

Short Communication

Showcase to illustrate how the web-server iRNA-Methyl is working

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Short Commentary

In 2015 a very powerful web-server predictor has been established for identifying N⁶-methyladenosine (m⁶A), which is one of the most abundant modifications in RNA [1].

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

Step 1: Open the web server at <http://lin.uestc.edu.cn/server/iRNA-Methyl> and you will see the top page of the iRNA-Methyl predictor on your computer screen, as shown in Fig.1. Click on the [Read Me](#) button to see a brief introduction about the predictor and the caveat when using it.

Step 2: Either type or copy/paste the query RNA sequences into the input box at the center of Fig.1. The input sequence should be in FASTA format. For the examples of RNA 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 example, if you use the query RNA sequences in the [Example](#) window as the input, you will see the following shown on the screen of your computer. (1) RNA sequence-1 contains 5 “GAC” (with adenine at its middle) consensus motifs, of which only those at the sequence positions 128 is predicted to be the methylation sites or site, and all the others are not. (2) RNA sequence-2 contains 8 “GAC” consensus motifs, of which only those at the sequence positions 332 is predicted to be the methylation sites, while all the others are not. All these results are fully consistent with the experimental observations.

Step 4: Click on the [Data](#) button to download the datasets used to train and test the model.

Step 5: Click on the [Citation](#) button to find the relevant paper that document the detailed development and algorithm of iRNA-Methyl.

It is instructive to point out 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., [2–14] and three comprehensive review papers [15–17]: (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.

Moreover, it has not escaped our notice that during the development of iRNA-Methyl web-server, the approach of general pseudo amino acid components [18] or PseAAC [19] had been utilized and hence its accuracy would be much higher than its counterparts, as concurred by many investigators [15, 18–266].

It is anticipated that iRNA-Methyl may become a useful high throughput tool for conducting genome analysis as well as drug development.

For the remarkable and awesome roles of the “5-steps rule” in driving proteome, genome analyses and drug development, see a series of recent papers [16, 17, 267–276] where the rule and its wide applications have been very impressively presented from various aspects or at different angles.

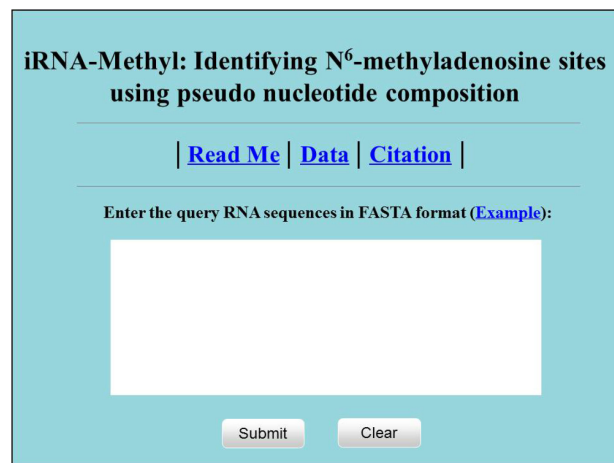


Figure 1. A semi screenshot for the top page of iRNA-Methyl (Adapted from [1] with permission).

References

1. Chen W, Feng P, Ding H, Lin H, Chou KC (2015) iRNA-Methyl: Identifying N⁶-methyladenosine sites using pseudo nucleotide composition. *Analytical Biochemistry* 490: 26–33. [Crossref]
2. 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 *Current Genomics*.
3. Cheng X, Lin WZ, Xiao X, Chou KC (2019) pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. *Bioinformatics* 35: 398–406. [Crossref]

