

Special Article - Carbohydrates

The pLoc_Bal-Mplant is a Powerful Artificial Intelligence Tool for Predicting the Subcellular Localization of Plant Proteins Purely based on their Sequence Information

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Short Communication

Recently a very useful web-server, or AI (Artificial Intelligence) tool, has been developed for predicting the subcellular localization of plant 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 ID (identification) needs two or more labels as well, namely the “multi-label mark” [2].

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

Clicking the link at http://www.jci-bioinfo.cn/pLoc_bal-mPlant/, you will see the top page of the pLoc_bal-mPlant web-server prompted on your computer screen (Figure 1). Then, just doing what the Step 2 and Step 3 say in [8], you will see Figure 2 on the screen of your computer. You can see from there: nearly all the success rates achieved by the AI tool for the plant proteins in each of the 12 subcellular locations are within the range of 97-100%. 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 constructed by strictly complying with the “Chou’s 5-steps rule” and hence possesses the following terrific merits as concurred by many investigators ([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 wonderful and awesome roles of the “5-steps rule” in driving proteome, genome analyses and drug development, see a series of recent papers [2,93-102] where the rule and its wide applications have been very impressively presented from various

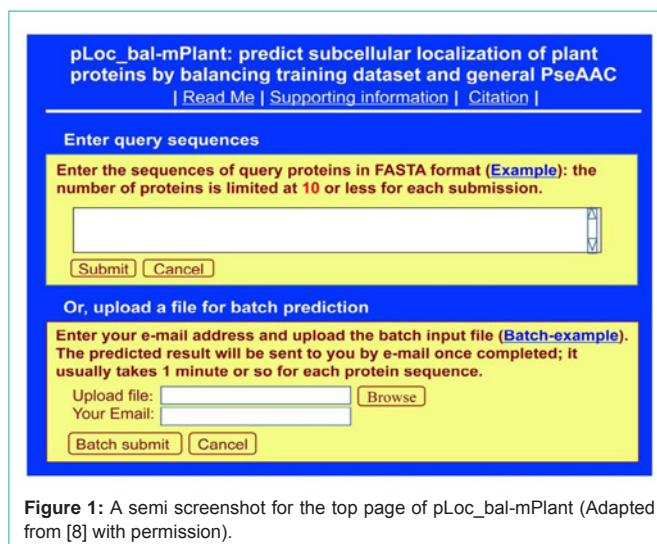


Figure 1: A semi screenshot for the top page of pLoc_bal-mPlant (Adapted from [8] with permission).

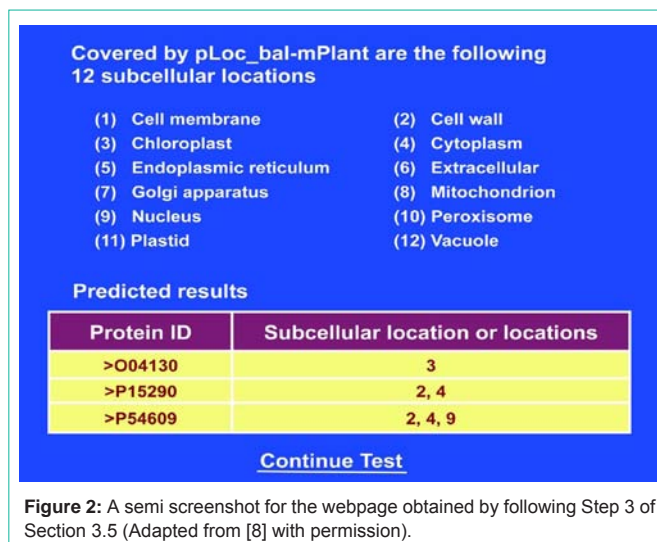


Figure 2: A semi screenshot for the webpage obtained by following Step 3 of Section 3.5 (Adapted from [8] with permission).

aspects or at different angles.

References

1. Chou KC, Shen HB. Recent progresses in protein subcellular location prediction. *Analytical Biochemistry*. 2007; 370: 1-16.
2. Chou KC. Advance in predicting subcellular localization of multi-label proteins and its implication for developing multi-target drugs. *Current Medicinal Chemistry*. 2019; 26: 4918-4943.
3. Xiao X, Cheng X, Chen G, Mao Q, Chou KC. pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. *Med Chem*.

