https://www.scirp.org/journal/ns Natural Science, 2020, Vol. 12, (No. 3), pp: 125-161

Gordon Life Science Institute and Its Impacts on Computational Biology and Drug Development

Kuo-Chen Chou

Gordon Life Science Institute, Boston, Massachusetts 02478, USA

Correspondence to: Kuo-Chen Chou, kcchou@gordonlifescience.org, kcchou38@gmail.com

Keywords: Bioinformatics, Drug Development, Reform And Opening, Free Communication, Sweden, Cradle, San Diego, Boston, Door-Opening, Productive and Bi-Productive Outcomes

Received: February 25, 2020 **Accepted:** March 15, 2020 **Published:** March 18, 2020

ABSTRACT

Gordon Life Science Institute is the first Internet Research Institute ever established in the world. It is a non-profit institute. Those scientists who really dedicate themselves to science and loving science more than anything else can become its member. In the friendly door-opened Institute, they can maximize their time and energy to engage in their scientific creativity. They have also believed that science would be more truthful and wonderful if scientists do not have to spend a lot of time on funding application, and that great scientific findings and creations in history were often made by those who were least supported or funded but driven by interesting imagination and curiosity. Recollected in this review article is its establishing and developing processes, as well as its philosophy and accomplishments. Particularly, its productive and by-productive outcomes have covered the following five very hot topics in bioinformatics and drug development: 1) PseAAC and PseKNC; 2) Disported key theory; 3) Wenxiang diagram; 4) Multi-label system prediction; 5) 5-steps rule. Their impacts on the proteomics and genomics as well as drug development are substantially and awesome.

1. INTRODUCTION

The Gordon Life Science Institute was established in 2003 and its cradle was in San Diego of California, USA. Its mission is to develop and apply new mathematical tools and physical concepts for understanding biological phenomena. For a briefing about its history and philosophy, click https://gordonlifescience.org/GordonLifeScience.html.

The Institute is a newly emerging academic organization in the Age of Information and Internet, founded by Professor Dr. Kuo-Chen Chou, right after he was retired from Pfizer Global Research and Development in 2003. Its mission is to develop and apply new mathematical tools and physical concepts for

understanding biological phenomena.

The Institute's name reflects an interesting historical story. After the Cultural Revolution, China started to open its door, the founder was invited by Professor Sture Forsén, the then Chairman of Nobel Prize Committee, to work in Chemical Center of Lund University as a Visiting Professor. To make Swedish people easier to pronounce his name, Professor Chou used "Gordon" as his name in Sweden. About a quarter of century later, the same name was used for the Institute, meaning that "Reform and Opening" and "Free Communication" can stimulate a lot of great creativities.

The current liaison site of Gordon Life Science Institute is in Boston of Massachusetts, USA; gls@gordonlifescience.org.

2. MISSION AND ORGANIZATION

The Institute has no physical boundaries. Its members do not have to work in a same building or campus. Distributed over different countries of the world (**Figure 1**), they shall freely collaborate, exchange ideas, and share information and findings via a variety of modern communication methods. This versatile system allows the members to focus completely on science without having to cope with the troubles in obtaining visas and in paying for relocation expenses, among many others.

The Gordon Life Science Institute is a non-profit organization. It is a gift to science and human beings. Its founding principle is to pursue the excellence in science: anyone who has proved his/her creativity in science can become a member regardless of his/her age, occupation, and nationality. Accordingly, the Institute has provided an ideal society or organization for those scientists who really dedicate themselves to science and loving science more than anything else. In the friendly door-opened Institute, these scientists can maximize their time and energy to engage in their scientific creativity.

Members of the Institute believe science would be more truthful and wonderful if scientists do not have to spend a lot of time on funding application. We also note that great scientific findings and creations in history were often made by those who were least supported or funded but driven by interesting imagination and curiosity. As pointed out by Albert Einstein, "Imagination is more important than knowledge. For knowledge is limited, whereas imagination embraces the entire world, stimulating progress, giving birth to evolution".

Figure 1. A schematic illustration to show the members of Gordon Life Science Institute are distributed over different countries of the world, exchanging ideas and findings via a variety of modern communication methods.

3. ACCOMPLISHMENTS

Up to March 2019, the Institute has 26 members. Among them 5 have been selected by Thompson Reuter and Clarivate Analytics as the "Highly Cited Researcher": 1) Kuo-Chen Chou for continuously 5 years (2014, 2015, 2016, 2017, and 2018), 2) Hong-Bin Shen (2014 and 2015), 3) Wei Chen (2018), 4) Hao Lin (2018), and 5) Xoan Xiao (2018).

Listed below are just some represented works produced by the Gordon Life Science Institute.

3.1. Extension of Special PseAAC to the General One

With the explosive growth of biological sequences in the post-genomic era, one of the most challenging problems in computational biology is how to express a biological sequence with a discrete model or a vector, yet still keep considerable sequence-order information or key pattern characteristic. This is because all the existing machine-learning algorithms (such as "Optimization" algorithm [1], "Covariance Discriminant" or "CD" algorithm [2, 3], "Nearest Neighbor" or "NN" algorithm [4], and "Support Vector Machine" or "SVM" algorithm [4, 5]) can only handle vectors as elaborated in a comprehensive review [6]. However, a vector defined in a discrete model may completely lose all the sequence-pattern information. To avoid completely losing the sequence-pattern information for proteins, the pseudo amino acid composition [7] or PseAAC [8] was proposed. Ever since then, it has been widely used in nearly all the areas of computational proteomics [3, 9-61, 58-60, 62-272].

Because it has been widely and increasingly used, four powerful open access soft-wares, called "PseAAC" [273], "PseAAC-Builder" [274], "propy" [275], and "PseAAC-General" [276], were established: the former three are for generating various modes of Chou's special PseAAC [276]; while the 4th one for those of Chou's general PseAAC [278], including not only all the special modes of feature vectors for proteins but also the higher level feature vectors such as "Functional Domain" mode (see Eqs.9-10 of [278]), "Gene Ontology" mode (see Eqs.11-12 of [278]), and "Sequential Evolution" or "PSSM" mode (see Eqs.13-14 of [278]).

3.2. Extension of PseAAC to PseKNC

Encouraged by the successes of using PseAAC to deal with protein/peptide sequences, the concept of PseKNC (Pseudo K-tuple Nucleotide Composition) [279] was developed for generating various feature vectors for DNA/RNA sequences that have proved very useful as well [268, 279-295]. Particularly, in 2015 a very powerful web-server called "Pse-in-One" [296] and its updated version "Pse-in-One2.0" [297] have been established that can be used to generate any desired feature vectors for protein/peptide and DNA/RNA sequences according to the need of users' studies.

3.3. Distorted Key Theory for Peptide Drugs

According to Fisher's "lock and key" model [298], Koshland's "induced fit" theory [298], and the "rack mechanism" [299], the prerequisite condition for a peptide to be cleaved by the disease-causing enzyme is a good fit and tightly binding with the enzyme's active site (**Figure 2**). However, such a peptide, after a modification on its scissile bond with some simple chemical procedure, will no longer be cleavable by the enzyme but it can still tightly bind to its active site. An illustration about the distorted key theory is given in **Figure 3**, where panel 1) shows an effective binding of a cleavable peptide to the active site of HIV protease, while panel 2) the peptide has become a non-cleavable one after its scissile bond is modified although it can still bind to the active site. Such a modified peptide, or "distorted key", will automatically become an inhibitor candidate against HIV protease. Even for non-peptide inhibitors, the information derived from the cleavable peptides can also provide useful insights about the key binding groups and fitting conformation in the sense of microenvironment. Besides, peptide drugs usually have no toxicity in vivo under the physiological concentration [300]. For more discussion about the distorted key theory, see a comprehensive review paper [301]. It was based on such a distorted key theory that many investigators

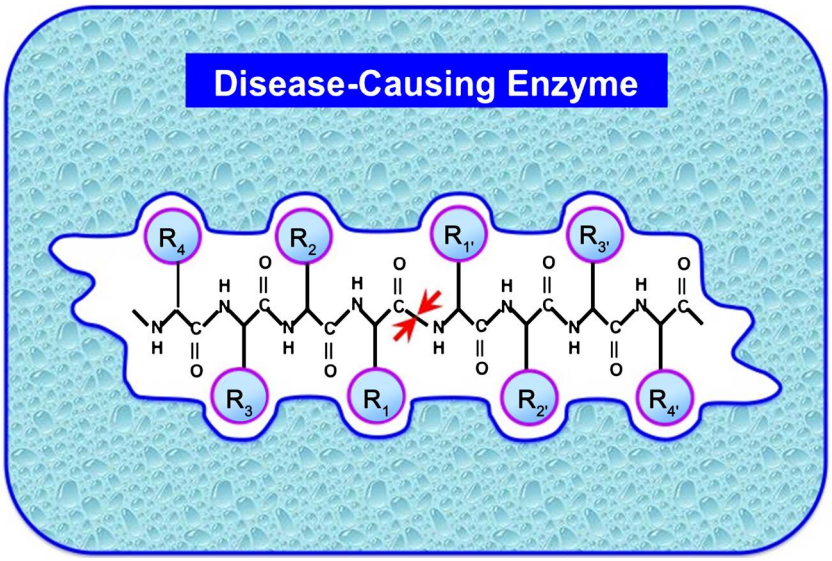

Figure 2. A schematic illustration to show a peptide in good fitting and tightly binding with the enzyme's active site before it is cleaved by the latter. Adapted from [301] with permission.

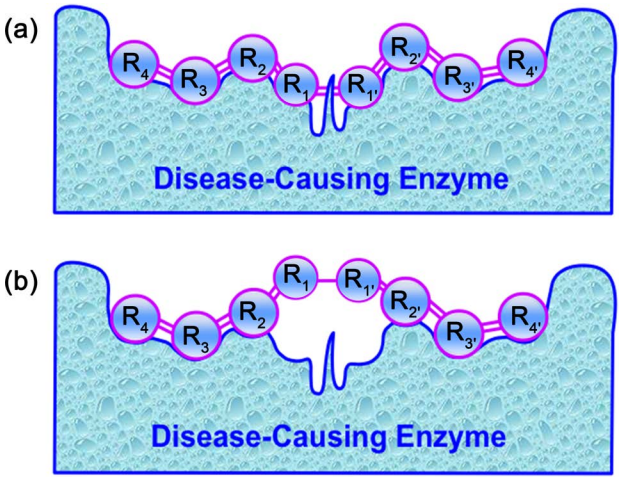

Figure 3. Schematic drawing to illustrate the "Distorted Key" theory, where panel (a) shows an effective binding of a cleavable peptide to the active site of a disease-causing enzyme, while panel (b) the same peptide has become a non-cleavable one after its scissile bond is modified although it can still bind to the active site. Such a modified peptide, or "distorted key", will automatically become an inhibitor candidate against the disease-causing enzyme. Adapted from [301] with permission.

were enthusiastic to develop various methods for predicting the protein cleavage sites by disease-causing enzymes (see, e.g., [300, 302-307]). Furthermore, a web-server called "HIVcleave" [304] has been established for predicting HIV protease cleavage sites in proteins. Its website address is at http://chou.med.harvard.edu/bioinf/HIV/.