4. Chou KC, Cheng X, Xiao X (2019) pLoc_bal-mHum: predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. *Genomics* 111: 1274–1282. [Crossref]
5. 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: 472–485. [Crossref]
6. Ehsan A, Mahmood MK, Khan YD, Barukab OM, Khan SA, et al. (2019) 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* 20: 124–133. [Crossref]
7. Feng P, Yang H, Ding H, Lin H, Chen W, et al. (2019) iDNA6mA-PseKNC: Identifying DNA N(6)-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics* 111: 96–102. [Crossref]
8. Hussain W, Khan SD, 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. [Crossref]
9. Hussain W, Khan YD, Rasool N, Khan SA, Chou KC (2019) 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* 468: 1–11. [Crossref]
10. Ilyas S, Hussain W, Ashraf A, Khan YD, Khan SA, Chou KC (2019) iMethylK-PseAAC: Improving accuracy for lysine methylation sites identification by incorporating statistical moments and position relative features into general PseAAC via Chou's 5-steps rule. *Current Genomics*
11. Jia J, Li X, Qiu W, Xiao X, Chou KC (2019) iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. *Journal of Theoretical Biology* 460: 195–203. [Crossref]
12. Khan YD, Batool A, Rasool N, Khan A, Chou KC (2019) Prediction of nitrosocysteine sites using position and composition variant features. *Letters in Organic Chemistry* 16: 283–293.
13. Khan YD, Jamil M, Hussain W, Rasool N, Khan SA, et al. (2019) pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. *J Theor Biol* 463: 47–55. [Crossref]
14. YLu SA, Wang S, Wang J, Zhou G, Zhang Q et al. (2019) An Epidemic Avian Influenza Prediction Model Based on Google Trends. *Letters in Organic Chemistry* 16: 303–310.
15. Chou KC (2011) Some remarks on protein attribute prediction and pseudo amino acid composition (50th Anniversary Year Review, 5-steps rule). *Journal of Theoretical Biology* 273: 236–247. [Crossref]
16. Chou KC (2019) Advance in predicting subcellular localization of multi-label proteins and its implication for developing multi-target drugs. *Current Medicinal Chemistry* 26: 4918–4943. [Crossref]
17. Chou KC (2019) Impacts of pseudo amino acid components and 5-steps rule to proteomics and proteome analysis. *Current Topics in Medicinal Chemistry* 19: 2283–2300. [Crossref]
18. Chou KC (2001) Prediction of protein cellular attributes using pseudo amino acid composition. *Proteins* 43: 246–255. [Crossref]
19. Chou KC (2005) Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. *Bioinformatics* 21: 10–19. [Crossref]
20. Guo ZM (2002) Prediction of membrane protein types by using pattern recognition method based on pseudo amino acid composition.
21. 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: 407–411. [Crossref]
22. Chou KC, Cai YD (2003) Predicting protein quaternary structure by pseudo amino acid composition. *Proteins* 53: 282–289. [Crossref]
23. 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: 1250–1260. [Crossref]
24. Pan YX, Zhang ZZ, Guo ZM, Feng GY, Huang ZD, et al. (2003) Application of pseudo amino acid composition for predicting protein subcellular location: stochastic signal processing approach. *Journal of Protein Chemistry* 22: 395–402. [Crossref]
25. Chou KC, Cai YD (2004) Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo amino acid composition. *Journal of Cellular Biochemistry* 91: 1197–1203. [Crossref]
26. 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. 17: 509–516.
27. Cai YD, Chou KC (2005) Predicting enzyme subclass by functional domain composition and pseudo amino acid composition. *Journal of Proteome Research* 4: 967–971. [Crossref]
28. Cai YD, Zhou GP, Chou KC (2005) Predicting enzyme family classes by hybridizing gene product composition and pseudo amino acid composition. *Journal of Theoretical Biology* 234: 145–149. [Crossref]
29. Gao Y, Shao SH, Xiao X, Ding YS, Huang YS (2005) Using pseudo amino acid composition to predict protein subcellular location: approached with Lyapunov index, Bessel function, and Chebyshev filter. *Amino Acids* 28: 373–376. [Crossref]
30. H Liu, J Yang, M Wang, L Xue, KC Chou (2005) Using Fourier spectrum analysis and pseudo amino acid composition for prediction of membrane protein types. *The Protein Journal* 24: 385–389. [Crossref]