- 2019; 15: 496-509.
4. Xiao X, Cheng X, Chen G, Mao Q, Chou KC. pLoc_bal-mGpos: predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. *Genomics*. 2019; 111: 886-892.
 5. Chou KC, Cheng X, Xiao X. pLoc_bal-mEuk: predict subcellular localization of eukaryotic proteins by general PseAAC and quasi-balancing training dataset. *Med Chem*. 2019; 15: 472-485.
 6. Chou KC, Cheng X, Xiao X. pLoc_bal-mHum: predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. *Genomics*. 2019; 111: 1274-1282.
 7. Cheng X, Lin WZ, Xiao X, Chou KC. pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. *Bioinformatics*. 2019; 35: 398-406.
 8. Cheng X, Xiao X, Chou KC. pLoc_bal-mPlant: predict subcellular localization of plant proteins by general PseAAC and balancing training dataset *Curr Pharm Des*. 2018; 24: 4013-4022.
 9. Cheng X, Xiao X, Chou KC. pLoc_bal-mGneg: predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. *Journal of Theoretical Biology*. 2018; 458: 92-102.
 10. Butt AH, Khan YD. Prediction of S-Sulfenylation Sites Using Statistical Moments Based Features via Chou's 5-Step Rule. *International Journal of Peptide Research and Therapeutics (IJPR)*. 2018.
 11. Awais M, Hussain W, Khan YD, Rasool N, Khan SA, Chou KC. iPhosH-PseAAC: Identify phosphohistidine sites in proteins by blending statistical moments and position relative features according to the Chou's 5-step rule and general pseudo amino acid composition. *IEEE/ACM Trans Comput Biol Bioinform*. 2019.
 12. Barukab O, Khan YD, Khan SA, Chou KC. iSulfoTyr-PseAAC: Identify tyrosine sulfation sites by incorporating statistical moments via Chou's 5-steps rule and pseudo components. *Current Genomics*. 2019.
 13. Butt AH, Khan YD. Prediction of S-Sulfenylation Sites Using Statistical Moments Based Features via Chou's 5-Step Rule. *International Journal of Peptide Research and Therapeutics (IJPR)*. 2019.
 14. Chen Y, Fan X. Use of Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangshen Pingfei San on Idiopathic Pulmonary Fibrosis. *Current Molecular Medicine*. 2019.
 15. Du X, Diao Y, Liu H, Li S. MsDBP: Exploring DNA-binding Proteins by Integrating Multi-scale Sequence Information via Chou's 5-steps Rule. *Journal of Proteome Research*. 2019; 18: 3119-3132.
 16. Ehsan MK, Mahmood YD, Khan OM, Barukab SA, Khan KC, Chou. iHyd-PseAAC (EPSV): Identify hydroxylation sites in proteins by extracting enhanced position and sequence variant feature via Chou's 5-step rule and general pseudo amino acid composition. *Current Genomics*. 2019; 20: 124-133.
 17. Hussain W, Khan SD, Rasool N, Khan SA, Chou KC. 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*. 2019; 568: 14-23.
 18. Hussain W, Khan YD, Rasool N, Khan SA, Chou KC. SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins. *J Theor Biol*. 2019; 468: 1-11.
 19. Ju Z, Wang SY. Prediction of lysine formylation sites using the composition of k-spaced amino acid pairs via Chou's 5-steps rule and general pseudo components. *Genomics*. 2019.
 20. Kabir M, Ahmad S, Iqbal M, Hayat M. iNR-2L: A two-level sequence-based predictor developed via Chou's 5-steps rule and general PseAAC for identifying nuclear receptors and their families. *Genomics*. 2019.
 21. Khan ZU, Ali F, Khan IA, Hussain Y, Pi D. iRSpot-SPI: Deep learning-based recombination spots prediction by incorporating secondary sequence information coupled with physio-chemical properties via Chou's 5-step rule and pseudo components. *Chemometrics and Intelligent Laboratory Systems (CHEMOLAB)*. 2019; 189: 169-180.