3.4. Introduction of Wenxiang Diagram

Using graphic approaches to study biological and medical systems can provide an intuitive vision and useful insights for helping analyze complicated relations therein, as indicated by many previous studies on a series of important biological topics (see, e.g., [308]). The "wenxiang" diagram (**Figure 4**) [309, 310] is a

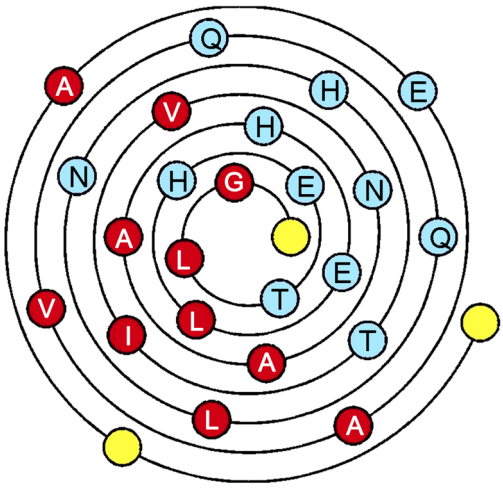

Figure 4. Schematic drawing to show the "wenxiang diagram". Adapted from [309] with permission.

special kind of graphical approach, which is very useful for in-depth studying protein-protein interaction mechanism [311, 312]. Also, the wenxiang diagram has also been used to study drug-metabolism system [313]. The name of "wenxiang" came from that its shape looks quite like the Chinese wenxiang (蚊香), a coil-like incense widely used in China to repel mosquitos. In the wenxiang graphs each residue is represented by a circle with a letter to indicate its code: a hydrophobic residue is denoted by a filled circle with a white code symbol, a hydrophilic residue is denoted by an open circle with a black code symbol, whereas the invalid residue is denoted by a yellow-filled circle.

3.5. Predictors for Multi-Label Systems

Information of subcellular localization for a protein is indispensable for revealing its biological function. Therefore, one of the fundamental goals in molecular cell biology and proteomics is to determine the subcellular locations of proteins in an entire cell. Before 2007, most efforts in this regard were focused on the single-label system by assuming that each of the constitute proteins in a cell had one, and only one, subcellular location (see, e.g., [314-318]). However, with more experimental data uncovered, it has been found that many proteins may simultaneously occur or move between two or more location sites in a cell and hence need multiple labels to mark them. Proteins with multiple locations are also called multiplex proteins [319, 320], which are often the special targets for drug development [320-326]). Therefore, how to deal with this kind of multi-label systems is a critical challenge. To take the challenge, the Institute has developed the following four series of predictors: 1) [320, 327-333]; 2) [334-339]; 3) [203, 204, 215, 224-226, 340]; 4) [227-230, 254, 265, 266]. All these predictors have yielded very high success rates, both globally and locally, as summarized in a comprehensive review paper [341]. In studying the multi-label systems, we need two kinds of metrics to measure performance quality of a predictor: one is for the accuracy of global prediction and the other for the accuracy of local prediction [342]. As a showcase, let us consider the multi-label predictor of pLoc_bal-mHum [229], which was developed for studying the 14 organelles or subcellular locations (**Figure 5**) in a human cell. 1) Click the link at http://www.jci-bioinfo.cn/pLoc_bal-mHum/, you'll see the top page of the predictor prompted on your computer screen (**Figure 6**). 2) You can either type or copy/paste the sequences of query human proteins into the input box at the center of **Figure 6**. The input sequence should be in the FASTA format. You can click the Example button right above the input box to see the sequences in FASTA format. c) Click on the Submit button to see the predicted result; e.g., if you use the four protein sequences in the Example window as the input, after 10 seconds or so, you will see a new screen (**Figure 7**) occurring. On its upper part are listed the names of the subcellular locations numbered from (1) to (14) covered by the current predictor. On its lower part are the predicted results: the query protein "O15382" of example-1 corresponds to "10", meaning it belongs to "Mitochondrion" only;

the query protein "P08962" of example-2 corresponds to "8, 13", meaning it belongs to "Lysosome" and "Plasma membrane"; the query protein "P12272" of example-3 corresponds to "2, 6, 11", meaning it belongs to "Cytoplasm", "Extracellular", and "Nucleus". All these results are perfectly consistent with experimental observations.

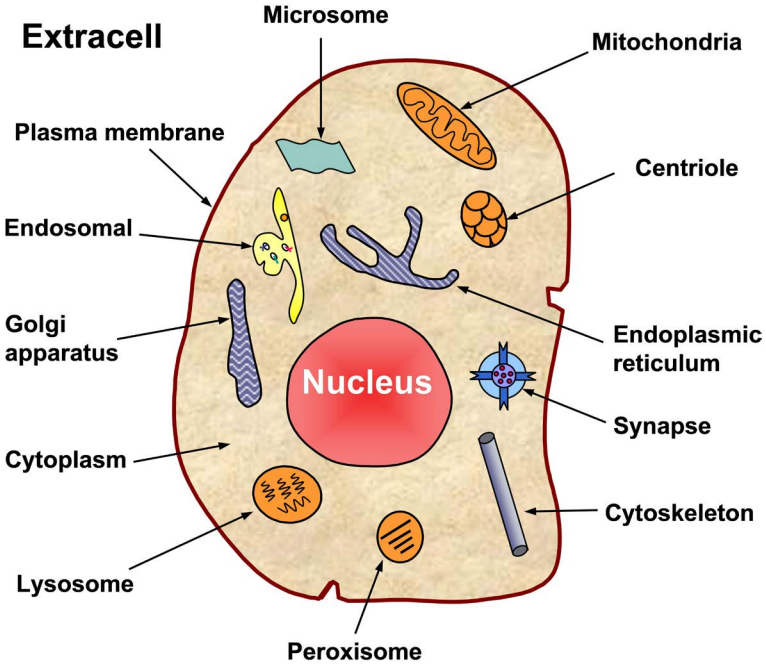

Figure 5. Schematic illustration to show the 14 subcellular locations of human proteins: 1) centriole, 2) cytoplasm, 3) cytoskeleton, 4) endoplasmic reticulum, 5) endosome, 6) extra cell, 7) Golgi apparatus, 8) lysosome, 9) microsome, 10) mitochondrion, 11) nucleus, 12) peroxisome, 13) plasma membrane, and 14) synapse. Adapted from [439] with permission.

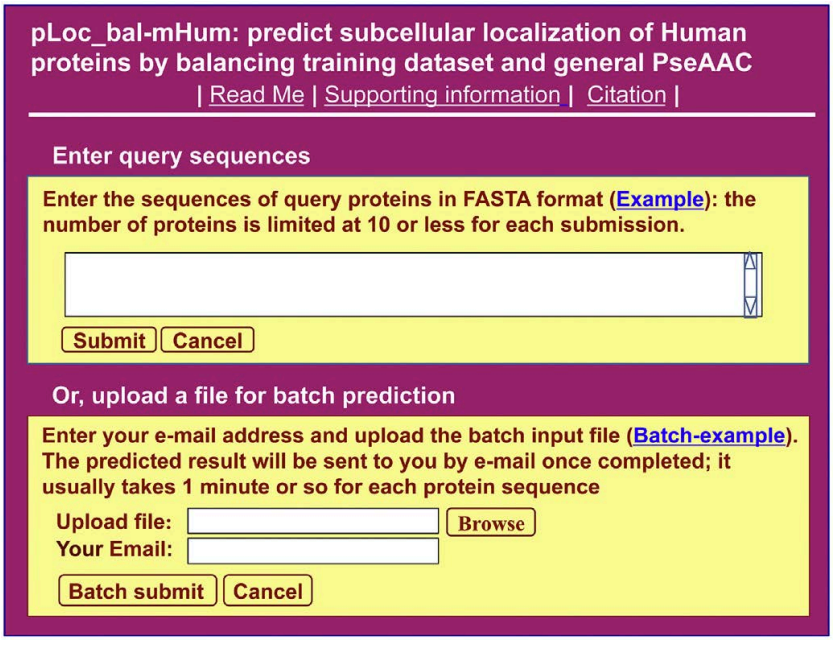

Figure 6. A semi-screenshot for the top page of pLoc_bal-mHum. Adapted from [229] with permission.

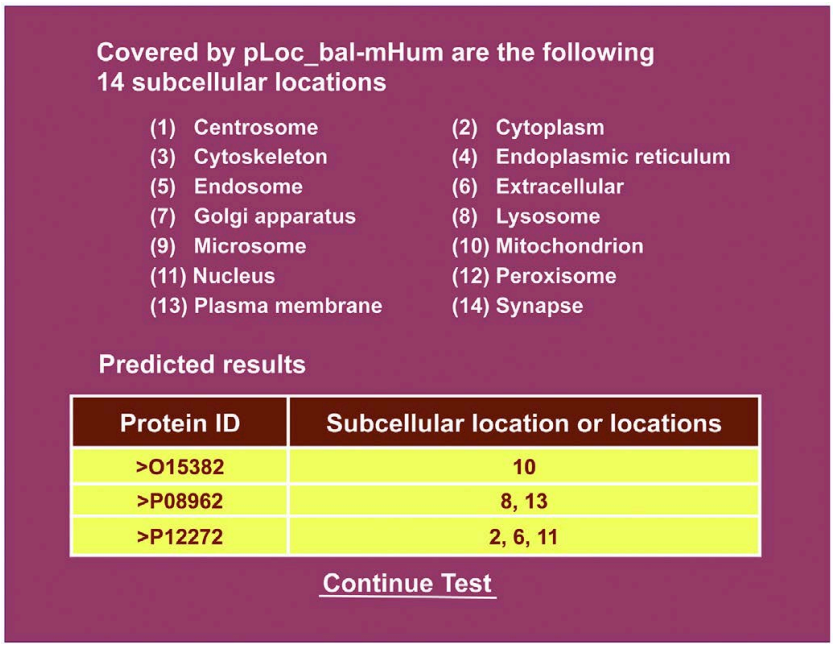

Figure 7. A semi-screenshot for the webpage obtained by following Step 3 of Section 2.4. Adapted from [229] with permission.

3.6. Five-Steps Rule

The Institute was the birth place of the famous 5-steps rule [278], which has been used in nearly all the areas of computational biology [203, 204, 215, 224-230, 233, 251, 254-256, 259-261, 264, 265, 283, 285, 294, 340, 341, 343-382]), material science [383], and even the commercial science (e.g., the bank account systems). The only difference between them is how to formulate the statistical samples or events with an effective mathematical expression that can truly reflect their intrinsic correlation with the target to be predicted. It just likes the case of many machine-learning algorithms. They can be widely used in nearly all the areas of statistical analysis.

