

# Analyze the Role of “Pseudo Amino Acid Composition” in Stimulating the Drug Development (Short Communication)

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## Short Communication

About 20 years ago a very important paper on “Some remarks on protein attribute prediction and pseudo amino acid composition” was published [1]. Ever since then, a series of papers for using the “Pseudo Amino Acid Composition” [1] or PseAAC [2] have been stimulated to formulate protein sequences for developing drugs against various diseases [3-167]. It has also stimulated the eight masterpieces papers [168-175] by the then Chairman of Nobel Prize Committee.

## Reference

1. Chou KC (2001) Prediction of protein cellular attributes using pseudo amino acid composition. *PROTEINS: Structure Function and Genetics* 44(60): 246-255.
2. Chou KC (2005) Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. *Bioinformatics* 21: 10-19.
3. Cai YD, Chou KC (2003) Nearest neighbour algorithm for predicting protein subcellular location by combining functional domain composition and pseudo amino acid composition. *Biochem Biophys Res Comm* 305(2): 407-411.
4. Chou KC, Cai YD (2003) Predicting protein quaternary structure by pseudo amino acid composition. *Proteins: Struct Funct Genet* 53(2): 282-289.
5. Chou KC, Cai YD (2003) Prediction and classification of protein subcellular location: sequence-order effect and pseudo amino acid composition. *Journal of Cellular Biochemistry* 90(6): 1250-1260.
6. Chou KC, Cai YD (2004) Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo amino acid composition. *J Cell Biochem* 91(6): 1197-1203.
7. Wang M, Yang J, Liu GP, Xu ZJ, Chou KC (2004) Weighted-support vector machines for predicting membrane protein types based on pseudo amino acid composition. *Protein Engineering Design and Selection* 17: 509-516.
8. Cai YD, Chou KC (2005) Predicting enzyme subclass by functional domain composition and pseudo amino acid composition. *Journal of Proteome Researc* 4(3): 967-971.
9. Cai YD, Zhou GP, Chou KC (2005) Predicting enzyme family classes by hybridizing gene product composition and pseudo amino acid composition. *J Theor Biol* 234(1): 145-149.
10. Gao Y, Shao SH, Xiao X, Ding YS, Huang YS, et al. (2005) Using pseudo amino acid composition to predict protein subcellular location: approached with Lyapunov index, Bessel function, and Chebyshev filter. *Amino Acids* 28(4): 373-376.
11. Liu H, Yang J, Wang M, Xue L, Chou KC (2005) Using Fourier spectrum analysis and pseudo amino acid composition for prediction of membrane protein types. *The Protein Journal* 24: 385-389.
12. Shen HB, Chou KC (2005) Using optimized evidence-theoretic K-nearest neighbor classifier and pseudo amino acid composition to predict membrane protein types. *Biochemical & Biophysical Research Communications* 334: 288-292.
13. Shen HB, Chou KC (2005) Predicting protein subnuclear location with optimized evidence-theoretic K-nearest classifier and pseudo amino acid composition. *Biochem Biophys Res Comm* 337(3): 752-756.
14. Cai YD, Chou KC (2006) Predicting membrane protein type by functional domain composition and pseudo amino acid composition. *J Theor Biol* 238: 395-400.
15. Shen HB, Yang J, Chou KC (2006) Fuzzy KNN for predicting membrane protein types from pseudo amino acid composition. *J Theor Biol* 240(1): 9-13.
16. Wang SQ, Yang J, Chou KC (2006) Using stacked generalization to predict membrane protein types based on pseudo amino acid composition. *J Theor Biol* 242(4): 941-946.
17. Xiao X, Shao SH, Ding YS, Huang ZD, Chou KC (2006) Using cellular automata images and pseudo amino acid composition to predict protein subcellular location. *Amino Acids* 30: 49-54.
18. Xiao X, Shao SH, Huang ZD, Chou KC (2006) Using pseudo amino acid composition to predict protein structural classes: approached with complexity measure factor. *J Comput Chem* 27: 478-482.
19. Ding YS, Zhang TL, Chou KC (2007) Prediction of protein structure classes with pseudo amino acid composition and fuzzy support vector machine network. *Protein & Peptide Letters* 14(8): 811-815.
20. Oxenoid K, Rice AJ, Chou JJ (2007) Comparing the structure and dynamics of phospholamban pentamer in its unphosphorylated and pseudo-phosphorylated states. *Protein Sci* 16(9): 1977-1983.

21. Shen HB, Chou KC (2008) PseAAC: a flexible web-server for generating various kinds of protein pseudo amino acid composition. *Anal Biochem* 373(2): 386-388.
22. Xiao X, Lin WZ, Chou KC (2008) Using grey dynamic modeling and pseudo amino acid composition to predict protein structural classes. *J Comput Chem* 29(12): 2018-2024.