 22. Lan J, Liu J, Liao C, Merkler DJ, Han Q, Li J. A Study for Therapeutic Treatment against Parkinson's Disease via Chou's 5-steps Rule. *Current Topics in Medicinal Chemistry*. 2019.
 23. Le NQK. iN6-methylat (5-step): identifying DNA N⁶-methyladenine sites in rice genome using continuous bag of nucleobases via Chou's 5-step rule. *Mol Genet Genomics*. 2019; 294: 1173-1182.
 24. Le NQK, Yapp EKY, Ho QT, Nagasundaram N, Ou YY, Yeh HY. iEnhancer-5Step: Identifying enhancers using hidden information of DNA sequences via Chou's 5-step rule and word embedding. *Anal Biochem*. 2019; 571: 53-61.
 25. Le NQK, Yapp EKY, Ou YY, Yeh HY. iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. *Anal Biochem*. 2019; 575: 17-26.
 26. Liang R, Xie J, Zhang C, Zhang M, Huang H, Huo H, et al. Identifying Cancer Targets Based on Machine Learning Methods via Chou's 5-steps Rule and General Pseudo Components. *Current Topics in Medicinal Chemistry*. 2019.
 27. Liang Y, Zhang S. Identifying DNase I hypersensitive sites using multi-features fusion and F-score features selection via Chou's 5-steps rule. *Biophys Chem*. 2019; 253: 106227.
 28. Malebary SJ, Rehman MSU, Khan YD. iCrotoK-PseAAC: Identify lysine crotonylation sites by blending position relative statistical features according to the Chou's 5-step rule. *PLoS One*. 2019; 14: e0223993.
 29. Nazari M, Tahir H, Tayari KT, Chong. iN6-Methyl (5-step): Identifying RNA N⁶-methyladenosine sites using deep learning mode via Chou's 5-step rules and Chou's general PseKNC. *Chemometrics and Intelligent Laboratory Systems (CHEMOLAB)*. 2019.
 30. Ning Q, Ma Z, Zhao X. dForml(KNN)-PseAAC: Detecting formylation sites from protein sequences using K-nearest neighbor algorithm via Chou's 5-step rule and pseudo components. *J Theor Biol*. 2019; 470: 43-49.
 31. Salman M, Khan N, Iqbal T, Hussain S, Afzal KC, Chou. A two-level computation model based on deep learning algorithm for identification of piRNA and their functions via Chou's 5-steps rule. *International Journal of Peptide Research and Therapeutics (IJPR)*. 2019.
 32. Tahir M, Tayara H, Chong KT. iDNA6mA (5-step rule): Identification of DNA N⁶-methyladenine sites in the rice genome by intelligent computational model via Chou's 5-step rule. *CHEMOLAB*. 2019; 189: 96-101.
 33. Vishnoi S, Garg P, Arora P. Physicochemical n-Grams Tool: A tool for protein physicochemical descriptor generation via Chou's 5-steps rule. *Chem Biol Drug Des*. 2019.
 34. Wiktorowicz A, Wit A, Dziewierz A, Rzeszutko L, Dudek D, Kleczynski P. Calcium Pattern Assessment in Patients with Severe Aortic Stenosis Via the Chou's 5-Steps Rule. *Current Pharmaceutical Design*. 2019.
 35. Yang L, Lv Y, Wang S, Zhang Q, Pan Y, Su D, et al. Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule. *Genomics*. 2019.
 36. Khan YD, Amin N, Hussain W, Rasool N, Khan SA, Chou KC. iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. *Anal Biochem*. 2020; 588: 113477.
 37. Xu Y, Ding J, Wu LY, Chou KC. iSNO-PseAAC: Predict cysteine S-nitrosylation sites in proteins by incorporating position specific amino acid propensity into pseudo amino acid composition. *PLoS ONE*. 2013; 8: e55844.
 38. Xu Y, Shao XJ, Wu LY, Deng NY, Chou KC. iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine S-nitrosylation sites in proteins. *PeerJ*. 2013; 1: e171.
 39. Xu Y, Wen X, Shao XJ, Deng NY, Chou KC. iHyd-PseAAC: Predicting hydroxyproline and hydroxylysine in proteins by incorporating dipeptide position-specific propensity into pseudo amino acid composition.