Working in such Institute filled with this kind of philosophy and atmosphere, the scientists would be more prone to be stimulated by the eight pioneering papers from the then Chairman of Nobel Prize Committee Sture Forsen [384-391] and many of their follow-up papers [172, 189, 310, 311, 392-430], so as to drive them substantially more creative and productive.

4. CONCLUSION AND PERSPECTIVE

In comparison with the conventional institutes, Gordon Life Science Institute has the following unique advantages: it can 1) attract those scientists who are really loving science more than anything else; 2) maximize their creativity in science and minimize the distraction or disturbance caused by the relocation and various followed-up tedious things; 3) provide them with an ideal environment to completely focus on doing science; 4) drive their motivation by insightful imagination and intriguing curiosity; and 5) create the atmosphere to guide their scientific results more truthful, fantastic, wonderful, and awesome.

Accordingly, it would not be surprising to see that a total of five members of Gordon Life Scientist have been selected by Clarivate Analytics as Highly Cited Researcher or HCR (see Section 3), indicating that for the ratio of HCR per member, the "Gordon Life Science Institute" has already exceeded the "Broad Institute of MIT and Harvard, USA", becoming the top in the world.

It is anticipated that more significant accomplishments will be achieved by the Gordon Life Science Institute for many years to come, as indicated by a series of very recent papers (see, e.g., [230, 431-438]).

ETHICAL APPROVAL STATEMENT

This article does not contain any studies with human or animal participants.

CONFLICTS OF INTEREST

The author declares no conflicts of interest regarding the publication of this paper.

REFERENCES

1. Zhang, C.T. and Chou, K.C. (1992) An optimization Approach to Predicting Protein Structural Class from Amino acid Composition. *Protein Science*, **1**, 401-408. https://doi.org/10.1002/pro.5560010312
2. Chou, K.C. and Elrod, D.W. (2002) Bioinformatical Analysis of G-Protein-Coupled Receptors. *Journal of Proteome Research*, **1**, 429-433. https://doi.org/10.1021/pr025527k
3. Chou, K.C. and Cai, Y.D. (2003) Prediction and Classification of Protein Subcellular Location: Sequence-Order Effect and Pseudo Amino Acid Composition. *Journal of Cellular Biochemistry*, **90**, 1250-1260. (Addendum, ibid., 2004, Vol. 91, 1085) https://doi.org/10.1002/jcb.10719
4. Hu, L., Huang, T., Shi, X., Lu, W.C., Cai, Y.D. and Chou, K.C. (2011) Predicting Functions of Proteins in Mouse Based on Weighted Protein-Protein Interaction Network and Protein Hybrid Properties. *PLoS ONE*, **6**, e14556. https://doi.org/10.1371/journal.pone.0014556
5. Cai, Y.D., Feng, K.Y., Lu, W.C. and Chou, K.C. (2006) Using LogitBoost Classifier to Predict Protein Structural Classes. *Journal of Theoretical Biology*, **238**, 172-176. https://doi.org/10.1016/j.jtbi.2005.05.034
6. Chou, K.C. (2015) Impacts of Bioinformatics to Medicinal Chemistry. *Medicinal Chemistry*, **11**, 218-234. https://doi.org/10.2174/1573406411666141229162834
7. Chou, K.C. (2001) Prediction of Protein Cellular Attributes Using Pseudo Amino Acid Composition. *PROTEINS*: *Structure*, *Function*, *and Genetics*, **43**, 246-255. (Erratum: ibid., 2001, Vol. 44, 60) https://doi.org/10.1002/prot.1035
8. Chou, K.C. (2005) Using Amphiphilic Pseudo Amino Acid Composition to Predict Enzyme Subfamily Classes. *Bioinformatics*, **21**, 10-19. https://doi.org/10.1093/bioinformatics/bth466
9. Guo, Z.M. (2002) Prediction of Membrane Protein Types by Using Pattern Recognition Method Based on Pseudo Amino Acid Composition. Master Thesis, Bio-X Life Science Research Center, Shanghai Jiao Tong University, Shanghai.
10. Chou, K.C. and Cai, Y.D. (2003) Predicting Protein Quaternary Structure by Pseudo Amino Acid Composition. *PROTEINS*: *Structure*, *Function*, *and Genetics*, **53**, 282-289. https://doi.org/10.1002/prot.10500
11. Pan, Y.X., Zhang, Z.Z., Guo, Z.M., Feng, G.Y., Huang, Z.D. and He, L. (2003) Application of Pseudo Amino Acid Composition for Predicting Protein Subcellular Location: Stochastic Signal Processing Approach. *Journal of Protein Chemistry*, **22**, 395-402. https://doi.org/10.1023/A:1025350409648
12. Chou, K.C. and Cai, Y.D. (2004) Predicting Subcellular Localization of Proteins by Hybridizing Functional Domain Composition and Pseudo Amino Acid Composition. *Journal of Cellular Biochemistry*, **91**, 1197-1203. https://doi.org/10.1002/jcb.10790
13. Wang, M., Yang, J., Liu, G.P., Xu, Z.J. and Chou, K.C. (2004) Weighted-Support Vector Machines for Predicting Membrane Protein Types Based on Pseudo Amino Acid Composition. *Protein Engineering*, *Design*, *and Selection*, **17**, 509-516. https://doi.org/10.1093/protein/gzh061
14. Cai, Y.D. and Chou, K.C. (2005) Predicting Enzyme Subclass by Functional Domain Composition and Pseudo Amino Acid Composition. *Journal of Proteome Research*, **4**, 967-971. https://doi.org/10.1021/pr0500399

15. Cai, Y.D., Zhou, G.P. and Chou, K.C. (2005) Predicting Enzyme Family Classes by Hybridizing Gene Product Composition and Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **234**, 145-149. https://doi.org/10.1016/j.jtbi.2004.11.017

16. Gao, Y., Shao, S.H., Xiao, X., Ding, Y.S., Huang, Y.S., Huang, Z.D. and Chou, K.C. (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. https://doi.org/10.1007/s00726-005-0206-9

17. Liu, H., Yang, J., Wang, M., Xue, L. and Chou, K.C. (2005) Using Fourier Spectrum Analysis and Pseudo Amino Acid Composition for Prediction of Membrane Protein Types. *The Protein Journal*, **24**, 385-389. https://doi.org/10.1007/s10930-005-7592-4

18. Shen, H.B. and Chou, K.C. (2005) Using Optimized Evidence-Theoretic K-Nearest Neighbor Classifier and Pseudo Amino Acid Composition to Predict Membrane Protein Types. *Biochemical & Biophysical Research Communications* (*BBRC*), **334**, 288-292. https://doi.org/10.1016/j.bbrc.2005.06.087

19. Shen, H.B. and Chou, K.C. (2005) Predicting Protein Subnuclear Location with Optimized Evidence-Theoretic K-Nearest Classifier and Pseudo Amino acid Composition. *Biochemical & Biophysical Research Communications* (*BBRC*), **337**, 752-756. https://doi.org/10.1016/j.bbrc.2005.09.117

20. Cai, Y.D. and Chou, K.C. (2006) Predicting Membrane Protein Type by Functional Domain Composition and Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **238**, 395-400. https://doi.org/10.1016/j.jtbi.2005.05.035

21. Chen, C., Tian, Y.X., Zou, X.Y., Cai, P.X. and Mo, J.Y. (2006) Using Pseudo Amino Acid Composition and Support Vector Machine to Predict Protein Structural Class. *Journal of Theoretical Biology*, **243**, 444-448. https://doi.org/10.1016/j.jtbi.2006.06.025

22. Chen, C., Zhou, X., Tian, Y., Zou, X. and Cai, P. (2006) Predicting Protein Structural Class with Pseudo Amino Acid Composition and Support Vector Machine Fusion Network. *Analytical Biochemistry*, **357**, 116-121. https://doi.org/10.1016/j.ab.2006.07.022

23. Du, P. and 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. https://doi.org/10.1186/1471-2105-7-518

24. Mondal, S., Bhavna, R., Mohan Babu, R. and Ramakumar, S. (2006) Pseudo Amino Acid Composition and Multi-Class Support Vector Machines Approach for Conotoxin Superfamily Classification. *Journal of Theoretical Biology*, **243**, 252-260. https://doi.org/10.1016/j.jtbi.2006.06.014

25. Shen, H.B., Yang, J. and Chou, K.C. (2006) Fuzzy KNN for Predicting Membrane Protein Types from Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **240**, 9-13. https://doi.org/10.1016/j.jtbi.2005.08.016

26. Wang, S.Q., Yang, J. and Chou, K.C. (2006) Using Stacked Generalization to Predict Membrane Protein Types Based on Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **242**, 941-946. https://doi.org/10.1016/j.jtbi.2006.05.006

27. Xiao, X., Shao, S.H., Ding, Y.S., Huang, Z.D. and Chou, K.C. (2006) Using Cellular Automata Images and Pseudo amino Acid Composition to Predict Protein Subcellular Location. *Amino Acids*, **30**, 49-54. https://doi.org/10.1007/s00726-005-0225-6

28. Xiao, X., Shao, S.H., Huang, Z.D. and Chou, K.C. (2006) Using Pseudo Amino Acid Composition to Predict Protein Structural Classes: Approached with Complexity Measure Factor. *Journal of Computational Chemistry*, **27**, 478-482. https://doi.org/10.1002/jcc.20354

29. Zhang, S.W., Pan, Q., Zhang, H.C., Shao, Z.C. and Shi, J.Y. (2006) Prediction Protein Homo-Oligomer Types by Pseudo Amino Acid Composition: Approached with an Improved Feature Extraction and Naive Bayes Feature

Fusion. *Amino Acids*, **30**, 461-468. https://doi.org/10.1007/s00726-006-0263-8

