

# 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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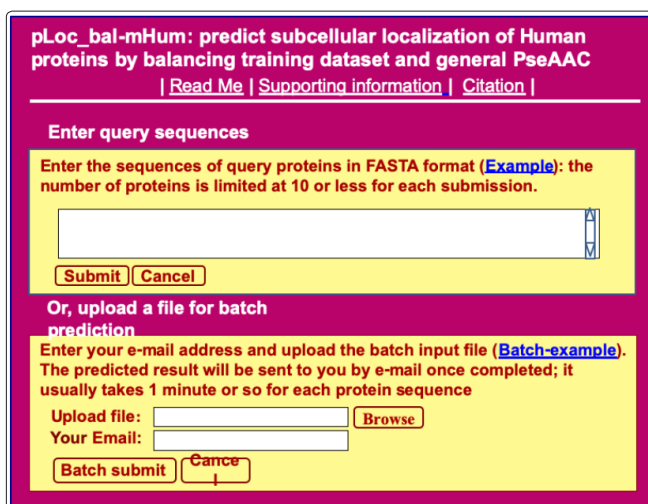
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**Showcase For pLoc\_bal-mHum**

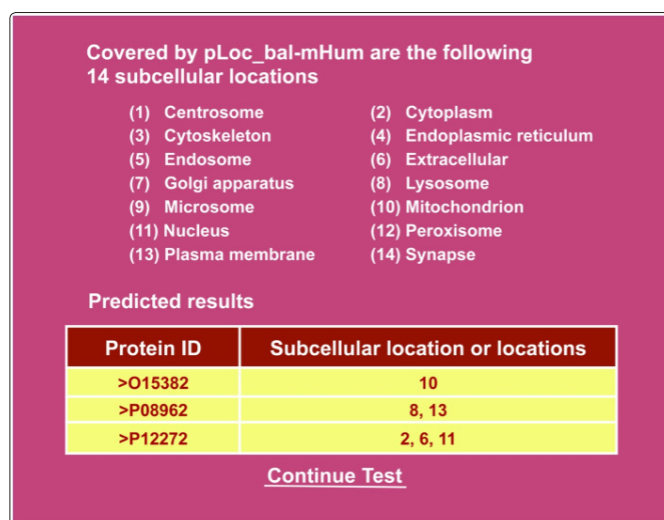
In 2019 a very powerful web-server, or AI (Artificial Intelligence) tool, has been developed for predicting the subcellular localization of human proteins purely according to their information for the multi-label systems, in which a same protein may appear or travel between two or more locations and hence its identification needs the multi-label mark [1, 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 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 [3-9].

Clicking the link at [http://www.jci-bioinfo.cn/pLoc\\_bal-mHum/](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, you will see Figure 2 on the screen of your computer [5]. 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.



**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)

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 three comprehensive review papers [2, 10-93].

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 where the rule and its wide applications have been very impressively presented from various aspects or at different angles [2, 93-101].

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