31. 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. [Crossref]
32. 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: 752–756. [Crossref]
33. Cai YD, Chou KC (2006) Predicting membrane protein type by functional domain composition and pseudo amino acid composition. *Journal of Theoretical Biology* 238: 395–400. [Crossref]
34. Chen C, Tian YX, Zou XY, Cai PX, Mo JY (2006) Using pseudo amino acid composition and support vector machine to predict protein structural class. *J Theor Biol* 243 444–448. [Crossref]
35. Chen C, Zhou X, Tian Y, Zou X, Cai P (2006) Predicting protein structural class with pseudo amino acid composition and support vector machine fusion network. *Analytical Biochemistry* 357: 116–121. [Crossref]
36. Du P, Li Y (2006) Prediction of protein submitochondria locations by hybridizing pseudo amino acid composition with various physicochemical features of segmented sequence. *BMC Bioinformatics* 7: 518. [Crossref]
37. Mondal S, Bhavna R, Mohan Babu R, Ramakumar S (2006) Pseudo amino acid composition and multi-class support vector machines approach for conotoxin superfamily classification. *J Theor Biol* 243: 252–260. [Crossref]
38. Shen HB, Yang J, Chou KC (2006) Fuzzy KNN for predicting membrane protein types from pseudo amino acid composition. *Journal of Theoretical Biology* 240: 9–13. [Crossref]
39. Wang SQ, Yang J, Chou KC (2006) Using stacked generalization to predict membrane protein types based on pseudo amino acid composition. *Journal of Theoretical Biology* 242: 941–946. [Crossref]
40. Xiao X, Shao SH, YS Ding SH, Huang ZD, Chou KC (2006) Using cellular automata images and pseudo amino acid composition to predict protein subcellular location. *Amino Acids* 30: 49–54. [Crossref]
41. Xiao X, Shao SH, Huang ZD, Chou KC (2006) Using pseudo amino acid composition to predict protein structural classes: approached with complexity measure factor. *Journal of Computational Chemistry* 27: 478–482.
42. Zhang SW, Pan Q, Zhang HC, Shao ZC, Shi JY (2006) Prediction protein homooligomer types by pseudo amino acid composition: Approached with an improved feature extraction and naive Bayes feature fusion. *Amino Acids* 30 461–468. [Crossref]
43. Zhou GP, Cai YD (2006) Predicting protease types by hybridizing gene ontology and pseudo amino acid composition. *Proteins* 63: 681–684. [Crossref]
44. Chen YL, Li QZ (2007) Prediction of apoptosis protein subcellular location using improved hybrid approach and pseudo amino acid composition. *Journal of Theoretical Biology* 248: 377–381. [Crossref]
45. 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: 811–815. [Crossref]
46. Lin H, Li QZ (2007) Predicting conotoxin superfamily and family by using pseudo amino acid composition and modified Mahalanobis discriminant. *Biochem Biophys Res Commun* 354: 548–551. [Crossref]
47. Lin H, Li QZ (2007) Using Pseudo Amino Acid Composition to Predict Protein Structural Class: Approached by Incorporating 400 Dipeptide Components. *Journal of Computational Chemistry* 28: 1463–1466. [Crossref]
48. Mundra P, Kumar M, Kumar KK, Jayaraman VK, Kulkarni BD (2007) Using pseudo amino acid composition to predict protein subnuclear localization: Approached with PSSM. *Pattern Recognition Letters* 28: 1610–1615.
49. Shi JY, Zhang SW, Pan Q, Cheng Y M, J Xie (2007) Prediction of protein subcellular localization by support vector machines using multi-scale energy and pseudo amino acid composition. *Amino Acids* 33: 69–74. [Crossref]
50. Zhang TL, Ding YS (2007) Using pseudo amino acid composition and binary-tree support vector machines to predict protein structural classes. *Amino Acids* 33: 623–629. [Crossref]
51. Zhou XB, Chen C, Li ZC, Zou XY (2007) Using Chou's amphiphilic pseudo amino acid composition and support vector machine for prediction of enzyme subfamily classes. *Journal of Theoretical Biology* 248 546–551. [Crossref]
52. Diao Y, Ma D, Wen Z, Yin J, Xiang J et al. (2008) Using pseudo amino acid composition to predict transmembrane regions in protein: cellular automata and Lempel-Ziv complexity. *Amino Acids* 34: 111–117. [Crossref]