23. Xiao X, Wang P, Chou KC (2008) Predicting protein structural classes with pseudo amino acid composition: an approach using geometric moments of cellular automaton image. *J Theor Biol* 254: 691-696.
24. Zhang TL, Ding YS, Chou KC (2008) Prediction protein structural classes with pseudo amino acid composition: approximate entropy and hydrophobicity pattern. *J Theor Biol* 250(1): 186-193.
25. Xiao X, Wang P, Chou KC (2009) Predicting protein quaternary structural attribute by hybridizing functional domain composition and pseudo amino acid composition. *J Appl Crystallogr* 42(2): 169-173.
26. Ding YS, Zhang TL (2008) Using Chou's pseudo amino acid composition to predict subcellular localization of apoptosis proteins: an approach with immune genetic algorithm-based ensemble classifier. *Pattern Recognition Letters* 29(13): 1887-1892.
27. Fang Y, Guo Y, Feng Y, Li M (2008) Predicting DNA-binding proteins: approached from Chou's pseudo amino acid composition and other specific sequence features. *Amino Acids* 34(1): 103-109.
28. Jiang X, Wei R, Zhang TL, Gu Q (2008) Using the concept of Chou's pseudo amino acid composition to predict apoptosis proteins subcellular location: an approach by approximate entropy. *Protein & Peptide Letters* 15(4): 392-396.
29. Jiang X, Wei R, Zhao Y, Zhang T (2008) Using Chou's pseudo amino acid composition based on approximate entropy and an ensemble of AdaBoost classifiers to predict protein subnuclear location. *Amino Acids* 34(4): 669-675.
30. Li FM, Li QZ (2008) Predicting protein subcellular location using Chou's pseudo amino acid composition and improved hybrid approach. *Protein & Peptide Letters* 15(6): 612-616.
31. Lin H (2008) The modified Mahalanobis discriminant for predicting outer membrane proteins by using Chou's pseudo amino acid composition. *J Theor Biol* 252(2): 350-356.
32. Lin H, Ding H, Feng-Biao Guo FB, Zhang AY, Huang J (2008) Predicting subcellular localization of mycobacterial proteins by using Chou's pseudo amino acid composition. *Protein & Peptide Letters* 15(7): 739-744.
33. Nanni L, Lumini A (2008) Genetic programming for creating Chou's pseudo amino acid based features for submitochondria localization. *Amino Acids* 34(4): 653-660.
34. Zhang GY, Li HC, Gao JQ, Fang BS (2008) Predicting lipase types by improved Chou's pseudo amino acid composition. *Protein & Peptide Letters* 15(10): 1132-1137.
35. Zhang SW, Chen W, Yang F, Pan Q (2008) Using Chou's pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. *Amino Acids* 35(3): 591-598.
36. Zhang SW, Zhang YL, Yang HF, Zhao CH, Pan Q (2008) Using the concept of Chou's pseudo amino acid composition to predict protein subcellular localization: an approach by incorporating evolutionary information and von Neumann entropies. *Amino Acids* 34: 565-572.
37. Chen C, Chen L, Zou X, Cai P (2009) Prediction of protein secondary structure content by using the concept of Chou's pseudo amino acid composition and support vector machine. *Protein & Peptide Letters* 16(1): 27-31.
38. Georgiou DN, Karakasidis TE, Nieto JJ, Torres A (2009) Use of fuzzy clustering technique and matrices to classify amino acids and its impact to Chou's pseudo amino acid composition. *J Theor Biol* 257(1): 17-26.
39. Li ZC, Zhou XB, Dai Z, Zou XY (2009) Prediction of protein structural classes by Chou's pseudo amino acid composition: approached using continuous wavelet transform and principal component analysis. *Amino Acids* 37(2): 415-425.
40. Lin H, Wang H, Ding H, Chen YL, Li QZ (2009) Prediction of Subcellular Localization of Apoptosis Protein Using Chou's Pseudo Amino Acid Composition. *Acta Biotheoretica* 57(3): 321-330.
41. Qiu JD, Huang JH, Liang RP, Lu XQ (2009) Prediction of G-protein-coupled receptor classes based on the concept of Chou's pseudo amino acid composition: an approach from discrete wavelet transform. *Anal Biochem* 390(1): 68-73.
42. Zeng YH, Guo YZ, Xiao RQ, Yang L, Yu LZ, et al. (2009) Using the augmented Chou's pseudo amino acid composition for predicting protein submitochondria locations based on auto covariance approach. *J Theor Biol* 259(2): 366-372.
43. Esmaeili M, Mohabatkar H, Mohsenzadeh S (2010) Using the concept of Chou's pseudo amino acid composition for risk type prediction of human papillomaviruses. *J Theor Biol* 263(2): 203-209.
44. Gu Q, Ding YS, Zhang TL (2010) Prediction of G-Protein-Coupled Receptor Classes in Low Homology Using Chou's Pseudo Amino Acid Composition with Approximate Entropy and Hydrophobicity Patterns. *Protein & Peptide Letters* 17(5): 559-567.
