Journal of Pharmaceutics & Drug Development
Volume 7 | Issue 1
ISSN: 2348-9782

Editorial Article **Open Access**

Showcase to Illustrate How the Web-Server Psuc-Lys is working

Chou K-C[*]

Gordon Life Science Institute, Boston, Massachusetts, USA

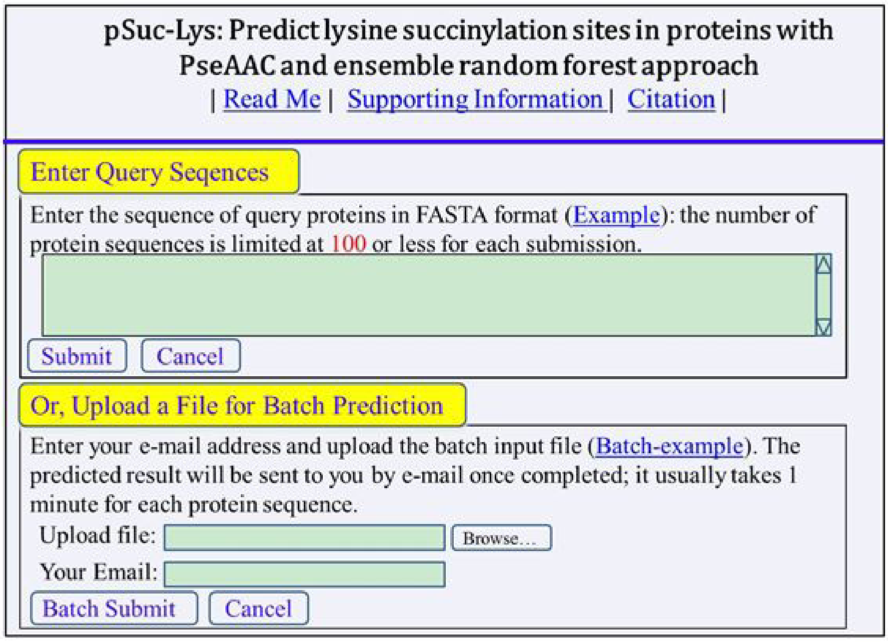
[*]**Corresponding author:** Chou K-C, Gordon Life Science Institute, Boston, Massachusetts 02478, USA, E-mail: kcchou@gordonlifescience.org

Citation: Chou K-C (2020) Showcase to Illustrate How the Web-Server Psuc-Lys is working. J Pharma Drug Develop 7(1): 101

Received Date: February 19, 2020 **Accepted Date:** August 24, 2020 **Published Date:** August 26, 2020

In 2016 a very powerful web-server predictor has been established for predicting lysine succinylation sites in protein [1], which is one of the most important modifications in proteins.

Step 1: Opening the web-server at http://www.jci-bioinfo.cn/pSuc-Lys, you will see the top page of pSuc-Lys on your computer screen, as shown in (Figure 1). Click on the Read Me button to see a brief introduction about the predictor.



pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach

| Read Me | Supporting Information | Citation |

Enter Query Seqences

Enter the sequence of query proteins in FASTA format (Example): the number of protein sequences is limited at 100 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 for each protein sequence.

Upload file:

Your Email:

Figure 1: A semi-screenshot for the top page of the web server pSuc-Lys at http://www.jci-bioinfo.cn/iSuc-Lys. (Adapted from [1] with permission)

Step 2: Either type or copy/paste your query protein sequences 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 the Submit button to get the predicted result. For example, if you use the Example window as the input, the corresponding predicted results are quite consistent with experimental observations.

Step 4: As shown on the lower panel of (Figure 1), 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.

Step 5: Click the Supporting Information button to download the benchmark dataset used in this study.

Step 6: Click the Citation button to find the relevant papers that document the detailed development and algorithm of **iSuc-PseOpt.**

It is anticipated that the Web-Server will be very useful because the vast majority of biological scientists can easily get their desired results without the need to go through the complicated equations in [1] that were presented just for the integrity in developing the predictor.

Also, note that 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., [2,3] and three comprehensive review papers [4-6]): (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.

It has not escaped our notice that during the development of iSuc-PseOpt web-server, the approach of general pseudo amino acid components [7] or PseAAC [8] had been utilized and hence its accuracy would be much higher than its counterparts, as concurred by many investigators (see, e.g., [9,10].

For the wonderful and awesome roles of the "5-steps rule" in driving proteome, genome analyses and drug development, see a series of recent papers [11-32] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

References

1. Jia J, Liu Z, Xiao X, Liu B, Chou KC (2016) pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. J Theor Biol 394: 223-30.

2. Hussain W, Khan YD, Rasool N, Khan SA, Chou KC (2019) SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins. Anal Biochem 568: 14-23.

3. Barukab O, Khan YD, Khan SA, Chou KC (2019) iSulfoTyr-PseAAC: Identify Tyrosine Sulfation Sites by Incorporating Statistical Moments via Chou's 5-steps Rule and Pseudo Components. Curr Genomics 20: 306-20.