53. 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: 1887–1892.
54. 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: 103–109. [Crossref]
55. Gu Q, Ding Y, Zhang T (2008) Prediction of G-protein-coupled receptor classes with pseudo amino acid composition.
56. 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: 392–396. [Crossref]
57. X Jiang, R Wei, Y Zhao, T Zhang (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: 669–675. [Crossref]
58. Li FM, Li QZ (2008) Using pseudo amino acid composition to predict protein subnuclear location with improved hybrid approach. *Amino Acids* 34: 119–125. [Crossref]
59. Li FM, Li QZ (2008) Predicting protein subcellular location using Chou's pseudo amino acid composition and improved hybrid approach. *Protein & Peptide Letters* 15: 612–616. [Crossref]
60. Lin H (2008) The modified Mahalanobis discriminant for predicting outer membrane proteins by using Chou's pseudo amino acid composition. *Journal of Theoretical Biology* 252: 350–356. [Crossref]
61. 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: 739–744. [Crossref]
62. Nanni L, Lumini A (2008) Genetic programming for creating Chou's pseudo amino acid based features for submitochondria localization. *Amino Acids* 34: 653–660. [Crossref]
63. Shen HB, Chou KC (2008) PseAAC: a flexible web-server for generating various kinds of protein pseudo amino acid composition. *Analytical Biochemistry* 373: 386–388. [Crossref]
64. Shi JY, Zhang SW, Pan Q, Zhou GP (2008) Using Pseudo Amino Acid Composition to Predict Protein Subcellular Location: Approached with Amino Acid Composition Distribution. *Amino Acids* 35: 321–327. [Crossref]
65. Xiao X, Lin WZ, Chou KC (2008) Using grey dynamic modeling and pseudo amino acid composition to predict protein structural classes. *Journal of Computational Chemistry* 29: 2018–2024. [Crossref]
66. 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. *Journal of Theoretical Biology* 254: 691–696. [Crossref]
67. Zhang GY, Fang BS (2008) Predicting the cofactors of oxidoreductases based on amino acid composition distribution and Chou's amphiphilic pseudo amino acid composition. *Journal of Theoretical Biology* 253: 310–315. [Crossref]
68. Zhang GY, Li HC, Gao JQ, Fang BS (2008) Predicting lipase types by improved Chou's pseudo amino acid composition. *Protein & Peptide Letters* 15: 1132–1137. [Crossref]
69. 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: 591–598. [Crossref]
70. 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. [Crossref]
71. Zhang TL, Ding YS, Chou KC (2008) Prediction protein structural classes with pseudo amino acid composition: approximate entropy and hydrophobicity pattern. *Journal of Theoretical Biology* 250: 186–193. [Crossref]
72. 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: 27–31. [Crossref]
73. Chou KC (2009) Pseudo amino acid composition and its applications in bioinformatics, proteomics and system biology. *Current Proteomics* 6: 262–274.
74. Ding H, Luo L, Lin H (2009) Prediction of cell wall lytic enzymes using Chou's amphiphilic pseudo amino acid composition. *Protein & Peptide Letters* 16: 351–355. [Crossref]
75. Du P, Cao S, Li Y (2009) SubChlo: predicting protein subchloroplast locations with pseudo amino acid composition and the evidence-theoretic K-nearest neighbor (ET-KNN) algorithm. *Journal of Theoretical Biology* 261: 330–335. [Crossref]
76. Gao QB, Jin ZC, Ye XF, Wu C, He J (2009) Prediction of nuclear receptors with optimal pseudo amino acid composition. *Analytical Biochemistry* 387: 54–59. [Crossref]
77. 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. *Journal of Theoretical Biology* 257 17–26. [Crossref]
78. http://en.wikipedia.org/wiki/Pseudo_amino_acid_composition, Pseudo amino acid composition, Wikipedia, 2009
79. 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* 37 415–425. [Crossref]
80. Lin H, Wang H, H Ding, YL Chen, QZ Li (2009) Prediction of Subcellular Localization of Apoptosis Protein Using Chou's Pseudo Amino Acid Composition. *Acta Biotheoretica* 57: 321–330. [Crossref]
81. Qiu, 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. *Analytical Biochemistry* 390: 68–73. [Crossref]
82. Xiao X, Wang P, Chou KC (2009) Predicting protein quaternary structural attribute by hybridizing functional domain composition and pseudo amino acid composition. *Journal of Applied Crystallography* 42: 169–173.
83. 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. *Journal of Theoretical Biology* 259: 366–372.
84. Esmaili M, Mohabatkar H, Mohsenzadeh S (2010) Using the concept of Chou's pseudo amino acid composition for risk type prediction of human papillomaviruses. *Journal of Theoretical Biology* 263: 203–209. [Crossref]
85. Gao QB, Ye XF, Jin ZC, He J (2010) Improving discrimination of outer membrane proteins by fusing different forms of pseudo amino acid composition. *Analytical Biochemistry* 398: 52–59. [Crossref]
86. Gu Q, Ding Y, Zhang T, Shen Y (2010) Prediction of G-protein-coupled receptor classes with pseudo amino acid composition. 27: 500–504.
87. 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: 559–567. [Crossref]
88. Kandaswamy KK, Pugalenth G, Moller S, Hartmann E, Kalies KU et al. (2010) Prediction of Apoptosis Protein Locations with Genetic Algorithms and Support Vector Machines Through a New Mode of Pseudo Amino Acid Composition. *Protein and Peptide Letters* 17: 1473–1479.
89. Liu T, Zheng X, Wang C, Wang J (2010) Prediction of Subcellular Location of Apoptosis Proteins using Pseudo Amino Acid Composition: An Approach from Auto Covariance Transformation. *Protein & Peptide Letters* 17: 1263–1269. [Crossref]
90. Mohabatkar H (2010) Prediction of cyclin proteins using Chou's pseudo amino acid composition. *Protein & Peptide Letters* 17 1207–1214. [Crossref]
91. Nanni H, Brahnam S, Lumini A (2010) High performance set of PseAAC and sequence based descriptors for protein classification. *Journal of Theoretical Biology* 266: 1–10. [Crossref]
92. Niu XH, Li NN, Shi F, Hu XH, Xia JB, et al. (2010) Predicting protein solubility with a hybrid approach by pseudo amino acid composition. *Protein and Peptide Letters* 17: 1466–1472. [Crossref]
93. 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: 715–722. [Crossref]
94. 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: 320–327.
95. Wang YC, Wang XB, Yang ZX, Deng NY (2010) Prediction of enzyme subfamily class via pseudo amino acid composition by incorporating the conjoint triad feature. *Protein & Peptide Letters* 17: 1441–1449. [Crossref]
96. Wu J, Li ML, Yu LZ, Wang C (2010) An ensemble classifier of support vector machines used to predict protein structural classes by fusing auto covariance and pseudo amino acid composition. *Protein J* 29: 62–67. [Crossref]
97. YuL, Guo Y, LiY, Li G, Li M (2010) SecretP: Identifying bacterial secreted proteins by fusing new features into Chou's pseudo amino acid composition. *Journal of Theoretical Biology* 267: 1–6. [Crossref]
98. Ding H, Liu L, Guo FB, Huang J, Lin H (2011) Identify Golgi protein types with modified mahalanobis discriminant algorithm and pseudo amino acid composition. *Protein & Peptide Letters* 18: 58–63. [Crossref]
99. 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: 1612–1617. [Crossref]
100. Hayat M, Khan A (2011) Predicting membrane protein types by fusing composite protein sequence features into pseudo amino acid composition. *Journal of Theoretical Biology* 271: 10–17. [Crossref]
101. Hu L, Zheng L, Wang Z, Li B, Liu L (2011) Using pseudo amino acid composition to predict protease families by incorporating a series of protein biological features. *Protein and Peptide Letters* 18: 552–558. [Crossref]