45. Mohabatkar H (2010) Prediction of cyclin proteins using Chou's pseudo amino acid composition. *Protein & Peptide Letters* 17: 1207-1214.
46. Qiu JD, Huang JH, Shi SP, Liang RP (2010) Using the concept of Chou's pseudo amino acid composition to predict enzyme family classes: an approach with support vector machine based on discrete wavelet transform. *Protein & Peptide Letters* 17(6): 715-722.
47. Sahu SS, Panda G (2010) A novel feature representation method based on Chou's pseudo amino acid composition for protein structural class prediction. *Computational Biology and Chemistry* 34(5-6): 320-327.
48. Yu L, Guo Y, Li Y, Li G, Li M, et al. (2010) SecretP: Identifying bacterial secreted proteins by fusing new features into Chou's pseudo amino acid composition. *J Theor Biol* 267(1): 1-6.
49. Guo J, Rao N, Liu G, Yang Y, Wang G (2011) Predicting protein folding rates using the concept of Chou's pseudo amino acid composition. *Journal of Computational Chemistry* 32(8): 1612-1617.
50. Lin J, Wang Y (2011) Using a novel AdaBoost algorithm and Chou's pseudo amino acid composition for predicting protein subcellular localization. *Protein & Peptide Letters* 18(12): 1219-1225.
51. Lin J, Wang Y, Xu X (2011) A novel ensemble and composite approach for classifying proteins based on Chou's pseudo amino acid composition. *African Journal of Biotechnology* 10(74): 16963-16968.
52. Mohabatkar H, Mohammad Beigi M, Esmaeili A (2011) Prediction of GABA(A) receptor proteins using the concept of Chou's pseudo amino acid composition and support vector machine. *J Theor Biol* 281(1): 18-23.
53. Mohammad BM, Behjati M, Mohabatkar H (2011) Prediction of metalloproteinase family based on the concept of Chou's pseudo amino acid composition using a machine learning approach. *Journal of Structural and Functional Genomics* 12(4): 191-197.
54. Qiu JD, Suo SB, Sun XY, Shi SP, Liang RP (2011) OligoPred: A web-server for predicting homo-oligomeric proteins by incorporating discrete wavelet transform into Chou's pseudo amino acid composition. *Journal of Molecular Graphics & Modelling* 30: 129-134.
55. Zou D, He Z, He J, Xia Y (2011) Supersecondary structure prediction using Chou's pseudo amino acid composition. *J Comput Chem* 32(2): 271-278.
56. Cao JZ, Liu WQ, Gu H (2012) Predicting Viral Protein Subcellular Localization with Chou's Pseudo Amino Acid Composition and

- Imbalance-Weighted Multi-Label K-Nearest Neighbor Algorithm. *Protein and Peptide Letters* 19(11): 1163-1169.
57. Chen C, Shen ZB, Zou XY (2012) Dual-Layer Wavelet SVM for Predicting Protein Structural Class Via the General Form of Chou's Pseudo Amino Acid Composition. *Protein & Peptide Letters* 19: 422-429.
58. Du P, Wang X, Xu C, Gao Y (2012) PseAAC-BUILDER: A cross-platform stand-alone program for generating various special Chou's pseudo amino acid compositions. *Anal Biochem* 425(2): 117-119.
59. Fan GL, Li QZ (2012) Predict mycobacterial proteins subcellular locations by incorporating pseudo-average chemical shift into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 304: 88-95.
60. Fan GL, Li QZ (2012) Predicting protein submitochondria locations by combining different descriptors into the general form of Chou's pseudo amino acid composition. *Amino Acids* 43: 545-555.
61. Li LQ, Zhang Y, Zou LY, Zhou Y, Zheng XQ (2012) Prediction of Protein Subcellular Multi-Localization Based on the General form of Chou's Pseudo Amino Acid Composition. *Protein & Peptide Letters* 19: 375-387.
62. Liu L, Hu XZ, Liu XX, Wang Y, Li SB (2012) Predicting Protein Fold Types by the General Form of Chou's Pseudo Amino Acid Composition: Approached from Optimal Feature Extractions. *Protein & Peptide Letters* 19: 439-449.
63. Nanni L, Brahnam S, Lumini A (2012) Wavelet images and Chou's pseudo amino acid composition for protein classification. *Amino Acids* 43(2): 657-665.
64. Nanni L, Lumini A, Gupta D, Garg A (2012) Identifying bacterial virulent proteins by fusing a set of classifiers based on variants of Chou's pseudo amino acid composition and on evolutionary information. *IEEE-ACM Transaction on Computational Biology and Bioinformatics* 9(2): 467-475.
65. Niu XH, Hu XH, Shi F, Xia JB (2012) Predicting Protein Solubility by the General Form of Chou's Pseudo Amino Acid Composition: Approached from Chaos Game Representation and Fractal Dimension. *Protein & Peptide Letters* 19(9): 940-948.