30. Zhou, G.P. and Cai, Y.D. (2006) Predicting Protease Types by Hybridizing Gene Ontology and Pseudo Amino Acid Composition. *PROTEINS*: *Structure*, *Function*, *and Bioinformatics*, **63**, 681-684. https://doi.org/10.1002/prot.20898
31. Chen, Y.L. and Li, Q.Z. (2007) Prediction of Apoptosis Protein Subcellular Location Using Improved Hybrid Approach and Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **248**, 377-381. https://doi.org/10.1016/j.jtbi.2007.05.019
32. Ding, Y.S., Zhang, T.L. and Chou, K.C. (2007) Prediction of Protein Structure Classes with Pseudo Amino Acid Composition and Fuzzy Support Vector Machine Network. *Protein & Peptide Letters*, **14**, 811-815. https://doi.org/10.2174/092986607781483778
33. Lin, H. and Li, Q.Z. (2007) Predicting Conotoxin Superfamily and Family by Using Pseudo Amino Acid Composition and Modified Mahalanobis Discriminant. *Biochemical and Biophysical Research Communications*, **354**, 548-551. https://doi.org/10.1016/j.bbrc.2007.01.011
34. Lin, H. and Li, Q.Z. (2007) Using Pseudo Amino Acid Composition to Predict Protein Structural Class: Approached by Incorporating 400 Dipeptide Components. *Journal of Computational Chemistry*, **28**, 1463-1466. https://doi.org/10.1002/jcc.20554
35. Mundra, P., Kumar, M., Kumar, K.K., Jayaraman, V.K. and Kulkarni, B.D. (2007) Using Pseudo Amino Acid Composition to Predict Protein Subnuclear Localization: Approached with PSSM. *Pattern Recognition Letters*, **28**, 1610-1615. https://doi.org/10.1016/j.patrec.2007.04.001
36. Shi, J.Y., Zhang, S.W., Pan, Q., Cheng, Y.-M. and Xie, J. (2007) Prediction of Protein Subcellular Localization by Support Vector Machines Using Multi-Scale Energy and Pseudo Amino Acid Composition. *Amino Acids*, **33**, 69-74. https://doi.org/10.1007/s00726-006-0475-y
37. Zhang, T.L. and Ding, Y.S. (2007) Using Pseudo Amino Acid Composition and Binary-Tree Support Vector Machines to Predict Protein Structural Classes. *Amino Acids*, **33**, 623-629. https://doi.org/10.1007/s00726-007-0496-1
38. Zhou, X.B., Chen, C., Li, Z.C. and Zou, X.Y. (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. https://doi.org/10.1016/j.jtbi.2007.06.001
39. Diao, Y., Ma, D., Wen, Z., Yin, J., Xiang, J. and Li, M. (2008) Using Pseudo Amino Acid Composition to Predict Transmembrane Regions in Protein: Cellular Automata and Lempel-Ziv Complexity. *Amino Acids*, **34**, 111-117. https://doi.org/10.1007/s00726-007-0550-z
40. Ding, Y.S. and Zhang, T.L. (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. https://doi.org/10.1016/j.patrec.2008.06.007
41. Fang, Y., Guo, Y., Feng, Y. and 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. https://doi.org/10.1007/s00726-007-0568-2
42. Gu, Q., Ding, Y. and Zhang, T. (2008) Prediction of G-Protein-Coupled Receptor Classes with Pseudo Amino Acid Composition. 2*nd International Conference on Bioinformatics and Biomedical Engineering*, Shanghai, 16-18 May 2008, 876-879. https://doi.org/10.1109/ICBBE.2008.215
43. Jiang, X., Wei, R., Zhang, T.L. and 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. https://doi.org/10.2174/092986608784246443

44. Jiang, X., Wei, R., Zhao, Y. and 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**, 669-675. https://doi.org/10.1007/s00726-008-0034-9

45. Li, F.M. and Li, Q.Z. (2008) Using Pseudo Amino Acid Composition to Predict Protein Subnuclear Location with Improved Hybrid Approach. *Amino Acids*, **34**, 119-125. https://doi.org/10.1007/s00726-007-0545-9

46. Li, F.M. and Li, Q.Z. (2008) Predicting Protein Subcellular Location Using Chou's Pseudo Amino Acid Composition and Improved Hybrid Approach. *Protein & Peptide Letters*, **15**, 612-616. https://doi.org/10.2174/092986608784966930

47. 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. https://doi.org/10.1016/j.jtbi.2008.02.004

48. Lin, H., Ding, H., Guo, F.-B., Zhang, A.Y. and Huang, J. (2008) Predicting Subcellular Localization of Mycobacterial Proteins by Using Chou's Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **15**, 739-744. https://doi.org/10.2174/092986608785133681

49. Shi, J.Y., Zhang, S.W., Pan, Q. and Zhou, G.P. (2008) Using Pseudo Amino Acid Composition to Predict Protein Subcellular Location: Approached with Amino Acid Composition Distribution. *Amino Acids*, **35**, 321-327. https://doi.org/10.1007/s00726-007-0623-z

50. Xiao, X., Lin, W.Z. and Chou, K.C. (2008) Using Grey Dynamic Modeling and Pseudo Amino Acid Composition to Predict Protein Structural Classes. *Journal of Computational Chemistry*, **29**, 2018-2024. https://doi.org/10.1002/jcc.20955

51. Xiao, X., Wang, P. and Chou, K.C. (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. https://doi.org/10.1016/j.jtbi.2008.06.016

52. Zhang, G.Y. and Fang, B.S. (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. https://doi.org/10.1016/j.jtbi.2008.03.015

53. Zhang, G.Y., Li, H.C., Gao, J.Q. and Fang, B.S. (2008) Predicting Lipase Types by Improved Chou's Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **15**, 1132-1137. https://doi.org/10.2174/092986608786071184

54. Zhang, S.W., Chen, W., Yang, F. and 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. https://doi.org/10.1007/s00726-008-0086-x

55. Zhang, S.W., Zhang, Y.L., Yang, H.F., Zhao, C.H. and 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. https://doi.org/10.1007/s00726-007-0010-9

56. Zhang, T.L., Ding, Y.S. and Chou, K.C. (2008) Prediction Protein Structural Classes with Pseudo Amino Acid Composition: Approximate Entropy and Hydrophobicity Pattern. *Journal of Theoretical Biology*, **250**, 186-193. https://doi.org/10.1016/j.jtbi.2007.09.014

57. Chen, C., Chen, L., Zou, X. and 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. https://doi.org/10.2174/092986609787049420

58. Ding, H., Luo, L. and Lin, H. (2009) Prediction of Cell Wall Lytic Enzymes Using Chou's Amphiphilic Pseudo

Amino Acid Composition. *Protein & Peptide Letters*, **16**, 351-355. https://doi.org/10.2174/092986609787848045

59. Du, P., Cao, S. and 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. https://doi.org/10.1016/j.jtbi.2009.08.004
60. Gao, Q.B., Jin, Z.C., Ye, X.F., Wu, C. and He, J. (2009) Prediction of Nuclear Receptors with Optimal Pseudo Amino Acid Composition. *Analytical Biochemistry*, **387**, 54-59. https://doi.org/10.1016/j.ab.2009.01.018
61. Georgiou, D.N., Karakasidis, T.E., Nieto, J.J. and 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. https://doi.org/10.1016/j.jtbi.2008.11.003
62. Li, Z.C., Zhou, X.B., Dai, Z. and Zou, X.Y. (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. https://doi.org/10.1007/s00726-008-0170-2
63. Lin, H., Wang, H., Ding, H., Chen, Y.L. and Li, Q.Z. (2009) Prediction of Subcellular Localization of Apoptosis Protein Using Chou's Pseudo Amino Acid Composition. *Acta Biotheoretica*, **57**, 321-330. https://doi.org/10.1007/s10441-008-9067-4
64. Qiu, J.D., Huang, J.H., Liang, R.P. and Lu, X.Q. (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. https://doi.org/10.1016/j.ab.2009.04.009
65. Xiao, X., Wang, P. and Chou, K.C. (2009) Predicting Protein Quaternary Structural Attribute by Hybridizing Functional Domain Composition and Pseudo Amino Acid Composition. *Journal of Applied Crystallography*, **42**, 169-173. https://doi.org/10.1107/S0021889809002751
66. Zeng, Y.H., Guo, Y.Z., Xiao, R.Q., Yang, L., Yu, L.Z. and Li, M.L. (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. https://doi.org/10.1016/j.jtbi.2009.03.028
67. Esmaeili, M., Mohabatkar, H. and 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. https://doi.org/10.1016/j.jtbi.2009.11.016
68. Gao, Q.B., Ye, X.F., Jin, Z.C. and He, J. (2010) Improving Discrimination of Outer Membrane Proteins by Fusing Different Forms of Pseudo Amino Acid Composition. *Analytical Biochemistry*, **398**, 52-59. https://doi.org/10.1016/j.ab.2009.10.040
69. Gu, Q., Ding, Y., Zhang, T. and Shen, Y. (2010) [Prediction of G-Protein-Coupled Receptor Classes with Pseudo Amino Acid Composition]. *Journal of Biomedical Engineering*, **27**, 500-504.
70. Gu, Q., Ding, Y.S. and Zhang, T.L. (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. https://doi.org/10.2174/092986610791112693
71. Kandaswamy, K.K., Pugalenthi, G., Moller, S., Hartmann, E., Kalies, K.U., Suganthan, P.N. and Martinetz, T. (2010) Prediction of Apoptosis Protein Locations with Genetic Algorithms and Support Vector Machines Through a New Mode of Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **17**, 1473-1479. https://doi.org/10.2174/0929866511009011473
72. Liu, T., Zheng, X., Wang, C. and 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**, 1263-269. https://doi.org/10.2174/092986610792231528
73. Mohabatkar, H. (2010) Prediction of Cyclin Proteins Using Chou's Pseudo Amino Acid Composition. *Protein &*

Peptide Letters, **17**, 1207-1214. https://doi.org/10.2174/092986610792231564

74. Nanni, L., Brahnam, S. and Lumini, A. (2010) High Performance Set of PseAAC and Sequence Based Descriptors for Protein Classification. *Journal of Theoretical Biology*, **266**, 1-10. https://doi.org/10.1016/j.jtbi.2010.06.006
75. Niu, X.H., Li, N.N., Shi, F., Hu, X.H., Xia, J.B. and Xiong, H.J. (2010) Predicting Protein Solubility with a Hybrid Approach by Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **17**, 1466-1472. https://doi.org/10.2174/0929866511009011466
76. Qiu, J.D., Huang, J.H., Shi, S.P. and Liang, R.P. (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. https://doi.org/10.2174/092986610791190372
77. Sahu, S.S. and 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. https://doi.org/10.1016/j.compbiolchem.2010.09.002
78. Wang, Y.C., Wang, X.B., Yang, Z.X. and Deng, N.Y. (2010) Prediction of Enzyme Subfamily Class via Pseudo Amino Acid Composition by Incorporating the Conjoint Triad Feature. *Protein & Peptide Letters*, **17**, 1441-1449. https://doi.org/10.2174/0929866511009011441
79. Wu, J., Li, M.L., Yu, L.Z. and 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. *The Protein Journal*, **29**, 62-67. https://doi.org/10.1007/s10930-009-9222-z
80. Yu, L., Guo, Y., Li, Y., Li, G., Li, M., Luo, J., Xiong, W. and Qin, W. (2010) SecretP: Identifying Bacterial Secreted Proteins by Fusing New Features into Chou's Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **267**, 1-6. https://doi.org/10.1016/j.jtbi.2010.08.001
81. Ding, H., Liu, L., Guo, F.B., Huang, J. and Lin, H. (2011) Identify Golgi Protein Types with Modified Mahalanobis Discriminant Algorithm and Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **18**, 58-63. https://doi.org/10.2174/092986611794328708
82. Guo, J., Rao, N., Liu, G., Yang, Y. and Wang, G. (2011) Predicting Protein Folding Rates Using the Concept of Chou's Pseudo Amino Acid Composition. *Journal of Computational Chemistry*, **32**, 1612-1617. https://doi.org/10.1002/jcc.21740
83. Hayat, M. and 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. https://doi.org/10.1016/j.jtbi.2010.11.017
84. Hu, L., Zheng, L., Wang, Z., Li, B. and Liu, L. (2011) Using Pseudo Amino Acid Composition to Predict Protease Families by Incorporating A Series of Protein Biological Features. *Protein & Peptide Letters*, **18**, 552-558. https://doi.org/10.2174/092986611795222795
85. Huang, Y., Yang, L. and Wang, T. (2011) Phylogenetic Analysis of DNA Sequences Based on the Generalized Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **269**, 217-223. https://doi.org/10.1016/j.jtbi.2010.10.027
86. Xia, J.B., Zhang, S.L., Shi, F., Xiong, H.J., Hu, X.H., Niu, X.H. and Li, Z. (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. https://doi.org/10.1016/j.jtbi.2011.06.003
87. Liao, B., Jiang, J.B., Zeng, Q.G. and Zhu, W. (2011) Predicting Apoptosis Protein Subcellular Location with PseAAC by Incorporating Tripeptide Composition. *Protein & Peptide Letters*, **18**, 1086-1092.