- International Journal of Molecular Sciences (IJMS). 2014; 15: 7594-7610.
40. Xu Y, Wen X, Wen LS, Wu LY, Deng NY, Chou KC. iNitro-Tyr: Prediction of nitrotyrosine sites in proteins with general pseudo amino acid composition. *PLoS ONE*. 2014; 9: e105018.
 41. Xu Y, Chou KC. Recent progress in predicting posttranslational modification sites in proteins. *Curr Top Med Chem*. 2016; 16: 591-603.
 42. Liu LM, Xu Y, Chou KC. iPGK-PseAAC: identify lysine phosphoglycerylation sites in proteins by incorporating four different tiers of amino acid pairwise coupling information into the general PseAAC. *Med Chem*. 2017; 13: 552-559.
 43. Xu Y, Li C, Chou KC. iPreNy-PseAAC: identify C-terminal cysteine prenylation sites in proteins by incorporating two tiers of sequence couplings into PseAAC. *Med Chem*. 2017; 13: 544-551.
 44. Cai L, Wan CL, He L, Jong S, Chou KC. Gestational influenza increases the risk of psychosis in adults. *Medicinal Chemistry*. 2015; 11: 676-682.
 45. Liu J, Song J, Wang MY, He L, Cai L, Chou KC. Association of EGF rs4444903 and XPD rs13181 polymorphisms with cutaneous melanoma in Caucasians. *Medicinal Chemistry*. 2015; 11: 551-559.
 46. Cai L, Yang YH, He L, Chou KC. Modulation of cytokine network in the comorbidity of schizophrenia and tuberculosis. *Curr Top Med Chem*. 2016; 16: 655-665.
 47. Cai L, Yuan W, Zhang Z, He L, Chou KC. In-depth comparison of somatic point mutation callers based on different tumor next-generation sequencing depth data. *Scientific Reports*. 2016; 6: 36540.
 48. Zhu Y, Cong QW, Liu Y, Wan CL, Yu T, He G, et al. Antithrombin is an importantly inhibitory role against blood clots. *Curr Top Med Chem*. 2016; 16: 666-674.
 49. Zhang ZD, Liang K, Li K, Wang GQ, Zhang KW, Cai L, et al. *Chlorella vulgaris* induces apoptosis of human non-small cell lung carcinoma (NSCLC) cells. *Med Chem*. 2017; 13: 560-568.
 50. Cai L, Huang T, Su J, Zhang X, Chen W, Zhang F, et al. Implications of newly identified brain eQTL genes and their interactors in Schizophrenia. *Molecular Therapy - Nucleic Acids*. 2018; 12: 433-442.
 51. Niu B, Zhang M, Du P, Jiang L, Qin R, Su Q, et al. Small molecular florbundiquinone B derived from medicinal plants inhibits acetylcholinesterase activity. *Oncotarget*. 2017; 8: 57149-57162.
 52. Su Q, Lu W, Du D, Chen F, Niu B, Chou KC. Prediction of the aquatic toxicity of aromatic compounds to *tetrahymena pyriformis* through support vector regression. *Oncotarget*. 2017; 8: 49359-49369.
 53. Lu Y, Wang S, Wang J, Zhou G, Zhang Q, Zhou X, et al. An Epidemic Avian Influenza Prediction Model Based on Google Trends. *Letters in Organic Chemistry*. 2019; 16: 303-310.
 54. Niu B, Liang C, Lu Y, Zhao M, Chen Q, Zhang Y, et al. Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. *Genomics*. 2019.
 55. Jia J, Liu Z, Xiao X, Liu B, Chou KC. Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition (iPPBS-PseAAC). *J Biomol Struct Dyn (JBSD)*. 2016; 34: 1946-1961.
 56. Jia J, Liu Z, Xiao X, Liu B, Chou KC. iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. *Anal Biochem*. 2016; 497: 48-56.
 57. Jia J, Liu Z, Xiao X, Liu B, Chou KC. pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. *Journal of Theoretical Biology*. 2016; 394: 223-230.
 58. Jia J, Liu Z, Xiao X, Liu B, Chou KC. iCar-PseCp: identify carbonylation sites in proteins by Monto Carlo sampling and incorporating sequence coupled effects into general PseAAC. *Oncotarget*. 2016; 7: 34558-34570.