66. Ren LY, Zhang YS, Gutman I (2012) Predicting the Classification of Transcription Factors by Incorporating their Binding Site Properties into a Novel Mode of Chou's Pseudo Amino Acid Composition. *Protein & Peptide Letters* 19(11): 1170-1176.
67. Zhao XW, Ma ZQ, Yin MH (2012) Predicting protein-protein interactions by combing various sequence-derived features into the general form of Chou's Pseudo amino acid composition. *Protein & Peptide Letters* 19: 492-500.
68. Zia-ur-Rehman, Khan A (2012) Identifying GPCRs and their Types with Chou's Pseudo Amino Acid Composition: An Approach from Multi-scale Energy Representation and Position Specific Scoring Matrix. *Protein & Peptide Letters* 19(8): 890-903.
69. Chen YK, Li KB (2013) Predicting membrane protein types by incorporating protein topology, domains, signal peptides, and physicochemical properties into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 318: 1-12.
70. Fan GL, Li QZ (2013) Discriminating bioluminescent proteins by incorporating average chemical shift and evolutionary information into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 334: 45-51.
71. Georgiou DN, Karakasidis TE, Megaritis AC (2013) A short survey on genetic sequences, Chou's pseudo amino acid composition and its combination with fuzzy set theory. *The Open Bioinformatics Journal* 7(1): 41-48.
72. Gupta MK, Niyogi R, Misra M (2013) An alignment-free method to find similarity among protein sequences via the general form of Chou's pseudo amino acid composition. *SAR QSAR Environ Res* 24: 597-609.
73. Huang C, Yuan J (2013) Using radial basis function on the general form of Chou's pseudo amino acid composition and PSSM to predict subcellular locations of proteins with both single and multiple sites. *Biosystems* 113(1): 50-57.
74. Huang C, Yuan JQ (2013) A multilabel model based on Chou's pseudo amino acid composition for identifying membrane proteins with both single and multiple functional types. *J Membr Biol* 246(4): 327-334.
75. Huang C, Yuan JQ (2013) Predicting protein subchloroplast locations with both single and multiple sites via three different modes of Chou's pseudo amino acid compositions. *J Theor Biol* 335: 205-212.
76. Khosravian M, Faramarzi FK, Beigi MM, Behbahani M, Mohabatkar H (2013) Predicting Antibacterial Peptides by the Concept of Chou's Pseudo amino Acid Composition and Machine Learning Methods. *Protein & Peptide Letters* 20: 180-186.
77. Lin H, Ding C, Yuan LF, Chen W, Ding H, et al. (2013) Predicting subchloroplast locations of proteins based on the general form of Chou's pseudo amino acid composition: Approached from optimal tripeptide composition. *International Journal of Biometrics* 6: 1350003.
78. Liu B, Wang X, Zou Q, Dong Q, Chen Q (2013) Protein remote homology detection by combining Chou's pseudo amino acid composition and profile-based protein representation. *Molecular Informatics* 32: 775-782.
79. Mohabatkar H, Beigi MM, Abdolahi K, Mohsenzadeh S (2013) Prediction of Allergenic Proteins by Means of the Concept of Chou's Pseudo Amino Acid Composition and a Machine Learning Approach. *Medicinal Chemistry* 9: 133-137.
80. Qin YF, Zheng L, Huang J (2013) Locating apoptosis proteins by incorporating the signal peptide cleavage sites into the general form of Chou's Pseudo amino acid composition. *Int J Quantum Chem* 113: 1660-1667.
81. Sarangi AN, Lohani M, Aggarwal R (2013) Prediction of Essential Proteins in Prokaryotes by Incorporating Various Physico-chemical Features into the General form of Chou's Pseudo Amino Acid Composition. *Protein Pept Lett* 20(7): 781-795.
82. Wan S, Mak MW, Kung SY (2013) GOASVM: A subcellular location predictor by incorporating term-frequency gene ontology into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 323: 40-48.
83. Wang X, Li GZ, Lu WC (2013) Virus-ECC-mPLoc: a multi-label predictor for predicting the subcellular localization of virus proteins with both single and multiple sites based on a general form of Chou's pseudo amino acid composition. *Protein & Peptide Letters* 20: 309-317.
84. Xiaohui N, Nana L, Jingbo X, Dingyan C, Yuehua P, et al. (2013) Using the concept of Chou's pseudo amino acid composition to predict protein solubility: An approach with entropies in information theory. *J Theor Biol* 332: 211-217.
85. Du P, Gu S, Jiao Y (2014) PseAAC-General: Fast building various modes of general form of Chou's pseudo amino acid composition for large-scale protein datasets. *International Journal of Molecular Sciences* 15(3): 3495-3506.
86. Hajisharifi Z, Piryaiee M, Mohammad Beigi M, Behbahani M, Mohabatkar H (2014) Predicting anticancer peptides with Chou's pseudo amino acid composition and investigating their mutagenicity via Ames test. *J Theor Biol* 341: 34-40.
