

# Showcase to Illustrate How the Web-Server pLoc\_Deep-mEuk Is Working

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## Abstract

Recently, a very useful method called “pLoc\_Deep-mEuk” has been proposed for finding against the Pandemic COVID-19. Illustrated in this short report is a step-by-step guide for how to use its web-server.

## Keywords

Coronavirus, Eukaryotic Proteins, Multi-Label System, PseAAC, Five-Steps Rules

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In 2020, a very powerful web-server predictor has been established for identifying the subcellular localization of eukaryotic proteins based on the sequence information alone [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\_Deep-mEuk”, where “Deep” means the web-server has been further improved by the “Deep Learning” technique [3-6], and “m” means the capacity able to deal with the multi-label systems.

Moreover, its power has been further strengthened by using the “Pseudo Amino Acid Component” [7] or “PseAAC” [8] treatment widely used in computational biology (see, e.g., [9-136] and the “5-steps rules” [137] widely and increasingly used in system biology and biomedicine (see, e.g., [4, 138-160])).

To learn how the web-server is working, please do the following.

**Step 1.** Click the link at [http://www.jci-bioinfo.cn/pLoc\\_Deep-mEuk/](http://www.jci-bioinfo.cn/pLoc_Deep-mEuk/), the top page of the pLoc\_Deep-mEuk web-server will appear on your computer screen, as shown in **Figure 1**. Click on the Read Me button to see a brief introduction about the predictor.

**Step 2.** Either type or copy/paste the sequences of query eukaryotic proteins

into the input box at the center of **Figure 1**. The input sequence should be in the FASTA format. For the examples of sequences in FASTA format, click the [Example](#) button right above the input box.

**Step 3.** Click on the [Submit](#) button to see the predicted result. For instance, if you use the four protein sequences in the [Example](#) window as the input, after 10 seconds or so, you will see a new screen (**Figure 2**) occurring. On its upper part are listed the names of the subcellular locations numbered from (1) to (22) covered by the current predictor. On its lower part are the predicted results: the query protein Q63564 of example-1 corresponds to “1,” meaning it belonging to “Acrosome” only; the query protein P23276 of example-2 corresponds to “2, 8” meaning it belonging to “Cell membrane” and “Cytoskeleton”; the query protein Q9VVV9 of example-3 corresponds to “2, 7, 18”, meaning it belonging to “Cell membrane”, “Cytoplasm”, and “Nucleus”; the query protein Q673G8 of example-4 corresponds to “2, 7, 10, 18”, meaning it belonging to “Cell membrane”, “Cytoplasm”, “Endosome”, and “Nucleus”. All these results are perfectly consistent with experimental observations.

**Figure 1.** The top page of the web-server for pLoc\_Deep-mEuk.

Protein ID	Subcellular location or locations
>Q63564	1
>P23276	2, 8
>Q9VVV9	2, 7, 18
>Q673G8	2, 7, 10, 18

**Figure 2.** The new screen shown on your computer obtained by Step 2.

**Step 4.** As shown on the lower panel of **Figure 2**, you may also choose the batch prediction by entering your e-mail address and your desired batch input file (in FASTA format of course) via the Browse button. To see the sample of batch input file, click on the button Batch-example. After clicking the button Batch-submit, you will see “Your batch job is under computation; once the results are available, you will be notified by e-mail.”

**Step 5.** Click on the Citation button to find the papers that have played the key role in developing the current predictor of pLoc\_Deep-mEuk.

**Step 6.** Click the Supporting Information button to download the Supporting Informations mentioned in this paper.

## Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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