 59. Jia J, Liu Z, Xiao X, Liu B, Chou KC. iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. *Molecules*. 2016; 21: E95.
 60. Jia J, Zhang L, Liu Z, Xiao X, Chou KC. pSumo-CD: Predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. *Bioinformatics*. 2016; 32: 3133-3141.
 61. Liu Z, Xiao X, Yu DJ, Jia J, Qiu WR, Chou KC. pRNAm-PC: Predicting N-methyladenosine sites in RNA sequences via physical-chemical properties. *Anal Biochem*. 2016; 497: 60-67.
 62. Xiao X, Ye HX, Liu Z, Jia JH, Chou KC. iROS-gPseKNC: predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. *Oncotarget*. 2016; 7: 34180-34189.
 63. Qiu WR, Sun BQ, Xiao X, Xu ZC, Jia JH, Chou KC. iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. *Genomics*. 2018; 110: 239-246.
 64. Jia J, Li X, Qiu W, Xiao X, Chou KC. iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. *Journal of Theoretical Biology*. 2019; 460: 195-203.
 65. Chen W, Ding H, Feng P, Lin H, Chou KC. iACP: a sequence-based tool for identifying anticancer peptides. *Oncotarget*. 2016; 7: 16895-16909.
 66. Chen W, Feng P, Ding H, Lin H, Chou KC. Using deformation energy to analyze nucleosome positioning in genomes. *Genomics*. 2016; 107: 69-75.
 67. Chen W, Tang H, Ye J, Lin H, Chou KC. iRNA-PseU: Identifying RNA pseudouridine sites. *Molecular Therapy - Nucleic Acids*. 2016; 5: e332.
 68. Zhang CJ, Tang H, Li WC, Lin H, Chen W, Chou KC. iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. *Oncotarget*. 2016; 7: 69783-69793.
 69. Chen W, Feng P, Yang H, Ding H, Lin H, Chou KC. iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. *Oncotarget*. 2017; 8: 4208-4217.
 70. Feng P, Ding H, Yang H, Chen W, Lin H, Chou KC. iRNA-PseColl: Identifying the occurrence sites of different RNA modifications by incorporating collective effects of nucleotides into PseKNC. *Molecular Therapy - Nucleic Acids*. 2017; 7: 155-163.
 71. Chen W, Ding H, Zhou X, Lin H, Chou KC. iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. *Analytical Biochemistry*. 2018; 561-562: 59-65.
 72. Chen W, Feng P, Yang H, Ding H, Lin H, Chou KC. iRNA-3typeA: identifying 3-types of modification at RNA's adenosine sites. *Molecular Therapy: Nucleic Acid*. 2018; 11: 468-474.
 73. Su ZD, Huang Y, Zhang ZY, Zhao YW, Wang D, Chen W, et al. iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. *Bioinformatics*. 2018; 34: 4196-4204.
 74. Yang H, Qiu WR, Liu G, Guo FB, Chen W, Chou KC, et al. iRSpot-Pse6NC: Identifying recombination spots in *Saccharomyces cerevisiae* by incorporating hexamer composition into general PseKNC. *International Journal of Biological Sciences*. 2018; 14: 883-891.
 75. Feng P, Yang H, Ding H, Lin H, Chen W, Chou KC. iDNA6mA-PseKNC: Identifying DNA N(6)-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics*. 2019; 111: 96-102.
 76. Du QS, Wang SQ, Xie NZ, Wang QY, Huang RB, Chou KC. 2L-PCA: A two-level principal component analyzer for quantitative drug design and its applications. *Oncotarget*. 2017; 8: 70564-70578.
 77. Liu B, Fang L, Long R, Lan X, Chou KC. iEnhancer-2L: a two-layer predictor for identifying enhancers and their strength by pseudo k-tuple nucleotide composition. *Bioinformatics*. 2016; 32: 362-369.
 78. Liu B, Long R, Chou KC. iDHS-EL: Identifying DNase I hypersensitive sites by fusing three different modes of pseudo nucleotide composition into an ensemble learning framework. *Bioinformatics*. 2016; 32: 2411-2418.