87. Jia C, Lin X, Wang Z (2014) Prediction of Protein S-Nitrosylation Sites Based on Adapted Normal Distribution Bi-Profile Bayes and Chou's Pseudo Amino Acid Composition. *Int J Mol Sci* 15(6): 10410-10423.
88. Kong L, Zhang L, Lv J (2014) Accurate prediction of protein structural classes by incorporating predicted secondary structure information into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 344: 12-18.

89. Nanni L, Brahnam S, Lumini A (2014) Prediction of protein structure classes by incorporating different protein descriptors into general Chou's pseudo amino acid composition. *J Theor Biol* 360: 109-116.
90. Zhang J, Sun P, Zhao X, Ma Z (2014) PECM: Prediction of extracellular matrix proteins using the concept of Chou's pseudo amino acid composition. *J Theor Biol* 363: 412-418.
91. Zhang L, Zhao X, Kong L (2014) Predict protein structural class for low-similarity sequences by evolutionary difference information into the general form of Chou's pseudo amino acid composition. *J Theor Biol* 355: 105-110.
92. Zuo YC, Peng Y, Liu L, Chen W, Yang L, et al. (2014) Predicting peroxidase subcellular location by hybridizing different descriptors of Chou's pseudo amino acid patterns. *Anal Biochem* 458: 14-19.
93. Ali F, Hayat M (2015) Classification of membrane protein types using Voting Feature Interval in combination with Chou's Pseudo Amino Acid Composition. *J Theor Biol* 384: 78-83.
94. Fan GL, Zhang XY, Liu YL, Nang Y, Wang H (2015) DSPMP: Discriminating secretory proteins of malaria parasite by hybridizing different descriptors of Chou's pseudo amino acid patterns. *J Comput Chem* 36: 2317-2327.
95. Huang C, Yuan JQ (2015) Simultaneously Identify Three Different Attributes of Proteins by Fusing their Three Different Modes of Chou's Pseudo Amino Acid Compositions. *Protein Pept Lett* 22: 547-556.
96. Khan ZU, Hayat M, Khan MA (2015) Discrimination of acidic and alkaline enzyme using Chou's pseudo amino acid composition in conjunction with probabilistic neural network model. *J Theor Biol* 365: 197-203.
97. Kumar R, Srivastava A, Kumari B, Kumar M (2015) Prediction of beta-lactamase and its class by Chou's pseudo amino acid composition and support vector machine. *J Theor Biol* 365: 96-103.
98. Wang X, Zhang W, Zhang Q, Li GZ (2015) MultiP-SChlo: multi-label protein subchloroplast localization prediction with Chou's pseudo amino acid composition and a novel multi-label classifier. *Bioinformatics* 31(16): 2639-2645.
99. Jiao YS, Du PF (2016) Prediction of Golgi-resident protein types using general form of Chou's pseudo amino acid compositions: Approaches with minimal redundancy maximal relevance feature selection. *J Theor Biol* 402: 38-44.
100. Tang H, Chen W, Lin H (2016) Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. *Mol Biosyst* 12(4): 1269-1275.
101. Zou HL, Xiao X (2016) Predicting the Functional Types of Singleplex and Multiplex Eukaryotic Membrane Proteins via Different Models of Chou's Pseudo Amino Acid Compositions. *J Membr Biol* 249(1-2): 23-29.
102. Huo H, Li T, Wang S, Lv Y, Zuo Y, et al. (2017) Prediction of presynaptic and postsynaptic neurotoxins by combining various Chou's pseudo components. *Sci Rep* 7(1): 5827.
103. Rahimi M, Bakhtiarzadeh MR, Mohammadi-Sangcheshmeh A (2017) Oogenesis\_Pred: A sequence-based method for predicting oogenesis proteins by six different modes of Chou's pseudo amino acid composition. *J Theor Biol* 414: 128-136.
104. Tripathi P, Pandey PN (2017) A novel alignment-free method to classify protein folding types by combining spectral graph clustering with Chou's pseudo amino acid composition. *J Theor Biol* 424: 49-54.
105. Yu B, Lou L, Li S, Zhang Y, Qiu W, et al. (2017) Prediction of protein structural class for low-similarity sequences using Chou's pseudo amino acid composition and wavelet denoising. *J Mol Graph Model* 76: 260-273.
106. Al Maruf MA, Shatabda S (2018) iRSpot-SF: Prediction of recombination hotspots by incorporating sequence based features into Chou's Pseudo components. *Genomics* 18: 63-82.
107. Arif M, Hayat M, Jan Z (2018) iMem-2LSAAC: A two-level model for discrimination of membrane proteins and their types by extending the notion of SAAC into Chou's pseudo amino acid composition. *J Theor Biol* 442: 11-21.
