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Letter to Editor

Showcase to Illustrate How the Web-Server pLoc_bal-mEuk is Working

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Dear Editor,

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.

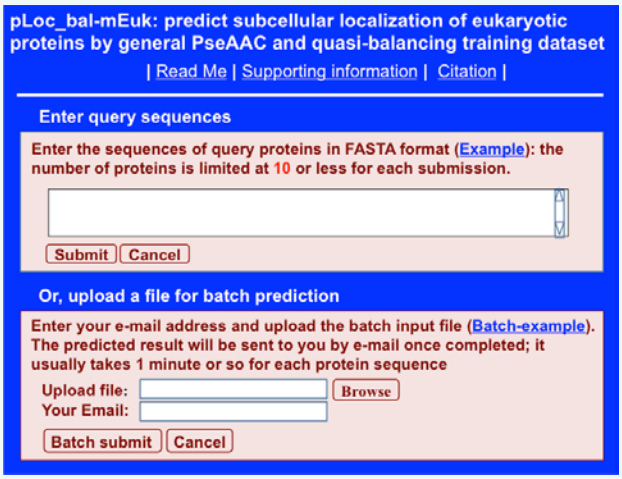

Figure 1 A semi screenshot for the top page of pLoc_bal-mEuk (Adapted from [5]).

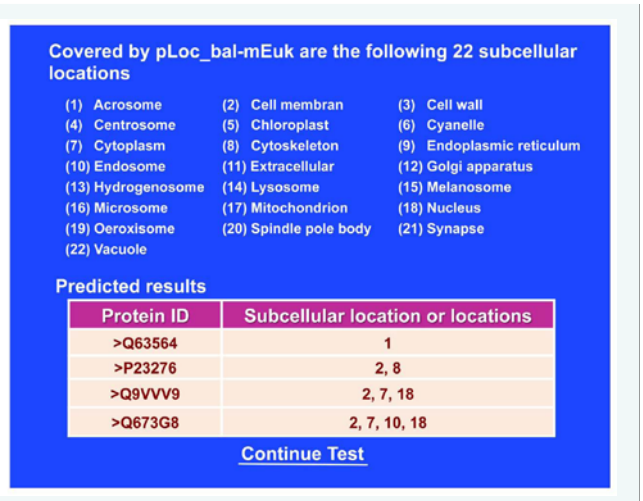

Figure 2 A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [5]).

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., [4-7,10-33] and three comprehensive review papers [2,34,35]): (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.

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