79. Liu B, Wang S, Long R, Chou KC. iRSpot-EL: identify recombination spots with an ensemble learning approach. *Bioinformatics*. 2017; 33: 35-41.
80. Liu B, Yang F, Chou KC. 2L-piRNA: A two-layer ensemble classifier for identifying piwi-interacting RNAs and their function. *Molecular Therapy - Nucleic Acids*. 2017; 7: 267-277.
81. Liu B, Li K, Huang DS, Chou KC. iEnhancer-EL: Identifying enhancers and their strength with ensemble learning approach. *Bioinformatics*. 2018; 34: 3835-3842.
82. Liu B, Weng F, Huang DS, Chou KC. iRO-3wPseKNC: Identify DNA replication origins by three-window-based PseKNC. *Bioinformatics*. 2018; 34: 3086-3093.
83. Liu B, Yang F, Huang DS, Chou KC. iPromoter-2L: a two-layer predictor for identifying promoters and their types by multi-window-based PseKNC. *Bioinformatics*. 2018; 34: 33-40.
84. Qiu WR, Sun BQ, Xiao X, Xu ZC, Chou KC. iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. *Oncotarget*. 2016; 7: 44310-44321.
85. Qiu WR, Sun BQ, Xiao X, Xu ZC, Chou KC. iPTM-mLys: identifying multiple lysine PTM sites and their different types. *Bioinformatics*. 2016; 32: 3116-3123.
86. Qiu WR, Xiao X, Xu ZC, Chou KC. iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. *Oncotarget*. 2016; 7: 51270-51283.
87. Qiu WR, Jiang SY, Sun BQ, Xiao X, Cheng X, Chou KC. iRNA-2methyl: identify RNA 2'-O-methylation sites by incorporating sequence-coupled effects into general PseKNC and ensemble classifier. *Medicinal Chemistry*. 2017; 13: 734-743.
88. Qiu WR, Jiang SY, Xu ZC, Xiao X, Chou KC. iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. *Oncotarget*. 2017; 8: 41178-41188.
89. Qiu WR, Sun BQ, Xiao X, Xu D, Chou KC. iPhos-PseEvo: Identifying human phosphorylated proteins by incorporating evolutionary information into general PseAAC via grey system theory. *Molecular Informatics*. 2017; 36.
90. Zhai X, Chen M, Lu W. Accelerated search for perovskite materials with higher Curie temperature based on the machine learning methods. *Computational Materials Science*. 2018; 151: 41-48.
91. Chou KC. Some remarks on protein attribute prediction and pseudo amino acid composition. (50th Anniversary Year Review, 5-steps rule). *Journal of Theoretical Biology*. 2011; 273: 236-247.
92. Chou KC. Impacts of pseudo amino acid components and 5-steps rule to proteomics and proteome analysis. *Current Topics in Medicinal Chemistry (CTMC)*. 2019; 19: 2283-2300.
93. Chou KC. Two kinds of metrics for computational biology. *Genomics*. 2019.
94. Chou KC. Proposing pseudo amino acid components is an important milestone for proteome and genome analyses. *International Journal for Peptide Research and Therapeutics (IJPRT)*. 2019.
95. Chou KC. An insightful recollection for predicting protein subcellular locations in multi-label systems. *Genomics*. 2019.
96. Chou KC. Progresses in predicting post-translational modification. *International Journal of Peptide Research and Therapeutics (IJPRT)*. 2019.
97. Chou KC. Recent Progresses in Predicting Protein Subcellular Localization with Artificial Intelligence (AI) Tools Developed Via the 5-Steps Rule. *Japanese Journal of Gastroenterology and Hepatology*. 2019.
98. Chou KC. An insightful recollection since the distorted key theory was born about 23 years ago. *Genomics*. 2019.
99. Chou KC. Artificial intelligence (AI) tools constructed via the 5-steps rule for predicting post-translational modifications. *Trends in Artificial Intelligence (TIA)*. 2019; 3: 60-74.
100. Chou KC. Distorted Key Theory and Its Implication for Drug Development. *Current Genomics*. 2020.
101. Chou KC. An insightful recollection since the birth of Gordon Life Science Institute about 17 years ago. *Advancement in Scientific and Engineering Research*. 2019; 4: 31-36.
102. Chou KC. Gordon Life Science Institute: Its philosophy, achievements, and perspective. *Annals of Cancer Therapy and Pharmacology*. 2019; 2: 001-26.