108. Cui X, Yu Z, Yu B, Wang M, Tian B, et al. (2018) UbiSitePred: A novel method for improving the accuracy of ubiquitination sites prediction by using LASSO to select the optimal Chou's pseudo components. *Chemometrics and Intelligent Laboratory Systems (CHEMOLAB)* 17: 512-538.
109. Mei J, Zhao J (2018) Prediction of HIV-1 and HIV-2 proteins by using Chou's pseudo amino acid compositions and different classifiers. *Sci Rep* 8(1): 2359.
110. Qiu W, Li S, Cui X, Yu Z, Wang M, et al. (2018) Predicting protein submitochondrial locations by incorporating the pseudo-position specific scoring matrix into the general Chou's pseudo-amino acid composition. *J Theor Biol* 450: 86-103.
111. Zhang L, Kong L (2018) iRSpot-ADPM: Identify recombination spots by incorporating the associated dinucleotide product model into Chou's pseudo components. *J Theor Biol* 441: 1-8.
112. Zhang S, Yang K, Lei Y, Song K (2018) iRSpot-DTS: Predict recombination spots by incorporating the dinucleotide-based spare-cross covariance information into Chou's pseudo components. *Genomics* 11: 457-464.
113. Zhao W, Wang L, Zhang TX, Zhao ZN, Du PF (2018) A brief review on software tools in generating Chou's pseudo-factor representations for all types of biological sequences. *Protein Pept Lett* 25(9): 822-829.
114. Al Maruf MA, Shatabda S (2019) iRSpot-SF: Prediction of recombination hotspots by incorporating sequence based features into Chou's Pseudo components. *Genomics* 111(4): 966-972.
115. Nosrati M, Mohabatkar H, Behbahani M (2019) Introducing of an integrated artificial neural network and Chou's pseudo amino acid composition approach for computational epitope-mapping of Crimean-Congo haemorrhagic fever virus antigens. *International Immunopharmacology* 78: 106020.
116. Pan Y, Wang S, Zhang Q, Lu Q, Su D, et al. (2019) Analysis and prediction of animal toxins by various Chou's pseudo components and reduced amino acid compositions. *J Theor Biol* 462: 221-229.
117. Tahir M, Tayara H, Chong KT (2019) iRNA-PseKNC(2methyl): Identify RNA 2'-O-methylation sites by convolution neural network and Chou's pseudo components. *J Theor Biol* 465: 1-6.
118. Tian B, Wu X, Chen C, Qiu W, Ma Q, et al. (2019) Predicting protein-protein interactions by fusing various Chou's pseudo components and using wavelet denoising approach. *J Theor Biol* 462: 329-346.
119. Zhang L, Kong L (2019) iRSpot-PDI: Identification of recombination spots by incorporating dinucleotide property diversity information into Chou's pseudo components. *Genomics* 111: 457-464.
120. Zhang S, Yang K, Lei Y, Song K (2019) iRSpot-DTS: Predict recombination spots by incorporating the dinucleotide-based spare-cross covariance information into Chou's pseudo components. *Genomics* 111: 1760-1770.
121. Chou KC (2020) The Significant and Profound Impacts of Chou's Pseudo Amino Acid Composition or PseAAC. *Natural Science* 12: 647-658.
122. Nosrati M, Mohabatkar H, Behbahani M (2020) Introducing of an integrated artificial neural network and Chou's pseudo amino acid composition approach for computational epitope-mapping of Crimean-Congo haemorrhagic fever virus antigens. *Int Immunopharmacol* 78: 106020.
123. Hayat M, Khan A (2012) Discriminating Outer Membrane Proteins with Fuzzy K-Nearest Neighbor Algorithms Based on the General Form of Chou's PseAAC. *Protein & Peptide Letters* 19(4): 411-421.

124. Liao B, Xiang Q, Li D (2012) Incorporating Secondary Features into the General form of Chou's PseAAC for Predicting Protein Structural Class. *Protein & Peptide Letters* 19: 1133-1138.
125. Mei S (2012) Multi-kernel transfer learning based on Chou's PseAAC formulation for protein submitochondria localization. *J Theor Biol* 293: 121-130.
126. Mei S (2012) Predicting plant protein subcellular multi-localization by Chou's PseAAC formulation based multi-label homolog knowledge transfer learning. *J Theor Biol* 310: 80-87.
127. Qin YF, Wang CH, Yu XQ, Zhu J, Liu TG, et al. (2012) Predicting Protein Structural Class by Incorporating Patterns of Over- Represented k-mers into the General form of Chou's PseAAC. *Protein & Peptide Letters* 19: 388-397.
128. Sun XY, Shi SP, Qiu JD, Suo SB, Huang SY, et al. (2012) Identifying protein quaternary structural attributes by incorporating physicochemical properties into the general form of Chou's PseAAC via discrete wavelet transform. *Molecular BioSystems* 8(12): 3178-3184.
129. Cao DS, Xu QS, Liang YZ (2013) propy: a tool to generate various modes of Chou's PseAAC. *Bioinformatics* 29: 960-962.