https://doi.org/10.2174/092986611797200931

88. Lin, H. and 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. https://doi.org/10.1016/j.jtbi.2010.10.019
89. Lin, J. and 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. https://doi.org/10.2174/092986611797642797
90. Lin, J., Wang, Y. and 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. https://doi.org/10.5897/AJB11.429
91. Liu, X.L., Lu, J.L. and Hu, X.H. (2011) Predicting Thermophilic Proteins with Pseudo Amino Acid Composition: Approached from Chaos Game Representation and Principal Component Analysis. *Protein & Peptide Letters*, **18**, 1244-1250. https://doi.org/10.2174/092986611797642661
92. Mahdavi, A. and 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. https://doi.org/10.1016/j.jtbi.2011.01.048
93. Mohabatkar, H., Mohammad Beigi, M. and Esmaeili, 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. https://doi.org/10.1016/j.jtbi.2011.04.017
94. Mohammad, B.M., Behjati, M. and 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. https://doi.org/10.1007/s10969-011-9120-4
95. Qiu, J.D., Sun, X.Y., Suo, S.B., Shi, S.P., Huang, S.Y., Liang, R.P. and Zhang, L. (2011) Predicting Homo-Oligomers and Hetero-Oligomers by Pseudo Amino Acid Composition: An Approach from Discrete Wavelet Transformation. *Biochimie*, **93**, 1132-1138. https://doi.org/10.1016/j.biochi.2011.03.010
96. Qiu, J.D., Suo, S.B., Sun, X.Y., Shi, S.P. and Liang, R.P. (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. https://doi.org/10.1016/j.jmgm.2011.06.014
97. Shi, R. and Xu, C. (2011) Prediction of Rat Protein Subcellular Localization with Pseudo Amino Acid Composition Based on Multiple Sequential Features. *Protein & Peptide Letters*, **18**, 625-633. https://doi.org/10.2174/092986611795222768
98. Shu, M., Cheng, X., Zhang, Y., Wang, Y., Lin, Y., Wang, L. and Lin, Z. (2011) Predicting the Activity of ACE Inhibitory Peptides with a Novel Mode of Pseudo Amino Acid Composition. *Protein & Peptide Letters*, **18**, 1233-1243. https://doi.org/10.2174/092986611797642706
99. Wang, D., Yang, L., Fu, Z. and 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. https://doi.org/10.2174/092986611795446085
100. Wang, W., Geng, X.B., Dou, Y., Liu, T. and Zheng, X. (2011) Predicting Protein Subcellular Localization by Pseudo Amino Acid Composition with a Segment-Weighted and Features-Combined Approach. *Protein & Peptide Letters*, **18**, 480-487. https://doi.org/10.2174/092986611794927947
101. Xiao, X. and Chou, K.C. (2011) Using Pseudo Amino Acid Composition to Predict Protein Attributes via Cellular Automata and Other Approaches. *Current Bioinformatics*, **6**, 251-260. https://doi.org/10.2174/1574893611106020251
102. Xiao, X., Wang, P. and Chou, K.C. (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. https://doi.org/10.1039/C0MB00170H

103. Zia Ur, R. and 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. https://doi.org/10.2174/092986611796011491
104. Zou, D., He, Z., He, J. and Xia, Y. (2011) Supersecondary Structure Prediction Using Chou's Pseudo Amino Acid Composition. *Journal of Computational Chemistry*, **32**, 271-278. https://doi.org/10.1002/jcc.21616
105. Cao, J.Z., Liu, W.Q. and 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 & Peptide Letters*, **19**, 1163-1169. https://doi.org/10.2174/092986612803216999
106. Chen, C., Shen, Z.B. and Zou, X.Y. (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. https://doi.org/10.2174/092986612799789332
107. Chen, Y.L., Li, Q.Z. and Zhang, L.Q. (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. https://doi.org/10.1007/s00726-010-0825-7
108. Fan, G.L. and Li, Q.Z. (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. https://doi.org/10.1016/j.jtbi.2012.03.017
109. Fan, G.L. and Li, Q.Z. (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. https://doi.org/10.1007/s00726-011-1143-4
110. Gao, Q.B., Zhao, H., Ye, X. and He, J. (2012) Prediction of Pattern Recognition Receptor Family Using Pseudo Amino Acid Composition. *Biochemical and Biophysical Research Communications*, **417**, 73-77. https://doi.org/10.1016/j.bbrc.2011.11.057
111. Hayat, M. and 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. https://doi.org/10.2174/092986612799789387
112. Li, L.Q., Zhang, Y., Zou, L.Y., Zhou, Y. and Zheng, X.Q. (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. https://doi.org/10.2174/092986612799789369
113. Liao, B., Xiang, Q. and 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. https://doi.org/10.2174/092986612803217051
114. Lin, W.Z., Fang, J.A., Xiao, X. and Chou, K.C. (2012) Predicting Secretory Proteins of Malaria Parasite by Incorporating Sequence Evolution Information into Pseudo Amino Acid Composition via Grey System Model. *PLoS ONE*, **7**, e49040. https://doi.org/10.1371/journal.pone.0049040
115. Liu, L., Hu, X.Z., Liu, X.X., Wang, Y. and Li, S.B. (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. https://doi.org/10.2174/092986612799789378
116. Mei, S. (2012) Multi-Kernel Transfer Learning Based on Chou's PseAAC Formulation for Protein Submitochondria Localization. *Journal of Theoretical Biology*, **293**, 121-130. https://doi.org/10.1016/j.jtbi.2011.10.015
117. 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. https://doi.org/10.1016/j.jtbi.2012.06.028

118. Nanni, L., Brahnam, S. and Lumini, A. (2012) Wavelet Images and Chou's Pseudo Amino Acid Composition for Protein Classification. *Amino Acids*, **43**, 657-665. https://doi.org/10.1007/s00726-011-1114-9
119. Nanni, L., Lumini, A., Gupta, D. and 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 Biolology and Bioinformatics*, **9**, 467-475. https://doi.org/10.1109/TCBB.2011.117
120. Niu, X.H., Hu, X.H., Shi, F. and Xia, J.B. (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. https://doi.org/10.2174/092986612802084492
121. Qin, Y.F., Wang, C.H., Yu, X.Q., Zhu, J., Liu, T.G. and Zheng, X.Q. (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. https://doi.org/10.2174/092986612799789350
122. Ren, L.Y., Zhang, Y.S. and 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. https://doi.org/10.2174/092986612803217088
123. Sun, X.Y., Shi, S.P., Qiu, J.D., Suo, S.B., Huang, S.Y. and Liang, R.P. (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. https://doi.org/10.1039/c2mb25280e
124. Wang, J., Li, Y., Wang, Q., You, X., Man, J., Wang, C. and Gao, X. (2012) ProClusEnsem: Predicting Membrane Protein Types by Fusing Different Modes of Pseudo Amino Acid Composition. *Computers in Biology and Medicine*, **42**, 564-574. https://doi.org/10.1016/j.compbiomed.2012.01.012
125. Yu, X., Zheng, X., Liu, T., Dou, Y. and 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. https://doi.org/10.1007/s00726-011-0848-8
126. Zhao, X.W., Ma, Z.Q. and Yin, M.H. (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. https://doi.org/10.2174/092986612800191080
127. Zia-ur-Rehman and 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. https://doi.org/10.2174/092986612801619589
128. Chang, T.H., Wu, L.C., Lee, T.Y., Chen, S.P., Huang, H.D. and Horng, J.T. (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. https://doi.org/10.1007/s10822-012-9628-0
129. Chen, Y.K. and Li, K.B. (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. https://doi.org/10.1016/j.jtbi.2012.10.033
130. Fan, G.-L., Li, Q.-Z. and Zuo, Y.-C. (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. https://doi.org/10.1016/j.procbio.2013.05.012
131. Fan, G.L. and Li, Q.Z. (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. https://doi.org/10.1016/j.jtbi.2013.06.003

132. Georgiou, D.N., Karakasidis, T.E. and Megaritis, A.C. (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. https://doi.org/10.2174/1875036201307010041
133. Gupta, M.K., Niyogi, R. and 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 and QSAR in Environmental Research*, **24**, 597-609. https://doi.org/10.1080/1062936X.2013.773378
134. Huang, C. and 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. https://doi.org/10.1016/j.biosystems.2013.04.005
135. Huang, C. and Yuan, J.Q. (2013) A Multilabel Model Based on Chou's Pseudo Amino Acid Composition for Identifying Membrane Proteins with Both Single and Multiple Functional Types. *The Journal of Membrane Biology*, **246**, 327-334. https://doi.org/10.1007/s00232-013-9536-9
136. Huang, C. and Yuan, J.Q. (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**, 205-212. https://doi.org/10.1016/j.jtbi.2013.06.034
137. Khosravian, M., Faramarzi, F.K., Beigi, M.M., Behbahani, M. and 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. https://doi.org/10.2174/092986613804725307
138. Lin, H., Ding, C., Yuan, L.F., Chen, W., Ding, H., Li, Z.Q., Guo, F.B., Hung, J. and Rao, N.N. (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*, **6**, Article No. 1350003. https://doi.org/10.1142/S1793524513500034
139. Liu, B., Wang, X., Zou, Q., Dong, Q. and 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. https://doi.org/10.1002/minf.201300084
140. Mohabatkar, H., Beigi, M.M., Abdolahi, K. and 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. https://doi.org/10.2174/157340613804488341
141. Pacharawongsakda, E. and 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. https://doi.org/10.1109/TNB.2013.2272014
142. Qin, Y.F., Zheng, L. and 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. https://doi.org/10.1002/qua.24383
143. Sarangi, A.N., Lohani, M. and 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 & Peptide Letters*, **20**, 781-795. https://doi.org/10.2174/0929866511320070008
144. Wan, S., Mak, M.W. and Kung, S.Y. (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. https://doi.org/10.1016/j.jtbi.2013.01.012
145. Wang, X., Li, G.Z. and Lu, W.C. (2013) Virus-ECC-mPLoc: A Multi-Label Predictor for Predicting the Subcel-

lular 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. https://doi.org/10.2174/092986613804910608

