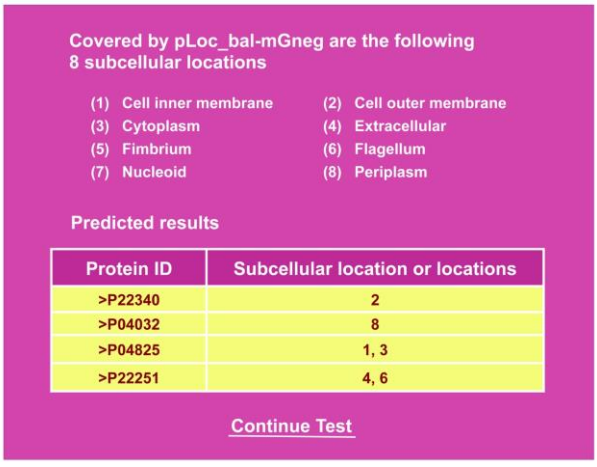

Figure 2. A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [4] with permission).

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In addition to the advantages of high accuracy and easy to use, the web-server has been constructed by strictly observing the "Chou's 5-steps rule" and hence bears the following fantastic merits as agreed and supported by many investigators (see, e.g., [10-91] as well as three comprehensive review papers [2, 92, 93]): (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.

Besides, the approach [94-96] of PseAAC (Pseudo Amino Acid Composition) has also been applied during developing the web-server predictor. It is a very powerful approach for representing the protein samples by catching their special or key features, as done by many scientists as well [97-222].

Furthermore, the IHTS (Inserting Hypothetical Training Samples) treatment has also been applied to balance or quasi-balance out the training dataset [57, 60, 84].

For the amazing and awesome roles of the "5-steps rule" and general "PseAAC" in driving proteome, genome analyses and drug development, see a series of recent papers [2, 93, 223-233] where both the "5-steps rule" and the general "PseAAC" as well as their huge impacts have been very impressively recollected at different angles or from varieties of aspects.

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