ONOMY Science

American journal of Virology & Disease
ISSN 2643-5357

Case report Open Access

Showcase to illustrate how the web-server pLoc_Deep-mAnimal is working

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Citation: Showcase to illustrate how the web-server pLoc_Deep-mAnimal is working. Am J of Viro and Dis. 2020; 2(2): 01-02.

Submitted: 22 May 2020; **Approved:** 27 May 2020; **Published:** 28 May 2020

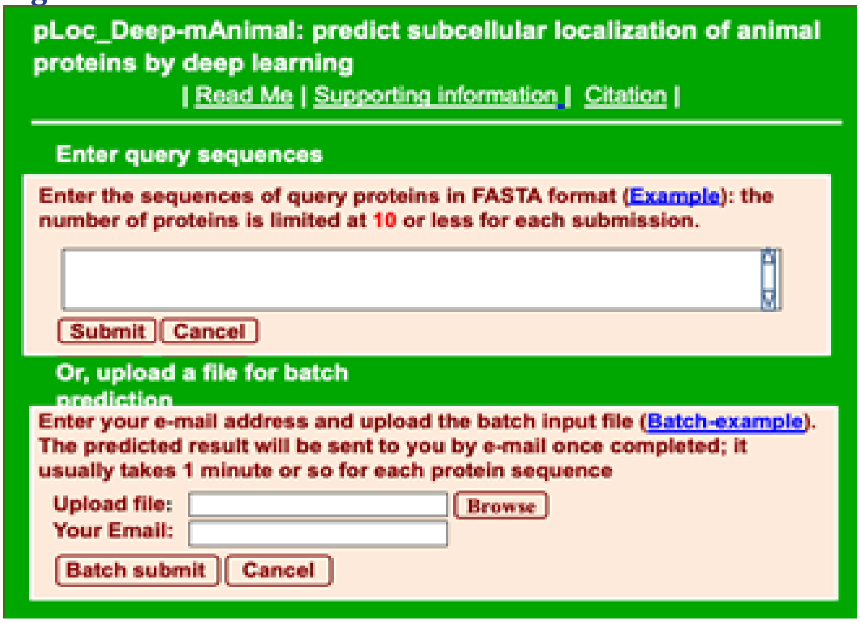
Short Title: Showcase for pLoc_Deep-mAnimal

In 2020, a very powerful web-server predictor has been established for identifying the subcellular localization of animal 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-mAnimal", 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. 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-mAnimal/, the top page of the pLoc_bal-mAnimal web-server will appear on your computer screen, as shown in Fig.1. Click on the Read Me button to see a brief introduction about the predictor.

Figure 1



pLoc_Deep-mAnimal: predict subcellular localization of animal proteins by deep learning

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

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

Step 2. Either type or copy/paste the sequences of query human proteins into the input box at the center of Fig.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 (Fig.2) occurring. On its upper part are listed the names of the subcellular locations

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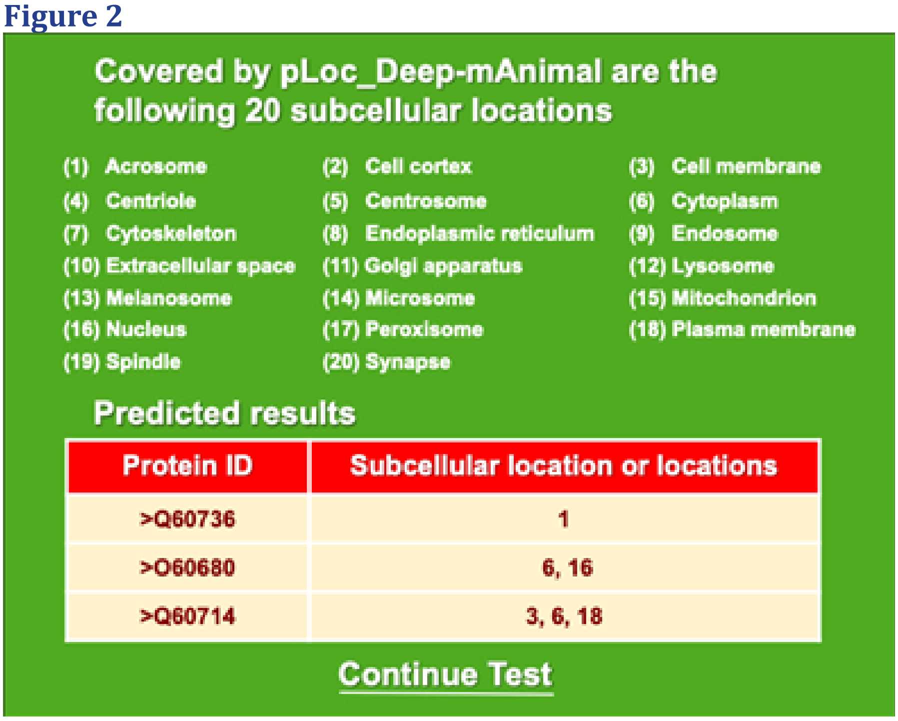
numbered from (1) to (20) covered by the current predictor. On its lower part are the predicted results: the query protein Q60736 of example-1 corresponds to “1,” meaning it belonging to “Acrosome” only; the query protein O60680 of example-2 corresponds to “6, 16” meaning it belonging to “Cytoplasm” and “Nucleus”; the query protein Q60714 of example-3 corresponds to “3, 6, 18”, meaning it belonging to “Cell Membrane”, “Cytoplasm”, and “Plasma membrane”. All these results are perfectly consistent with experimental observations.

Figure 2



Covered by pLoc_Deep-mAnimal are the following 20 subcellular locations

(1) Acrosome
(2) Cell cortex
(3) Cell membrane
(4) Centriole
(5) Centrosome
(6) Cytoplasm
(7) Cytoskeleton
(8) Endoplasmic reticulum
(9) Endosome
(10) Extracellular space
(11) Golgi apparatus
(12) Lysosome
(13) Melanosome
(14) Microsome
(15) Mitochondrion
(16) Nucleus
(17) Peroxisome
(18) Plasma membrane
(19) Spindle
(20) Synapse

Predicted results

Protein ID	Subcellular location or locations
>Q60736	1
>O60680	6, 16
>Q60714	3, 6, 18

Step 4. As shown on the lower panel of Fig.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-mAnimal.

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

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