146. Xiao, X., Min, J.L., Wang, P. and Chou, K.C. (2013) iCDI-PseFpt: Identify the Channel-Drug Interaction in Cellular Networking with PseAAC and Molecular Fingerprints. *Journal of Theoretical Biology*, **337**, 71-79. https://doi.org/10.1016/j.jtbi.2013.08.013
147. Niu, X.H., Li, N.N., Xia, J.B., Chen, D.Y., Peng, Y.H., Xiao, Y., Wei, W.Q., Wang, D.M. and Wang, Z.Z. (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. https://doi.org/10.1016/j.jtbi.2013.03.010
148. Xie, H.L., Fu, L. and Nie, X.D. (2013) Using Ensemble SVM to Identify Human GPCRs N-Linked Glycosylation Sites Based on the General Form of Chou's PseAAC. *Protein Engineering, Design and Selection*, **26**, 735-742. https://doi.org/10.1093/protein/gzt042
149. Xu, Y., Ding, J., Wu, L.Y. and Chou, K.C. (2013) iSNO-PseAAC: Predict Cysteine S-Nitrosylation Sites in Proteins by Incorporating Position Specific Amino Acid Propensity into Pseudo Amino Acid Composition. *PLoS ONE*, **8**, e55844. https://doi.org/10.1371/journal.pone.0055844
150. Xu, Y., Shao, X.J., Wu, L.Y., Deng, N.Y. and Chou, K.C. (2013) iSNO-AAPair: Incorporating Amino Acid Pairwise Coupling into PseAAC for Predicting Cysteine S-Nitrosylation Sites in Proteins. *PeerJ*, **1**, e171. https://doi.org/10.7717/peerj.171
151. Hajisharifi, Z., Piryaiee, M., Mohammad Beigi, M., Behbahani, M. and Mohabatkar, 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. https://doi.org/10.1016/j.jtbi.2013.08.037
152. Han, G.S., Yu, Z.G. and 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. *Journal of Theoretical Biology*, **344**, 31-39. https://doi.org/10.1016/j.jtbi.2013.11.017
153. Hayat, M. and 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**, 184-192. https://doi.org/10.1016/j.cmpb.2014.06.007
154. Jia, C., Lin, X. and Wang, Z. (2014) Prediction of Protein S-Nitrosylation Sites Based on Adapted Normal Distribution Bi-Profile Bayes and Chou's Pseudo Amino Acid Composition. *International Journal of Molecular Sciences*, **15**, 10410-10423. https://doi.org/10.3390/ijms150610410
155. Kong, L., Zhang, L. and 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. *Journal of Theoretical Biology*, **344**, 12-18. https://doi.org/10.1016/j.jtbi.2013.11.021
156. Li, L., Yu, S., Xiao, W., Li, Y., Li, M., Huang, L., Zheng, X., Zhou, S. and Yang, H. (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. https://doi.org/10.1016/j.biochi.2014.06.001
157. Liu, B., Xu, J., Lan, X., Xu, R., Zhou, J., Wang, X. and Chou, K.C. (2014) iDNA-Prot|dis: Identifying DNA-Binding Proteins by Incorporating Amino Acid Distance-Pairs and Reduced Alphabet Profile into the General Pseudo Amino Acid Composition. *PLoS ONE*, **9**, e106691. https://doi.org/10.1371/journal.pone.0106691
158. Mondal, S. and Pai, P.P. (2014) Chou's Pseudo Amino Acid Composition Improves Sequence-Based Antifreeze Protein Prediction. *Journal of Theoretical Biology*, **356**, 30-35. https://doi.org/10.1016/j.jtbi.2014.04.006

159. Nanni, L., Brahnam, S. and Lumini, A. (2014) Prediction of Protein Structure Classes by Incorporating Different Protein Descriptors into General Chou's Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **360**, 109-116. https://doi.org/10.1016/j.jtbi.2014.07.003

160. Qiu, W.R., Xiao, X. and Chou, K.C. (2014) iRSpot-TNCPseAAC: Identify Recombination Spots with Trinucleotide Composition and Pseudo Amino Acid Components. *International Journal of Molecular Sciences* (*IJMS*), **15**, 1746-1766. https://doi.org/10.3390/ijms15021746

161. Qiu, W.R., Xiao, X., Lin, W.Z. and Chou, K.C. (2014) iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. *BioMed Research International* (*BMRI*), **2014**, Article ID: 947416. https://doi.org/10.1155/2014/947416

162. Xu, Y., Wen, X., Shao, X.J., Deng, N.Y. and Chou, K.C. (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* (*IJMS*), **15**, 7594-7610. https://doi.org/10.3390/ijms15057594

163. Xu, Y., Wen, X., Wen, L.S., Wu, L.Y., Deng, N.Y. and Chou, K.C. (2014) iNitro-Tyr: Prediction of Nitrotyrosine Sites in Proteins with General Pseudo Amino Acid Composition. *PLoS ONE*, **9**, e105018. https://doi.org/10.1371/journal.pone.0105018

164. Zhang, J., Sun, P., Zhao, X. and 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. https://doi.org/10.1016/j.jtbi.2014.08.002

165. Zhang, J., Zhao, X., Sun, P. and Ma, Z. (2014) PSNO: Predicting Cysteine S-Nitrosylation Sites by Incorporating Various Sequence-Derived Features into the General Form of Chou's PseAAC. *International Journal of Molecular Sciences*, **15**, 11204-11219. https://doi.org/10.3390/ijms150711204

166. Zhang, L., Zhao, X. and 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. *Journal of Theoretical Biology*, **355**, 105-110. https://doi.org/10.1016/j.jtbi.2014.04.008

167. Ahmad, S., Kabir, M. and 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**, 165-174. https://doi.org/10.1016/j.cmpb.2015.07.005

168. Ali, F. and Hayat, M. (2015) Classification of Membrane Protein Types Using Voting Feature Interval in Combination with Chou's Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **384**, 78-83. https://doi.org/10.1016/j.jtbi.2015.07.034

169. Chen, L., Chu, C., Huang, T., Kong, X. and Cai, Y.D. (2015) Prediction and Analysis of Cell-Penetrating Peptides Using Pseudo Amino Acid Composition and Random Forest Models. *Amino Acids*, **47**, 1475-1493. https://doi.org/10.1007/s00726-015-1974-5

170. Dehzangi, A., Heffernan, R., Sharma, A., Lyons, J., Paliwal, K. and Sattar, A. (2015) Gram-Positive and Gram-Negative Protein Subcellular Localization by Incorporating Evolutionary-Based Descriptors into Chou's General PseAAC. *Journal of Theoretical Biology*, **364**, 284-294. https://doi.org/10.1016/j.jtbi.2014.09.029

171. Huang, C. and Yuan, J.Q. (2015) Simultaneously Identify Three Different Attributes of Proteins by Fusing Their Three Different Modes of Chou's Pseudo Amino Acid Compositions. *Protein & Peptide Letters*, **22**, 547-556. https://doi.org/10.2174/0929866522666150209151344

172. Jia, J., Liu, Z., Xiao, X. and Chou, K.C. (2015) iPPI-Esml: An Ensemble Classifier for Identifying the Interactions of Proteins by Incorporating Their Physicochemical Properties and Wavelet Transforms into PseAAC. *Journal of Theoretical Biology*, **377**, 47-56. https://doi.org/10.1016/j.jtbi.2015.04.011

173. Ju, Z., Cao, J.Z. and 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 Chous General PseAAC. *Journal of Theoretical Biology*, **385**, 50-57. https://doi.org/10.1016/j.jtbi.2015.07.030

174. Khan, Z.U., Hayat, M. and Khan, M.A. (2015) Discrimination of Acidic and Alkaline Enzyme Using Chou's Pseudo Amino Acid Composition in Conjunction with Probabilistic Neural Network Model. *Journal of Theoretical Biology*, **365**, 197-203. https://doi.org/10.1016/j.jtbi.2014.10.014

175. Kumar, R., Srivastava, A., Kumari, B. and Kumar, M. (2015) Prediction of Beta-Lactamase and Its Class by Chou's Pseudo Amino Acid Composition and Support Vector Machine. *Journal of Theoretical Biology*, **365**, 96-103. https://doi.org/10.1016/j.jtbi.2014.10.008

176. Liu, B., Chen, J. and Wang, X. (2015) Protein Remote Homology Detection by Combining Chou's Distance-Pair Pseudo Amino Acid Composition and Principal Component Analysis. *Molecular Genetics and Genomics*, **290**, 1919-1931. https://doi.org/10.1007/s00438-015-1044-4

177. Liu, B., Xu, J., Fan, S., Xu, R., Zhou, J. and Wang, X. (2015) PseDNA-Pro: DNA-Binding Protein Identification by Combining Chou's PseAAC and Physicochemical Distance Transformation. *Molecular Informatics*, **34**, 8-17. https://doi.org/10.1002/minf.201400025

178. Mandal, M., Mukhopadhyay, A. and 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. https://doi.org/10.1007/s11517-014-1238-7

179. Sanchez, V., Peinado, A.M., Perez-Cordoba, J.L. and Gomez, A.M. (2015) A New Signal Characterization and Signal-Based Chou's PseAAC Representation of Protein Sequences. *Journal of Bioinformatics and Computational Biology*, **13**, Article ID: 1550024. https://doi.org/10.1142/S0219720015500249

180. Sharma, R., Dehzangi, A., Lyons, J., Paliwal, K., Tsunoda, T. and Sharma, A. (2015) Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. *IEEE Transactions on Nanobioscience*, **14**, 915-926. https://doi.org/10.1109/TNB.2015.2500186

181. Wang, X., Zhang, W., Zhang, Q. and Li, G.Z. (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. https://doi.org/10.1093/bioinformatics/btv212

182. Xu, R., Zhou, J., Liu, B., He, Y.A., Zou, Q., Wang, X. and Chou, K.C. (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 and Dynamics* (*JBSD*), **33**, 1720-1730. https://doi.org/10.1080/07391102.2014.968624

183. Zhang, M., Zhao, B. and Liu, X. (2015) Predicting Industrial Polymer Melt Index via Incorporating Chaotic Characters into Chou's General PseAAC. *Chemometrics and Intelligent Laboratory Systems* (*CHEMOLAB*), **146**, 232-240. https://doi.org/10.1016/j.chemolab.2015.05.028

184. Zhang, S.L. (2015) Accurate Prediction of Protein Structural Classes by Incorporating PSSS and PSSM into Chou's General PseAAC. *Chemometrics and Intelligent Laboratory Systems* (*CHEMOLAB*), **142**, 28-35. https://doi.org/10.1016/j.chemolab.2015.01.004