130. Chang TH, Wu LC, Lee TY, Chen SP, Huang HD, et al. (2013) EuLoc: a web-server for accurately predict protein subcellular localization in eukaryotes by incorporating various features of sequence segments into the general form of Chou's PseAAC. *Journal of Computer-Aided Molecular Design* 27: 91-103.
131. Fan GL, Li QZ, Zuo YC (2013) Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. *Process Biochemistry* 48: 1048-1053.
132. Pacharawongsakda E, Theeramunkong T (2013) Predict Subcellular Locations of Singleplex and Multiplex Proteins by Semi-Supervised Learning and Dimension-Reducing General Mode of Chou's PseAAC. *IEEE Transactions on Nanobioscience* 12: 311-320.
133. Xie HL, Fu L, Nie XD (2013) Using ensemble SVM to identify human GPCRs N-linked glycosylation sites based on the general form of Chou's PseAAC. *Protein Eng Des Sel* 26: 735-742.
134. Han GS, Yu ZG, Anh V (2014) A two-stage SVM method to predict membrane protein types by incorporating amino acid classifications and physicochemical properties into a general form of Chou's PseAAC. *J Theor Biol* 344: 31-39.
135. Li L, Yu S, Xiao W, Li Y, Li M, et al. (2014) Prediction of bacterial protein subcellular localization by incorporating various features into Chou's PseAAC and a backward feature selection approach. *Biochimie* 104: 100-107.
136. Zhang J, Zhao X, Sun P, Ma Z (2014) PSNO: Predicting Cysteine S-Nitrosylation Sites by Incorporating Various Sequence-Derived Features into the General Form of Chou's PseAAC. *Int J Mol Sci* 15(7): 11204-11219.
137. Liu B, Xu J, Fan S, Xu R, Jiyun Zhou J, et al. (2015) PseDNA-Pro: DNA-binding protein identification by combining Chou's PseAAC and physicochemical distance transformation. *Molecular Informatics* 34: 8-17.
138. Mandal M, Mukhopadhyay A, Maulik U (2015) Prediction of protein subcellular localization by incorporating multiobjective PSO-based feature subset selection into the general form of Chou's PseAAC. *Medical & biological engineering & computing* 53: 331-344.
139. Sanchez V, Peinado AM, Perez-Cordoba JL, Gomez AM (2015) A new signal characterization and signal-based Chou's PseAAC representation of protein sequences. *Journal of bioinformatics and computational biology* 13: 1550024.
140. Kabir M, Hayat M (2016) iRSpot-GAEnsC: identifying recombination spots via ensemble classifier and extending the concept of Chou's PseAAC to formulate DNA samples. *Molecular Genetics and Genomics* 291(1): 285-296.
141. Tahir M, Hayat M (2016) iNuc-STNC: a sequence-based predictor for identification of nucleosome positioning in genomes by extending the concept of SAAC and Chou's PseAAC. *Mol Biosyst* 12: 2587-2593.
142. Ju Z, He JJ (2017) Prediction of lysine propionylation sites using biased SVM and incorporating four different sequence features into Chou's PseAAC. *J Mol Graph Model* 76: 356-363.
143. Yu B, Li S, Qiu WY, Chen C, Chen RX, et al. (2017) Accurate prediction of subcellular location of apoptosis proteins combining Chou's PseAAC and PsePSSM based on wavelet denoising. *Oncotarget* 8: 107640-107665.
144. Ahmad J, Hayat M (2018) MFSC: Multi-voting based Feature Selection for Classification of Golgi Proteins by Adopting the General form of Chou's PseAAC components. *J Theor Biol* 463: 99-109.
145. Akbar S, Hayat M (2018) iMethyl-STTNC: Identification of N(6)-methyladenosine sites by extending the Idea of SAAC into Chou's PseAAC to formulate RNA sequences. *J Theor Biol* 455: 205-211.
146. Contreras-Torres E (2018) Predicting structural classes of proteins by incorporating their global and local physicochemical and conformational properties into general Chou's PseAAC. *J Theor Biol* 454: 139-145.
147. Fu X, Zhu W, Liso B, Cai L, Peng L, et al. (2018) Improved DNA-binding protein identification by incorporating evolutionary information into the Chou's PseAAC. *IEEE Access* 18: 43-66.
148. Javed F, Hayat M (2018) Predicting subcellular localizations of multi-label proteins by incorporating the sequence features into Chou's PseAAC. *Genomics* 17: 793-821.
149. Mousavizadegan M, Mohabatkar H (2018) Computational prediction of antifungal peptides via Chou's PseAAC and SVM. *Journal of bioinformatics and computational biology* 16(4): 1850016.
150. Zhang S, Liang Y (2018) Predicting apoptosis protein subcellular localization by integrating auto-cross correlation and PSSM into Chou's PseAAC. *J Theor Biol* 457: 163-169.