102. Y Huang, L Yang, T Wang (2011) Phylogenetic analysis of DNA sequences based on the generalized pseudo amino acid composition. *Journal of Theoretical Biology* 269: 217–223. [Crossref]
103. X Jingbo, Z Silan, S Feng, X Huijuan, H Xuehai, et al. (2011) Using the concept of pseudo amino acid composition to predict resistance gene against *Xanthomonas oryzae* pv. *oryzae* in rice: An approach from chaos games representation. *Journal of Theoretical Biology* 284: 16–23. [Crossref]
104. B Liao, JB Jiang, QG Zeng, W Zhu (2011) Predicting Apoptosis Protein Subcellular Location with PseAAC by Incorporating Tripeptide Composition. *Protein & Peptide Letters* 18: 1086–1092. [Crossref]
105. Lin H, Ding H (2011) Predicting ion channels and their types by the dipeptide mode of pseudo amino acid composition. *Journal of Theoretical Biology* 269: 64–69. [Crossref]
106. 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: 1219–1225. [Crossref]
107. 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: 16963–16968.
108. Liu XL, Lu JL, Hu XH (2011) Predicting Thermophilic Proteins with Pseudo Amino Acid Composition: Approached from Chaos Game Representation and Principal Component Analysis. *Protein & Peptide Letters* 18: 1244–1250. [Crossref]
109. Mahdavi A, Jahandideh S (2011) Application of density similarities to predict membrane protein types based on pseudo amino acid composition. *Journal of Theoretical Biology* 276: 132–137. [Crossref]
110. Mohabatkar H, Mohammad Beigi M, Esmaili A (2011) Prediction of GABA(A) receptor proteins using the concept of Chou's pseudo amino acid composition and support vector machine. *Journal of Theoretical Biology* 281: 18–23. [Crossref]
111. Mohammad B.M, 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: 191–197. [Crossref]
112. Qiu JD, Sun XY, Suo SB, Shi SP, Huang SY, et al. (2011) Predicting homo-oligomers and hetero-oligomers by pseudo amino acid composition: an approach from discrete wavelet transformation. *Biochimie* 93: 1132–1138. [Crossref]
113. 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. [Crossref]
114. Shi R, Xu C (2011) Prediction of rat protein subcellular localization with pseudo amino acid composition based on multiple sequential features. *Protein and Peptide Letters* 18: 625–633. [Crossref]
115. Shu M, Cheng X, Zhang Y, Wang Y, Lin Y (2011) Predicting the Activity of ACE Inhibitory Peptides with a Novel Mode of Pseudo Amino Acid Composition. *Protein & Peptide Letters* 18: 1233–1243. [Crossref]
116. Wang D, Yang L, Fu Z, Xia J (2011) Prediction of thermophilic protein with pseudo amino acid composition: an approach from combined feature selection and reduction. *Protein & Peptide Letters* 18: 684–689. [Crossref]
117. Wang W, Geng XB, Dou Y, Liu T, Zheng X (2011) Predicting protein subcellular localization by pseudo amino acid composition with a segment-weighted and features-combined approach. *Protein and Peptide Letters* 18: 480–487. [Crossref]
118. Xiao X, Chou KC (2011) Using pseudo amino acid composition to predict protein attributes via cellular automata and other approaches. *Current Bioinformatics* 6: 251–260.
119. Xiao X, Wang P, Chou KC (2011) GPCR-2L: Predicting G protein-coupled receptors and their types by hybridizing two different modes of pseudo amino acid compositions. *Molecular Biosystems* 7: 911–919. [Crossref]
120. Zia Ur R, Khan A (2011) Prediction of GPCRs with Pseudo Amino Acid Composition: Employing Composite Features and Grey Incidence Degree Based Classification. *Protein & Peptide Letters* 18: 872–878. [Crossref]
121. Zou D, He Z, He J, Xia Y (2011) Supersecondary structure prediction using Chou's pseudo amino acid composition. *Journal of Computational Chemistry* 32: 271–278. [Crossref]
122. 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: 1163–1169. [Crossref]
123. 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. [Crossref]
124. Chen YL, Li QZ, Zhang LQ (2012) Using increment of diversity to predict mitochondrial proteins of malaria parasite: integrating pseudo amino acid composition and structural alphabet. *Amino Acids* 42: 1309–1316. [Crossref]
125. 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. *Analytical Biochemistry* 425: 117–119. [Crossref]
126. 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. *Journal of Theoretical Biology* 304: 88–95. [Crossref]
127. 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. [Crossref]
128. Gao QB, Zhao H, Ye X, He J (2012) Prediction of pattern recognition receptor family using pseudo amino acid composition. *Biochemical and Biophysical Research Communications* 417: 73–77. [Crossref]
129. 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: 411–421. [Crossref]
130. 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. [Crossref]
131. 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. [Crossref]
132. Lin WZ, Fang JA, Xiao X, Chou KC (2012) Predicting Secretory Proteins of Malaria Parasite by Incorporating Sequence Evolution Information into Pseudo Amino Acid Composition via Grey System Model.
133. 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. [Crossref]
134. Mei S (2012) Multi-kernel transfer learning based on Chou's PseAAC formulation for protein submitochondria localization. *Journal of Theoretical Biology* 293: 121–130. [Crossref]
135. Mei S (2012) Predicting plant protein subcellular multi-localization by Chou's PseAAC formulation based multi-label homolog knowledge transfer learning. *Journal of Theoretical Biology* 310: 80–87. [Crossref]
136. Nanni L, Brahnam S, Lumini A (2012) Wavelet images and Chou's pseudo amino acid composition for protein classification. *Amino Acids* 43: 657–665. [Crossref]
137. 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: 467–475.
138. 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: 940–948. [Crossref]
139. Qin YF, Wang CH, Yu XQ, Zhu J, Liu TG (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. [Crossref]
140. 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: 1170–1176. [Crossref]
141. Sun XY, Shi SP, Qiu JD, Suo SB, Huang SY (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: 3178–3184.
142. Wang J, Li Y, Wang Q, You X, Man J et al. (2012) ProClusEnsem: predicting membrane protein types by fusing different modes of pseudo amino acid composition. *Comput Biol Med* 42: 564–574. [Crossref]
143. Yu X, Zheng X, Liu T, Dou Y, Wang J (2012) Predicting subcellular location of apoptosis proteins with pseudo amino acid composition: approach from amino acid substitution matrix and auto covariance transformation. *Amino Acids* 42: 1619–1625. [Crossref]
144. Zhao XW, Ma ZQ, Yin MH (2012) Predicting protein-protein interactions by combining various sequence-derived features into the general form of Chou's Pseudo amino acid composition. *Protein & Peptide Letters* 19: 492–500. [Crossref]
145. 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: 890–903. [Crossref]
146. Cao DS, Xu QS, Liang YZ (2013) propy: a tool to generate various modes of Chou's PseAAC. *Bioinformatics* 29: 960–962. [Crossref]
147. 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. [Crossref]