185. Zhu, P.P., Li, W.C., Zhong, Z.J., Deng, E.Z., Ding, H., Chen, W. and Lin, H. (2015) Predicting the Subcellular Localization of Mycobacterial Proteins by Incorporating the Optimal Tripeptides into the General Form of Pseudo Amino Acid Composition. *Molecular BioSystems*, **11**, 558-563. https://doi.org/10.1039/C4MB00645C

186. Ahmad, K., Waris, M. and Hayat, M. (2016) Prediction of Protein Submitochondrial Locations by Incorporating Dipeptide Composition into Chou's General Pseudo Amino Acid Composition. *The Journal of Membrane Biology*, **249**, 293-304. https://doi.org/10.1007/s00232-015-9868-8

187. Behbahani, M., Mohabatkar, H. and 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. *Journal of Theoretical Biology*, **411**, 1-5. https://doi.org/10.1016/j.jtbi.2016.09.001

188. Fan, G.L., Liu, Y.L. and Wang, H. (2016) Identification of Thermophilic Proteins by Incorporating Evolutionary and Acid Dissociation Information into Chou's General Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **407**, 138-142. https://doi.org/10.1016/j.jtbi.2016.07.010

189. Jia, J., Liu, Z., Xiao, X., Liu, B. and Chou, K.C. (2016) Identification of Protein-Protein Binding Sites by Incorporating the Physicochemical Properties and Stationary Wavelet Transforms into Pseudo Amino Acid Composition (iPPBS-PseAAC). *Journal of Biomolecular Structure and Dynamics* (*JBSD*), **34**, 1946-1961. https://doi.org/10.1080/07391102.2015.1095116

190. Jia, J., Liu, Z., Xiao, X., Liu, B. and Chou, K.C. (2016) pSuc-Lys: Predict Lysine Succinylation Sites in Proteins with PseAAC and Ensemble Random Forest Approach. *Journal of Theoretical Biology*, **394**, 223-230. https://doi.org/10.1016/j.jtbi.2016.01.020

191. Jia, J., Liu, Z., Xiao, X., Liu, B. and Chou, K.C. (2016) iCar-PseCp: Identify Carbonylation Sites in Proteins by Monto Carlo Sampling and Incorporating Sequence Coupled Effects into General PseAAC. *Oncotarget*, **7**, 34558-34570. https://doi.org/10.18632/oncotarget.9148

192. Jia, J., Zhang, L., Liu, Z., Xiao, X. and Chou, K.C. (2016) pSumo-CD: Predicting Sumoylation Sites in Proteins with Covariance Discriminant Algorithm by Incorporating Sequence-Coupled Effects into General PseAAC. *Bioinformatics*, **32**, 3133-3141. https://doi.org/10.1093/bioinformatics/btw387

193. Jiao, Y.S. and Du, P.F. (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. *Journal of Theoretical Biology*, **402**, 38-44. https://doi.org/10.1016/j.jtbi.2016.04.032

194. Ju, Z., Cao, J.Z. and Gu, H. (2016) Predicting Lysine Phosphoglycerylation with Fuzzy SVM by Incorporating k-Spaced Amino Acid Pairs into Chou's General PseAAC. *Journal of Theoretical Biology*, **397**, 145-150. https://doi.org/10.1016/j.jtbi.2016.02.020

195. Kabir, M. and 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**, 285-296. https://doi.org/10.1007/s00438-015-1108-5

196. Qiu, W.R., Sun, B.Q., Xiao, X., Xu, Z.C. and Chou, K.C. (2016) iHyd-PseCp: Identify Hydroxyproline and Hydroxylysine in Proteins by Incorporating Sequence-Coupled Effects into General PseAAC. *Oncotarget*, **7**, 44310-44321. https://doi.org/10.18632/oncotarget.10027

197. Tahir, M. and 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. *Molecular BioSystems*, **12**, 2587-2593. https://doi.org/10.1039/C6MB00221H

198. Tang, H., Chen, W. and Lin, H. (2016) Identification of Immunoglobulins Using Chou's Pseudo Amino Acid Composition with Feature Selection Technique. *Molecular BioSystems*, **12**, 1269-1275. https://doi.org/10.1039/C5MB00883B

199. Tiwari, A.K. (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. https://doi.org/10.1016/j.cmpb.2016.07.004

200. Xu, C., Sun, D., Liu, S. and Zhang, Y. (2016) Protein Sequence Analysis by Incorporating Modified Chaos Game and Physicochemical Properties into Chou's General Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **406**, 105-115. https://doi.org/10.1016/j.jtbi.2016.06.034

201. Zou, H.L. and Xiao, X. (2016) Predicting the Functional Types of Singleplex and Multiplex Eukaryotic Membrane Proteins via Different Models of Chou's Pseudo Amino Acid Compositions. *The Journal of Membrane Biology*, **249**, 23-29. https://doi.org/10.1007/s00232-015-9830-9

202. Zou, H.L. and Xiao, X. (2016) Classifying Multifunctional Enzymes by Incorporating Three Different Models into Chou's General Pseudo Amino Acid Composition. *The Journal of Membrane Biology*, **249**, 561-567. https://doi.org/10.1007/s00232-016-9904-3

203. Cheng, X., Xiao, X. and Chou, K.C. (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. https://doi.org/10.1039/C7MB00267J

204. Cheng, X., Xiao, X. and Chou, K.C. (2017) pLoc-mVirus: Predict Subcellular Localization of Multi-Location Virus Proteins via Incorporating the Optimal GO Information into General PseAAC. *Gene*, **628**, 315-321. (Erratum: ibid., 2018, Vol. 644, 156-156) https://doi.org/10.1016/j.gene.2017.07.036

205. Ju, Z. and He, J.J. (2017) Prediction of Lysine Propionylation Sites Using Biased SVM and Incorporating Four Different Sequence Features into Chou's PseAAC. *Journal of Molecular Graphics and Modelling*, **76**, 356-363. https://doi.org/10.1016/j.jmgm.2017.07.022

206. Ju, Z. and He, J.J. (2017) Prediction of Lysine Crotonylation Sites by Incorporating the Composition of k-Spaced Amino Acid Pairs into Chou's General PseAAC. *Journal of Molecular Graphics and Modelling*, **77**, 200-204. https://doi.org/10.1016/j.jmgm.2017.08.020

207. Khan, M., Hayat, M., Khan, S.A. and Iqbal, N. (2017) Unb-DPC: Identify Mycobacterial Membrane Protein Types by Incorporating Un-Biased Dipeptide Composition into Chou's General PseAAC. *Journal of Theoretical Biology*, **415**, 13-19. https://doi.org/10.1016/j.jtbi.2016.12.004

208. Liang, Y. and Zhang, S. (2017) Predict Protein Structural Class by Incorporating Two Different Modes of Evolutionary Information into Chou's General Pseudo Amino Acid Composition. *Journal of Molecular Graphics and Modelling*, **78**, 110-117. https://doi.org/10.1016/j.jmgm.2017.10.003

209. Liu, L.M., Xu, Y. and Chou, K.C. (2017) iPGK-PseAAC: Identify Lysine Phosphoglycerylation Sites in Proteins by Incorporating Four Different Tiers of Amino Acid Pairwise Coupling Information into the General PseAAC. *Medicinal Chemistry*, **13**, 552-559. https://doi.org/10.2174/1573406413666170515120507

210. Meher, P.K., Sahu, T.K., Saini, V. and Rao, A.R. (2017) Predicting Antimicrobial Peptides with Improved Accuracy by Incorporating the Compositional, Physico-Chemical and Structural Features into Chou's General PseAAC. *Scientific Reports*, **7**, Article No. 42362. https://doi.org/10.1038/srep42362

211. Qiu, W.R., Sun, B.Q., Xiao, X., Xu, D. and Chou, K.C. (2017) iPhos-PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. *Molecular Informatics*, **36**, UNSP 1600010. https://doi.org/10.1002/minf.201600010

212. Qiu, W.R., Zheng, Q.S., Sun, B.Q. and 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. *Molecular Informatics*, **36**, UNSP 1600085. https://doi.org/10.1002/minf.201600085

213. Rahimi, M., Bakhtiarizadeh, M.R. and 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. *Journal of Theoretical Biology*, **414**, 128-136. https://doi.org/10.1016/j.jtbi.2016.11.028

214. Tripathi, P. and Pandey, P.N. (2017) A Novel Alignment-Free Method to Classify Protein Folding Types by Combining Spectral Graph Clustering with Chou's Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **424**, 49-54. https://doi.org/10.1016/j.jtbi.2017.04.027

215. Xiao, X., Cheng, X., Su, S., Nao, Q. and Chou, K.C. (2017) pLoc-mGpos: Incorporate Key Gene Ontology In-

formation into General PseAAC for Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. *Natural Science*, **9**, 331-349. https://doi.org/10.4236/ns.2017.99032

216. Xu, C., Ge, L., Zhang, Y., Dehmer, M. and Gutman, I. (2017) Prediction of Therapeutic Peptides by Incorporating q-Wiener Index into Chou's General PseAAC. *Journal of Biomedical Informatics*, **75**, 63-69. https://doi.org/10.1016/j.jbi.2017.09.011
217. Xu, Y., Li, C. and Chou, K.C. (2017) iPreny-PseAAC: Identify C-Terminal Cysteine Prenylation Sites in Proteins by Incorporating Two Tiers of Sequence Couplings into PseAAC. *Medicinal Chemistry*, **13**, 544-551. https://doi.org/10.2174/1573406413666170419150052
218. Yu, B., Li, S., Qiu, W.Y., Chen, C., Chen, R.X., Wang, L., Wang, M.H. and Zhang, Y. (2017) Accurate Prediction of Subcellular Location of Apoptosis Proteins Combining Chou's PseAAC and PsePSSM Based on Wavelet Denoising. *Oncotarget*, **8**, 107640-107665. https://doi.org/10.18632/oncotarget.22585
219. Yu, B., Lou, L., Li, S., Zhang, Y., Qiu, W., Wu, X., Wang, M. and Tian, B. (2017) Prediction of Protein Structural Class for Low-Similarity Sequences Using Chou's Pseudo Amino Acid Composition and Wavelet Denoising. *Journal of Molecular Graphics and Modelling*, **76**, 260-273. https://doi.org/10.1016/j.jmgm.2017.07.012
220. Ahmad, J. and Hayat, M. (2018) MFSC: Multi-Voting Based Feature Selection for Classification of Golgi Proteins by Adopting the General Form of Chou's PseAAC Components. *Journal of Theoretical Biology*, **463**, 99-109. https://doi.org/10.1016/j.jtbi.2018.12.017
221. Akbar, S. and 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. *Journal of Theoretical Biology*, **455**, 205-211. https://doi.org/10.1016/j.jtbi.2018.07.018
222. Arif, M., Hayat, M. and 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. *Journal of Theoretical Biology*, **442**, 11-21. https://doi.org/10.1016/j.jtbi.2018.01.008
223. Butt, A.H., Rasool, N. and Khan, Y.D. (2018) Predicting Membrane Proteins and Their Types by Extracting Various Sequence Features into Chou's General PseAAC. *Molecular Biology Reports*, **45**, 2295-2306. https://doi.org/10.1007/s11033-018-4391-5
224. Cheng, X., Xiao, X. and Chou, K.C. (2018) pLoc-mEuk: Predict Subcellular Localization of Multi-Label Eukaryotic Proteins by Extracting the Key GO Information into General PseAAC. *Genomics*, **110**, 50-58. https://doi.org/10.1016/j.ygeno.2017.08.005
225. Cheng, X., Xiao, X. and Chou, K.C. (2018) pLoc-mGneg: Predict Subcellular Localization of Gram-Negative Bacterial Proteins by Deep Gene Ontology Learning via General PseAAC. *Genomics*, **110**, 231-239. https://doi.org/10.1016/j.ygeno.2017.10.002
226. Cheng, X., Xiao, X. and Chou, K.C. (2018) pLoc-mHum: Predict Subcellular Localization of Multi-Location Human Proteins via General PseAAC to Winnow out the Crucial GO Information. *Bioinformatics*, **34**, 1448-1456. https://doi.org/10.1093/bioinformatics/btx711
227. Cheng, X., Xiao, X. and Chou, K.C. (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. https://doi.org/10.1016/j.jtbi.2018.09.005
228. Cheng, X., Xiao, X. and Chou, K.C. (2018) pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. *Current Pharmaceutical Design*, **24**, 4013-4022. https://doi.org/10.2174/1381612824666181119145030
229. Chou, K.C., Cheng, X. and Xiao, X. (2019) pLoc_bal-mHum: Predict Subcellular Localization of Human Proteins by PseAAC and Quasi-Balancing Training Dataset. *Genomics*, **111**, 1274-1282.

