

# Showcase to Illustrate How the Webserver pLoc\_Bal-Meuk Is Working

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## ARTICLE INFO

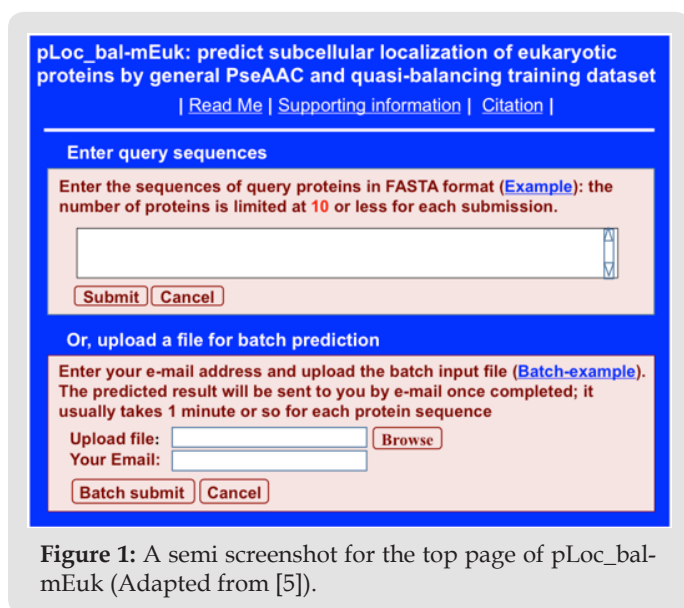
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## ABSTRACT

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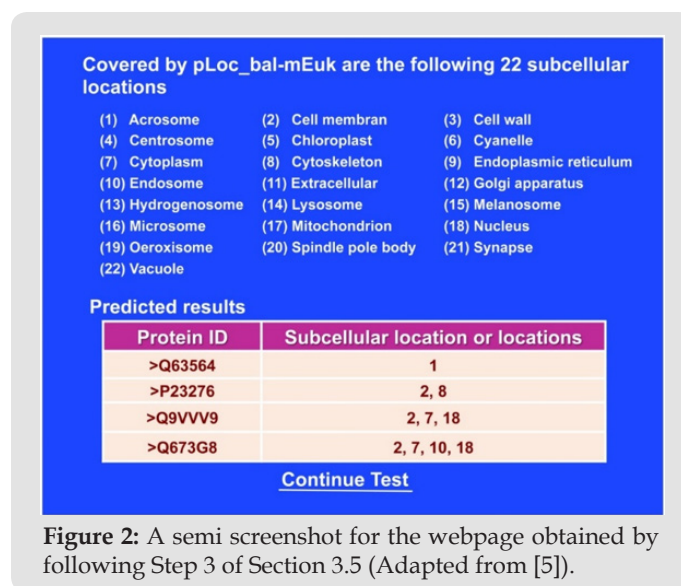
## Short Communication



**Figure 1:** A semi screenshot for the top page of pLoc\_bal-mEuk (Adapted from [5]).

Recently, a very powerful web-server predictor has been established for identifying the subcellular localization of a protein based on its sequence information alone for the multi-label systems [1], in which a same protein may occur or move between two or more location sites and hence needs to be marked with the multi-label approach [2-103]. The web-server predictor is called “pLoc\_bal-mEuk”, where “bal” means the web-server has been further improved by the “balance treatment” [3-9], and “m” means the capacity able to deal with the multi-label systems. To find how the webserver is working, please do the following. Click the link

at [http://www.jci-bioinfo.cn/pLoc\\_bal-mEuk/](http://www.jci-bioinfo.cn/pLoc_bal-mEuk/), the top page of the pLoc\_bal-mEuk webserver will appear on your computer screen, as shown in (Figure 1). Then by following the Step 2 and Step 3 in [5], you will see the predicted results shown on (Figure 2). Nearly all the success rates achieved by the web-server predictor for the eukaryotic proteins in each of the 22 subcellular locations are within the range of 90-100%, which is far beyond the reach of any of its counterparts. Besides, 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., [10-90] and three comprehensive review papers [2,91,92]):



**Figure 2:** A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [5]).

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 most experimental scientists.

For the fantastic and awesome roles of the “5-steps rule” in driving proteome, genome analyses and drug development, see a series of recent papers [2, 92-104] where the rule and its wide applications have been very impressively presented from various aspects or at different angles

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