148. 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. *Journal of Theoretical Biology* 318: 1–12. [Crossref]
149. 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. *Pocess Biochemistry* 48: 1048–1053.
150. 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. *Journal of Theoretical Biology* 334: 45–51. [Crossref]
151. 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: 41–48.
152. 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. [Crossref]
153. 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: 50–57. [Crossref]
154. 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: 327–34. [Crossref]
155. 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. *Journal of Theoretical Biology* 335: 205–12. [Crossref]
156. Khosravian M, Faramarzi FK, Beigi MM, Behbahani M, Mohabatkari 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. [Crossref]
157. Lin H, Ding C, Yuan LF, Chen W, Ding H (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 Biomathematics*
158. 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 Biomathematics*
159. 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.
160. Mohabatkari 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. [Crossref]
161. 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. *Transactions on Nanobioscience* 12: 311–320. [Crossref]
162. 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. *International Journal of Quantum Chemistry* 113: 1660–1667.
163. 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: 781–795. [Crossref]
164. 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. *Journal of Theoretical Biology* 323: 40–48. [Crossref]
165. 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. [Crossref]
166. Xiao X, Min JL, Wang P, Chou KC (2013) iCDI-PseFpt: Identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. *Journal of Theoretical Biology* 337: 71–79. [Crossref]
167. Xiaohui N, Nana L, Jingbo X, Dingyan C, Yuehua P (2013) Using the concept of Chou's pseudo amino acid composition to predict protein solubility: An approach with entropies in information theory. *Journal of Theoretical Biology* 332: 211–217. [Crossref]
168. 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. [Crossref]
169. Xu Y, Ding J, Wu LY, Chou KC (2013) iSNO-PseAAC: Predict cysteine S-nitrosylation sites in proteins by incorporating position specific amino acid propensity into pseudo amino acid composition
170. Xu Y, Shao XJ, Wu LY, Deng NY, Chou KC (2013) iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine S-nitrosylation sites in proteins. *PeerJ*
171. 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: 3495–3506.
172. Hajisharifi Z, Piryaei M, Mohammad Beigi M, Behbahani M, Mohabatkari H (2014) Predicting anticancer peptides with Chou's pseudo amino acid composition and investigating their mutagenicity via Ames test. *Journal of Theoretical Biology* 341: 34–40. [Crossref]
173. 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. [Crossref]
174. Hayat M, Iqbal N (2014) Discriminating protein structure classes by incorporating Pseudo Average Chemical Shift to Chou's general PseAAC and Support Vector Machine. *Comput Methods Programs Biomed* 116: 184–192. [Crossref]
175. 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: 10410–10423. [Crossref]
176. 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. [Crossref]
177. Li L, Yu S, Xiao W, Li Y, Li M (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.
178. Liu B, Xu J, Lan X, Xu R, Zhou J (2014) iDNA-ProTdis: identifying DNA-binding proteins by incorporating amino acid distance-pairs and reduced alphabet profile into the general pseudo amino acid composition.
179. Mondal S, Pai PP (2014) Chou's pseudo amino acid composition improves sequence-based antifreeze protein prediction. *J Theor Biol* 356: 30–35. [Crossref]
180. 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. [Crossref]
181. Qiu WR, Xiao X, Chou KC (2014) iRSpot-TNCPseAAC: Identify recombination spots with trinucleotide composition and pseudo amino acid components. *Int J Mol Sci* 15: 1746–1766. [Crossref]
182. Qiu WR, Xiao X, Lin WZ, Chou KC (2014) iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. *Biomed Res Int*. [Crossref]
183. Xu Y, Wen X, Shao XJ, Deng NY, Chou KC (2014) iHyd-PseAAC: Predicting hydroxyproline and hydroxylysine in proteins by incorporating dipeptide position-specific propensity into pseudo amino acid composition. *International Journal of Molecular Sciences* 15: 7594–7610. [Crossref]
184. Xu Y, Wen X, Wen LS, Wu LY, K.C. Chou (2014) iNitro-Tyr: Prediction of nitrotyrosine sites in proteins with general pseudo amino acid composition.
185. 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. *Journal of Theoretical Biology* 363: 412–418. [Crossref]
186. 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: 11204–11219. [Crossref]
187. 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. [Crossref]
188. Zuo YC, Peng Y, Liu L, Chen W, Yang L (2014) Predicting peroxidase subcellular location by hybridizing different descriptors of Chou's pseudo amino acid patterns. *Anal Biochem* 458: 14–19. [Crossref]
189. 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. *Comput Methods Programs Biomed* 122: 165–174. [Crossref]
190. 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. [Crossref]
191. Chen L, Chu C, Huang T, Kong X, Cai YD (2015) Prediction and analysis of cell-penetrating peptides using pseudo amino acid composition and random forest models. *Amino Acids* 47: 1485–1493. [Crossref]
192. Dehzangi A, Heffernan R, Sharma A, Lyons J, Paliwal K (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. [Crossref]