151. Ahmad J, Hayat M (2019) MFSC: Multi-voting based feature selection for classification of Golgi proteins by adopting the general form of Chou's PseAAC components. *J Theor Biol* 463: 99-109.
152. Butt AH, Rasool N, Khan YD (2019) Prediction of antioxidant proteins by incorporating statistical moments based features into Chou's PseAAC. *J Theor Biol* 473: 1-8.
153. Javed F, Hayat M (2019) Predicting subcellular localization of multi-label proteins by incorporating the sequence features into Chou's PseAAC. *Genomics* 111(6): 1325-1332.
154. Tahir M, Hayat M, Khan SA (2019) 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. *Molecular genetics and genomics* 294(1): 199-210.
155. Mehbahani M, Rabiei P, Mohabatkar H (2020) A Comparative Analysis of Allergen Proteins between Plants and Animals Using Several Computational Tools and Chou's PseAAC Concept. *Int Arch Allergy Immunol*.
156. Hayat M, Iqbal N (2014) Discriminating protein structure classes by incorporating Pseudo Average Chemical Shift to Chou's general PseAAC and Support Vector Machine. *Computer methods and programs in biomedicine* 116(3): 184-192.

157. Ahmad S, Kabir M, Hayat M (2015) Identification of Heat Shock Protein families and J-protein types by incorporating Dipeptide Composition into Chou's general PseAAC. *Computer methods and programs in biomedicine* 122(2): 165-174.
158. Dehzangi A, Heffernan R, Sharma A, Lyons J, Paliwal K, et al. (2015) Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. *J Theor Biol* 364: 284-294.
159. Sharma R, Dehzangi A, Lyons J, Paliwal K, Tsunoda T, et al. (2015) Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. *IEEE Trans Nanobioscience* 14: 915-926.
160. Zhang M, Zhao B, Liu X (2015) Predicting industrial polymer melt index via incorporating chaotic characters into Chou's general PseAAC. *Chemometrics and Intelligent Laboratory Systems* 146: 232-240.
161. Zhang SL (2015) Accurate prediction of protein structural classes by incorporating PSSS and PSSM into Chou's general PseAAC. *Chemometrics and Intelligent Laboratory Systems* 142: 28-35.
162. Ahmad K, Waris M, Hayat M (2016) Prediction of Protein Submitochondrial Locations by Incorporating Dipeptide Composition into Chou's General Pseudo Amino Acid Composition. *J Membr Biol* 249(3): 293-304.
163. Behbahani M, Mohabatkar H, Nosrati M (2016) Analysis and comparison of lignin peroxidases between fungi and bacteria using three different modes of Chou's general pseudo amino acid composition. *J Theor Biol* 411: 1-5.
164. Fan GL, Liu YL, Wang H (2016) Identification of thermophilic proteins by incorporating evolutionary and acid dissociation information into Chou's general pseudo amino acid composition. *J Theor Biol* 407: 138-142.
165. Ju Z, Cao JZ, Gu H (2016) Predicting lysine phosphoglycerylation with fuzzy SVM by incorporating k-spaced amino acid pairs into Chou's general PseAAC. *J Theor Biol* 397: 145-150.
166. Tiwari AK (2016) Prediction of G-protein coupled receptors and their subfamilies by incorporating various sequence features into Chou's general PseAAC. *Computer methods and programs in biomedicine* 134: 197-213.
167. Xu C, Sun D, Liu S, Zhang Y (2016) Protein Sequence Analysis by Incorporating Modified Chaos Game and Physicochemical Properties into Chou's General Pseudo Amino Acid Composition. *J Theor Biol* 406: 105-115.
168. Chou KC, Forsen S (1980) Diffusion-controlled effects in reversible enzymatic fast reaction system: Critical spherical shell and proximity rate constants. *Biophysical Chemistry* 12: 255-263.
169. Chou KC, Forsen S (1980) Graphical rules for enzyme-catalyzed rate laws. *Biochem J* 187: 829-835.
170. Chou KC, Forsen S, Zhou GQ (1980) Three schematic rules for deriving apparent rate constants. *Chemica Scripta* 16: 109-113.
171. Chou KC, Li TT, Forsen S (1980) The critical spherical shell in enzymatic fast reaction systems. *Biophysical Chemistry* 12: 265-269.
172. Li TT, Chou KC, Forsen S (1980) The flow of substrate molecules in fast enzyme-catalyzed reaction systems. *Chemica Scripta* 16: 192-196.
173. Chou KC, Carter RE, Forsen S (1981) A new graphical method for deriving rate equations for complicated mechanisms. *Chemica Scripta* 18: 82-86.
174. Chou KC, Chen NY, Forsen S (1981) The biological functions of low-frequency phonons: 2. Cooperative effects. *Chemica Scripta* 18: 126-132.
175. Chou KC, Forsen S (1981) Graphical rules of steady-state reaction systems. *Can J Chem* 59: 737-755.



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