4. Chou KC (2011) Some remarks on protein attribute prediction and pseudo amino acid composition. J Theor Biol 273: 236-47.

5. Chou KC (2019) Advances in Predicting Subcellular Localization of Multi-label Proteins and its Implication for Developing Multi-target Drugs. Curr Med Chem 26: 4918-43.

6. Chou KC (2019) Impacts of Pseudo Amino Acid Components and 5-steps Rule to Proteomics and Proteome Analysis. Curr Top in Med Chem 19: 2283-300.

7. Chou KC (2001) Prediction of protein cellular attributes using pseudo-amino acid composition. Proteins Struct Funct and Bioinf 43: 246-55.

8. Chou KC (2005) Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. Bioinf 21: 10-9.

9. Tahir M, Hayat M, Khan SA (2018) iNuc-ext-PseTNC: an efficient ensemble model for identification of nucleosome positioning by extending the concept of Chou's PseAAC to pseudo-tri-nucleotide composition. Mol Genet Genomics 294: 199-210.

10. Khan YD, Amin N, Hussain W, Rasool N, Khan SA, Chou KC, et al. (2020) iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. Anal Biochem 588: 113477.

11. Chou KC (2019) The Cradle of Gordon Life Science Institute and its Development and Driving Force. Biomed J Sci & Tech Res 23: 17848-63.

12. Chou KC (2019) Showcase to Illustrate How the Web-Server Idna6ma-Pseknc is Working. J Pathol Res Rev & Rep 1: 1-15.

13. Chou KC (2019) The pLoc_Bal-Mplant is a Powerful Artificial Intelligence Tool for Predicting the Subcellular Localization of Plant Proteins Purely based on their Sequence Information. Int J Nutr Sci 4: 1-4.

14. Chou KC, Cheng X, Xiao X (2019) pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-balancing Training Dataset. Med Chem 15: 472-85.

15. Chou KC (2019) Showcase to illustrate how the web-server iNitro-Tyr is working. Glo J of Com Sci and Infor Tec 2: 1-16.

16. Chou KC (2019) Gordon Life Science Institute: Its philosophy, achievements, and perspective. Ann of Cancer ther and Pharmacol 2: 1-26.

17. Chou KC (2020) Showcase to Illustrate How the Webserver ploc_BalMeuk Is Working. Biomed J Sci & Tech Res 24: 18156- 60.

18. Chou KC (2020) The pLoc_bal-mGneg Predictor is a Powerful Web-Server for Identifying the Subcellular Localization of Gram-Negative Bacterial Proteins based on their Sequences Information Alone. ijSci 9: 27-34.

19. Chou KC (2020) How the artificial intelligence tool iRNA-2methyl is working for RNA 2'-Omethylation Sites. J Med Care Res Rev 3: 347-65.

20. Chou KC (2020) Showcase to illustrate how the web-server iKcr-PseEns is working. J Med Care Res Rev 3: 331-46.

21. Chou KC (2020) The pLoc_bal-mVirus is a powerful artificial intelligence tool for predicting the subcellular localization of virus proteins according to their sequence information alone. J Gent Genome 4.

22. Chou KC (2019) How the artificial intelligence tool iSNO-PseAAC is working in predicting the cysteine S-nitrosylation sites in proteins. J Stem Cell Res Med 4: 1-9.

23. Chou KC (2020) Showcase to illustrate how the web-server iRNA-Methyl is working, J Mol Genet 3: 1-7.

24. Chou KC (2020) How the Artificial Intelligence Tool iRNA-PseU is Working in Predicting the RNA Pseudouridine Sites. Biomed J Sci Tech Res 24.

25. Chou KC (2020) Showcase to illustrate how the web-server iSNO-AAPair is working. J Gent Genome 4.

26. Chou KC (2020) The pLoc_bal-mHum is a Powerful Web-Serve for Predicting the Subcellular Localization of Human Proteins Purely Based on Their Sequence Information. Adv Bioeng Biomed Sci Res 3: 1-5.

27. Chou KC (2020) Showcase to Illustrate How the Web-server iPTM-mLys is working. Infotext J Infect Dis Ther 1: 1-16.

28. Chou KC (2020) The pLoc_bal-mGpos is a powerful artificial intelligence tool for predicting the subcellular localization of Gram-positive bacterial proteins according to their sequence information alone. Glo J Com Sci Infor Tec 2:1-13.

29. Chou KC (2020) Showcase to illustrate how the web-server iPreny-PseAAC is working. Glo J Com Sci Infor Tec 2: 1-15.

30. Chou KC (2020) Some illuminating remarks on molecular genetics and genomics as well as drug development. Mol Genet Genomics 295: 261-274.

31. Chou KC (2020) The Problem of Elsevier Series Journals Online Submission by Using Artificial Intelligence Nat Sci 12: 37-38.

32. Chou KC (2020) The Most Important Ethical Concerns in Science. Nat Sci 12: 35-36.