

Short Communication

Showcase to illustrate how the web-server pLoc_bal-mEuk is working

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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]. 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 web-server is working, please do the following.

Click the link at http://www.jci-bioinfo.cn/pLoc_bal-mEuk/, the top page of the pLoc_bal-mEuk web-server 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]: (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.

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, 92-103] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

pLoc_bal-mEuk: predict subcellular localization of eukaryotic proteins by general PseAAC and quasi-balancing training dataset
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Enter query sequences

Enter the sequences of query proteins in FASTA format ([Example](#)): the number of proteins is limited at 10 or less for each submission.

Or, upload a file for batch prediction

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 1 minute or so for each protein sequence

Upload file:
Your Email:

Figure 1. A semi screenshot for the top page of pLoc_bal-mEuk (Adapted from [5]).

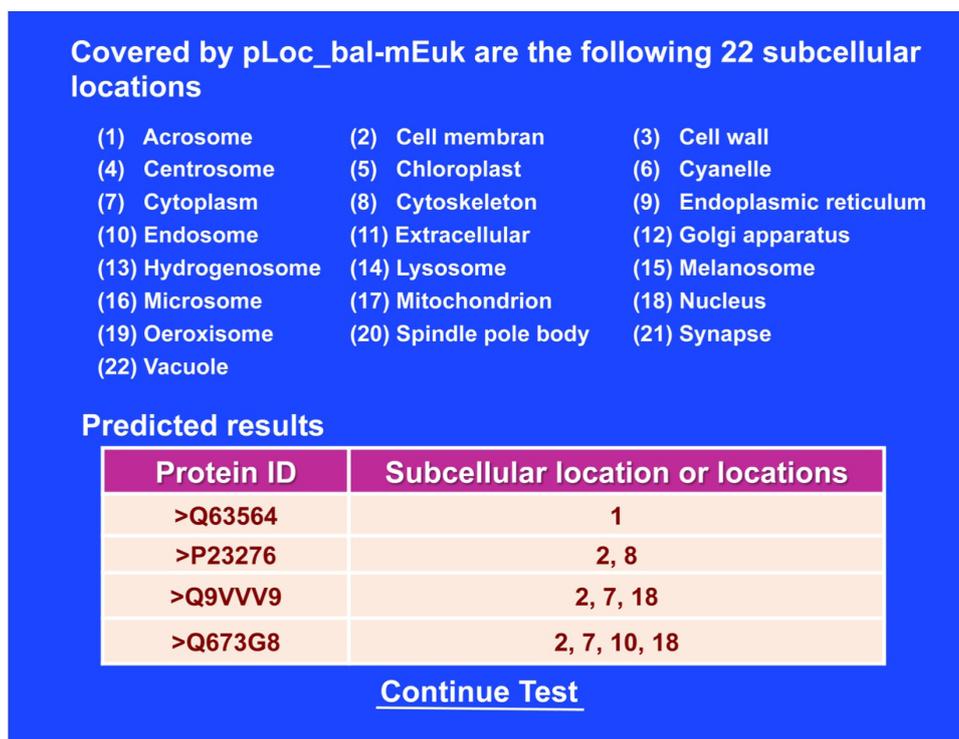


Figure 2. A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [5]).

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