193. 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. [Crossref]
194. 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. [Crossref]
195. Jia J, Liu Z, Xiao X, Chou KC (2015) iPPI-Esml: an ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. *J Theor Biol* 377: 47–56. [Crossref]
196. Ju Z, Cao JZ, Gu H (2015) iLM-2L: A two-level predictor for identifying protein lysine methylation sites and their methylation degrees by incorporating K-gap amino acid pairs into Chou's general PseAAC. *J Theor Biol* 385: 50–57. [Crossref]
197. 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. [Crossref]
198. 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. [Crossref]
199. Liu B, Chen J, Wang X (2015) Protein remote homology detection by combining Chou's distance-pair pseudo amino acid composition and principal component analysis. *Mol Genet Genomics* 290: 1919–1931.
200. 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. [Crossref]
201. Liu B, Xu J, Fan S, Xu R, 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. [Crossref]
202. 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. *Med Biol Eng Comput* 53: 331–344. [Crossref]
203. Sanchez V, Peinado AM, Perez-Cordoba JL, Gomez AM (2015) A new signal characterization and signal-based Chou's PseAAC representation of protein sequences. *J Bioinform Comput Biol* 13: 1550024. [Crossref]
204. 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. [Crossref]
205. 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: 2639–2645. [Crossref]
206. Xu R, Zhou J, Liu B, He Y, Zou Q, et al. (2015) Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. *Journal of Biomolecular Structure & Dynamics (JBSD)* 33: 1720–1730. [Crossref]
207. Zhang M, Zhao B, X. Liu (2015) Predicting industrial polymer melt index via incorporating chaotic characters into Chou's general PseAAC. *Chemometrics and Intelligent Laboratory Systems (CHEMOLAB)* 146: 232–240.
208. Zhang S (2015) Accurate prediction of protein structural classes by incorporating PSSM and PSSM into Chou's general PseAAC. *Chemometrics and Intelligent Laboratory Systems (CHEMOLAB)* 142: 28–35.
209. Zhu PP, Li WC, Zhong ZJ, Deng EZ, Ding H, et al. (2015) Predicting the subcellular localization of mycobacterial proteins by incorporating the optimal tripeptides into the general form of pseudo amino acid composition. *Mol Biosyst* 11: 558–563.
210. 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: 293–304.
211. 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. [Crossref]
212. 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. [Crossref]
213. Jia J, Liu Z, Xiao X, Liu B, Chou KC (2016) 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)* 34: 1946–1961. [Crossref]
214. 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. *Journal of Theoretical Biology* 394: 223–230. [Crossref]
215. Jia J, Liu Z, Xiao X, Liu B, Chou KC (2016) iCar-PseCp: Identify carbonylation sites in proteins by Monto Carlo sampling and incorporating sequence coupled effects into general PseAAC. *Oncotarget* 7: 34558–34570. [Crossref]
216. Jia J, Zhang L, Liu Z, Xiao X, Chou KC (2016) pSumo-CD: Predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. *Bioinformatics* 32: 3133–3141. [Crossref]
217. 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. [Crossref]
218. 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. [Crossref]
219. 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: 285–96. [Crossref]
220. Qiu WE, Sun BQ, Xiao X, Xu ZC, Chou KC (2016) iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. *Oncotarget* 7: 44310–44321. [Crossref]
221. 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. [Crossref]
222. Tang H, Chen W, Lin H (2016) Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. *Mol Biosyst* 12: 1269–1275. [Crossref]
223. Tiwari AK (2016) Prediction of G-protein coupled receptors and their subfamilies by incorporating various sequence features into Chou's general PseAAC. *Comput Methods Programs Biomed* 134: 197–213. [Crossref]
224. 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. [Crossref]
225. 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: 23–29. [Crossref]
226. Zou HL, Xiao X (2016) Classifying Multifunctional Enzymes by Incorporating Three Different Models into Chou's General Pseudo Amino Acid Composition (doi:10.1007/s00232-016-9904-3). *J Membr Biol* 249: 561–567. [Crossref]
227. Cheng X, Xiao X, Chou KC (2017) pLoc-mPlant: Predict subcellular localization of multi-location plant proteins via incorporating the optimal GO information into general PseAAC. *Molecular BioSystems* 13: 1722–1727. [Crossref]
228. Cheng X, Xiao X, Chou KC (2017) pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. *Gene* 628: 315–321. [Crossref]
229. 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.
230. Ju Z, He JJ (2017) Prediction of lysine crotonylation sites by incorporating the composition of k-spaced amino acid pairs into Chou's general PseAAC. *J Mol Graph Model* 77: 200–204. [Crossref]
231. Khan M, Hayat M, Khan SA, Iqbal N (2017) Unb-DPC: Identify mycobacterial membrane protein types by incorporating un-biased dipeptide composition into Chou's general PseAAC. *J Theor Biol* 415: 13–19.
232. Liang Y, Zhang S (2017) Predict protein structural class by incorporating two different modes of evolutionary information into Chou's general pseudo amino acid composition. *J Mol Graph Model* 78: 110–117.
233. Liu LM, Xu Y, Chou KC (2017) 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* 13: 552–559. [Crossref]
234. Meher PK, Sahu TK, Saini V, Rao AR (2017) Predicting antimicrobial peptides with improved accuracy by incorporating the compositional, physico-chemical and structural features into Chou's general PseAAC. *Sci Rep* 7: 42362. [Crossref]
235. Qiu WR, Sun BQ, Xiao X, Xu D, Chou KC (2017) iPhos-PseEvo: Identifying human phosphorylated proteins by incorporating evolutionary information into general PseAAC via grey system theory. *Molecular Informatics* 36: 5–6. [Crossref]
236. Qiu WR, Zheng QS, Sun BQ, Xiao X (2017) Multi-iPPseEvo: A Multi-label Classifier for Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into Chou's General PseAAC via Grey System Theory. *Mol Inform* 36.
237. Rahimi M, Bakhtiarizadeh 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.
238. 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. [Crossref]
239. Xiao X, Cheng X, Su S, Nao Q, Chou KC (2017) pLoc-mGpos: Incorporate key gene ontology information into general PseAAC for predicting subcellular localization of Gram-positive bacterial proteins. *Natural Science* 9: 331–349.

