

The Ploc_Bal-Mhum Is a Powerful Web-Serve for Predicting the Subcellular Localization of Human Proteins Purely Based on Their Sequence Information

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Running Title: Showcase for pLoc_bal-mHum

In 2019 a very powerful web-server, or AI (Artificial Intelligence) tool, has been developed for predicting the subcellular localization of human proteins purely according to their information for the multi-label systems [1], in which a same protein may appear or travel between two or more locations and hence its identification needs the multi-label mark [2].

The AI tool is named as “pLoc_bal-mEuk”, where “bal” stands for that the AI tool has been further treated by balancing the training dataset [3-9], and “m” for that the AI tool can be used to cope with multi-label systems. Below, let us show how the AI tool is working.

Clicking the link at http://www.jci-bioinfo.cn/pLoc_bal-mHum/, you will see the top page of the pLoc_bal-mHum web-server appearing on your computer screen (Figure 1). Then by following the Step 2 and Step 3 in [5], you will see Figure 2 on the screen of your computer. The corresponding detailed predicted results were given in ref. 5. As you can see from there: nearly all the success rates achieved by the AI tool for the

human proteins in each of the 14 subcellular locations are within the range of 94-100%. Such a high prediction quality is far beyond the reach of any of its counterparts.

In addition to the advantages of high accuracy and easy to use, the AI tool has been built up by strictly complying with the “Chou’s 5-steps rule” and hence bears the following remarkable and notable merits as concurred 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.

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, 93-104] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

pLoc_bal-mHum: predict subcellular localization of Human proteins by balancing training dataset and general PseAAC
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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-mHum (Adapted from [6] with permission).

**Covered by pLoc_bal-mHum are the following
14 subcellular locations**

(1) Centrosome	(2) Cytoplasm
(3) Cytoskeleton	(4) Endoplasmic reticulum
(5) Endosome	(6) Extracellular
(7) Golgi apparatus	(8) Lysosome
(9) Microsome	(10) Mitochondrion
(11) Nucleus	(12) Peroxisome
(13) Plasma membrane	(14) Synapse

Predicted results

Protein ID	Subcellular location or locations
>O15382	10
>P08962	8, 13
>P12272	2, 6, 11

Continue Test

Figure 2. A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [6] with permission).

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