240. Xu C, Ge L, Zhang Y, Dehmer M, Gutman I (2017) Prediction of therapeutic peptides by incorporating q-Wiener index into Chou's general PseAAC. *J Biomed Inform* 75: 63–69.
241. Xu Y, Wang Z, Li C, Chou KC (2017) iPreny-PseAAC: Identify C-terminal cysteine prenylation sites in proteins by incorporating two tiers of sequence couplings into PseAAC. *Med Chem* 13: 544–551. [Crossref]
242. 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. [Crossref]
243. 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.
244. 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. [Crossref]
245. 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. [Crossref]
246. 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. [Crossref]
247. Butt AH, Rasool N, Khan YD (2018) Predicting membrane proteins and their types by extracting various sequence features into Chou's general PseAAC. *Mol Biol Rep* 45: 2295–2306. [Crossref]
248. Cheng X, Xiao X, Chou KC (2018) pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. *Genomics* 110: 50–58. [Crossref]
249. Cheng X, Xiao X, Chou KC (2018) pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. *Genomics* 110: 231–239. [Crossref]
250. Cheng X, Xiao X, Chou KC (2018) pLoc-mHum: Predict subcellular localization of multi-location human proteins via general PseAAC to winnow out the crucial GO information. *Bioinformatics* 34 (2018) 1448–1456.
251. Cheng X, Xiao X, Chou KC (2018) pLoc_bal-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. *Journal of Theoretical Biology* 458: 92–102. [Crossref]
252. Cheng X, Xiao X, Chou KC (2018) pLoc_bal-mPlant: Predict subcellular localization of plant proteins by general PseAAC and balancing training dataset. *Curr Pharm Des* 24: 4013–4022.
253. 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. [Crossref]
254. 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* 20
255. Ghauri AW, Khan YD, Rasool N, Khan SA, Chou KC (2018) pNitro-Tyr-PseAAC: Predict nitrotyrosine sites in proteins by incorporating five features into Chou's general PseAAC. *Curr Pharm Des* 24: 4034–4043. [Crossref]
256. Javed F, Hayat M (2018) Predicting subcellular localizations of multi-label proteins by incorporating the sequence features into Chou's PseAAC. *Genomics* 111: 1325–1332.
257. Ju Z, Wang SY (2018) Prediction of citrullination sites by incorporating k-spaced amino acid pairs into Chou's general pseudo amino acid composition. *Gene* 664: 78–83. [Crossref]
258. Khan YD, Rasool N, Hussain W, Khan SA, Chou KC (2018) iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. *Analytical Biochemistry* 550: 109–116. [Crossref]
259. Khan YD, Rasool N, Hussain W, Khan SA, Chou KC (2018) iPhosY-PseAAC: Identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. *Mol Biol Rep* 45: 2501–2509. [Crossref]
260. Krishnan MS (2018) Using Chou's general PseAAC to analyze the evolutionary relationship of receptor associated proteins (RAP) with various folding patterns of protein domains. *J Theor Biol* 445: 62–74. [Crossref]
261. Mei J, Fu Y, Zhao J (2018) Analysis and prediction of ion channel inhibitors by using feature selection and Chou's general pseudo amino acid composition. *J Theor Biol* 456: 41–48. [Crossref]
262. 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: 2359.
263. Mei J, Zhao J (2018) Analysis and prediction of presynaptic and postsynaptic neurotoxins by Chou's general pseudo amino acid composition and motif features. *J Theor Biol* 427: 147–153. [Crossref]
264. Mousavizadegan M, Mohabatkar H (2018) Computational prediction of antifungal peptides via Chou's PseAAC and SVM. *J Bioinform Comput Biol*. [Crossref]
265. Rahman SM, Shatabda S, Saha S, Kaykobad M, Sohail Rahman M (2018) DPP-PseAAC: A DNA-binding Protein Prediction model using Chou's general PseAAC. *J Theor Biol* 452: 22–34. [Crossref]
266. Sankari ES, Manimegalai DD (2018) Predicting membrane protein types by incorporating a novel feature set into Chou's general PseAAC. *J Theor Biol* 455: 319–328.
267. Chou KC (2019) Two kinds of metrics for computational biology. *Genomics*.
268. Chou KC (2019) Proposing pseudo amino acid components is an important milestone for proteome and genome analyses. *International Journal for Peptide Research and Therapeutics*.
269. Chou K.C (2019) An insightful recollection for predicting protein subcellular locations in multi-label systems. *Genomics*.
270. Chou KC (2019) Progresses in predicting post-translational modification. *International Journal of Peptide Research and Therapeutics*.
271. Chou KC (2019) Recent Progresses in Predicting Protein Subcellular Localization with Artificial Intelligence (AI) Tools Developed Via the 5-Steps Rule. *Japanese Journal of Gastroenterology and Hepatology* 2: 1–4.
272. Chou KC (2019) An insightful recollection since the distorted key theory was born about 23 years ago. *Genomics*.
273. Chou KC (2019) Artificial intelligence (AI) tools constructed via the 5-steps rule for predicting post-translational modifications. *Trends in Artificial Intelligence* 3: 60–74.
274. Chou KC (2020) Distorted Key Theory and Its Implication for Drug Development. *Current Genomics*.
275. Chou KC (2019) An insightful recollection since the birth of Gordon Life Science Institute about 17 years ago. *Advancement in Scientific and Engineering Research* 4: 31–36.
276. Chou KC (2019) Gordon Life Science Institute: Its philosophy, achievements, and perspective. *Annals of Cancer Therapy and Pharmacology* 2: 1–26.

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