https://doi.org/10.1016/j.ygeno.2018.08.007

230. Chou, K.C., Cheng, X. and Xiao, X. (2019) pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-Balancing Training Dataset. *Medicinal Chemistry*, **15**, 472-485. https://doi.org/10.2174/1573406415666181218102517

231. Contreras-Torres, E. (2018) Predicting Structural Classes of Proteins by Incorporating Their Global and Local Physicochemical and Conformational Properties into General Chou's PseAAC. *Journal of Theoretical Biology*, **454**, 139-145. https://doi.org/10.1016/j.jtbi.2018.05.033

232. Fu, X., Zhu, W., Liso, B., Cai, L., Peng, L. and Yang, J. (2018) Improved DNA-Binding Protein Identification by Incorporating Evolutionary Information into the Chou's PseAAC. *IEEE Access*, **20**, 66545-66556. https://doi.org/10.1109/ACCESS.2018.2876656

233. Ghauri, A.W., Khan, Y.D., Rasool, N., Khan, S.A. and Chou, K.C. (2018) pNitro-Tyr-PseAAC: Predict Nitrotyrosine Sites in Proteins by Incorporating Five Features into Chou's General PseAAC. *Current Pharmaceutical Design*, **24**, 4034-4043. https://doi.org/10.2174/1381612825666181127101039

234. Javed, F. and Hayat, M. (2019) Predicting Subcellular Localizations of Multi-Label Proteins by Incorporating the Sequence Features into Chou's PseAAC. *Genomics*, **111**, 1325-1332. https://doi.org/10.1016/j.ygeno.2018.09.004

235. Ju, Z. and Wang, S.Y. (2018) Prediction of Citrullination Sites by Incorporating k-Spaced Amino Acid Pairs into Chou's General Pseudo Amino Acid Composition. *Gene*, **664**, 78-83. https://doi.org/10.1016/j.gene.2018.04.055

236. Khan, Y.D., Rasool, N., Hussain, W., Khan, S.A. and Chou, K.C. (2018) iPhosT-PseAAC: Identify Phosphothreonine Sites by Incorporating Sequence Statistical Moments into PseAAC. *Analytical Biochemistry*, **550**, 109-116. https://doi.org/10.1016/j.ab.2018.04.021

237. Khan, Y.D., Rasool, N., Hussain, W., Khan, S.A. and Chou, K.C. (2018) iPhosY-PseAAC: Identify Phosphotyrosine Sites by Incorporating Sequence Statistical Moments into PseAAC. *Molecular Biology Reports*, **45**, 2501-2509. https://doi.org/10.1007/s11033-018-4417-z

238. Krishnan, M.S. (2018) Using Chou's General PseAAC to Analyze the Evolutionary Relationship of Receptor Associated Proteins (RAP) with Various Folding Patterns of Protein Domains. *Journal of Theoretical Biology*, **445**, 62-74. https://doi.org/10.1016/j.jtbi.2018.02.008

239. Liang, Y. and Zhang, S. (2018) Identify Gram-Negative Bacterial Secreted Protein Types by Incorporating Different Modes of PSSM into Chou's General PseAAC via Kullback-Leibler Divergence. *Journal of Theoretical Biology*, **454**, 22-29. https://doi.org/10.1016/j.jtbi.2018.05.035

240. Mei, J., Fu, Y. and Zhao, J. (2018) Analysis and Prediction of Ion Channel Inhibitors by Using Feature Selection and Chou's General Pseudo Amino Acid Composition. *Journal of Theoretical Biology*, **456**, 41-48. https://doi.org/10.1016/j.jtbi.2018.07.040

241. Mei, J. and Zhao, J. (2018) Prediction of HIV-1 and HIV-2 Proteins by Using Chou's Pseudo Amino Acid Compositions and Different Classifiers. *Scientific Reports*, **8**, Article No. 2359. https://doi.org/10.1038/s41598-018-20819-x

242. Mei, J. and Zhao, J. (2018) Analysis and Prediction of Presynaptic and Postsynaptic Neurotoxins by Chou's General Pseudo Amino Acid Composition and Motif Features. *Journal of Theoretical Biology*, **427**, 147-153. https://doi.org/10.1016/j.jtbi.2018.03.034

243. Mousavizadegan, M. and Mohabatkar, H. (2018) Computational Prediction of Antifungal Peptides via Chou's PseAAC and SVM. *Journal of Bioinformatics and Computational Biology*, **16**, Article ID: 1850016. https://doi.org/10.1142/S0219720018500166

244. Rahman, S.M., Shatabda, S., Saha, S., Kaykobad, M. and Sohel Rahman, M. (2018) DPP-PseAAC: A DNA-Binding Protein Prediction Model Using Chou's General PseAAC. *Journal of Theoretical Biology*, **452**, 22-34.

https://doi.org/10.1016/j.jtbi.2018.05.006

245. Sankari, E.S. and Manimegalai, D.D. (2018) Predicting Membrane Protein Types by Incorporating a Novel Feature Set into Chou's General PseAAC. *Journal of Theoretical Biology*, **455**, 319-328. https://doi.org/10.1016/j.jtbi.2018.07.032

246. Srivastava, A., Kumar, R. and Kumar, M. (2018) BlaPred: Predicting and Classifying Beta-Lactamase Using a 3-Tier Prediction System via Chou's General PseAAC. *Journal of Theoretical Biology*, **457**, 29-36. https://doi.org/10.1016/j.jtbi.2018.08.030

247. Zhang, S. and Duan, X. (2018) Prediction of Protein Subcellular Localization with Oversampling Approach and Chou's General PseAAC. *Journal of Theoretical Biology*, **437**, 239-250. https://doi.org/10.1016/j.jtbi.2017.10.030

248. Zhang, S. and Liang, Y. (2018) Predicting Apoptosis Protein Subcellular Localization by Integrating Auto-Cross Correlation and PSSM into Chou's PseAAC. *Journal of Theoretical Biology*, **457**, 163-169. https://doi.org/10.1016/j.jtbi.2018.08.042

249. Adilina, S., Farid, D.M. and Shatabda, S. (2019) Effective DNA Binding Protein Prediction by Using Key Features via Chou's General PseAAC. *Journal of Theoretical Biology*, **460**, 64-78. https://doi.org/10.1016/j.jtbi.2018.10.027

250. Ahmad, J. and Hayat, M. (2019) MFSC: Multi-Voting Based Feature Selection for Classification of Golgi Proteins by Adopting the General form of Chou's PseAAC Components. *Journal of Theoretical Biology*, **463**, 99-109. https://doi.org/10.1016/j.jtbi.2018.12.017

251. Awais, M., Hussain, W., Khan, Y.D., Rasool, N., Khan, S.A. and Chou, K.C. (2019) iPhosH-PseAAC: Identify Phosphohistidine Sites in Proteins by Blending Statistical Moments and Position Relative Features According to the Chou's 5-Step Rule and General Pseudo Amino Acid Composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. https://doi.org/10.1109/TCBB.2019.2919025 https://www.ncbi.nlm.nih.gov/pubmed/31144645

252. Butt, A.H., Rasool, N. and Khan, Y.D. (2019) Prediction of Antioxidant Proteins by Incorporating Statistical Moments Based Features into Chou's PseAAC. *Journal of Theoretical Biology*, **473**, 1-8. https://doi.org/10.1016/j.jtbi.2019.04.019

253. Chen, G., Cao, M., Yu, J., Guo, X. and Shi, S. (2019) Prediction and Functional Analysis of Prokaryote Lysine Acetylation Site by Incorporating Six Types of Features into Chou's General PseAAC. *Journal of Theoretical Biology*, **461**, 92-101. https://doi.org/10.1016/j.jtbi.2018.10.047

254. Cheng, X., Lin, W.Z., Xiao, X. and Chou, K.C. (2019) pLoc_bal-mAnimal: Predict Subcellular Localization of Animal Proteins by Balancing Training Dataset and PseAAC. *Bioinformatics*, **35**, 398-406. https://doi.org/10.1093/bioinformatics/bty628

255. Ehsan, A., Mahmood, M.K., Khan, Y.D., Barukab, O.M., Khan, S.A. and Chou, K.C. (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. https://doi.org/10.2174/1389202920666190325162307

256. Hussain, W., Khan, S.D., Rasool, N., Khan, S.A. and Chou, K.C. (2019) SPalmitoylC-PseAAC: A Sequence-Based Model Developed via Chou's 5-Steps Rule and General PseAAC for Identifying S-Palmitoylation Sites in Proteins. *Analytical Biochemistry*, **568**, 14-23. https://doi.org/10.1016/j.ab.2018.12.019

257. Hussain, W., Khan, Y.D., Rasool, N., Khan, S.A. and Chou, K.C. (2019) SPrenylC-PseAAC: A Sequence-Based Model Developed via Chou's 5-Steps Rule and General PseAAC for Identifying S-Prenylation Sites in Proteins. *Journal of Theoretical Biology*, **468**, 1-11. https://doi.org/10.1016/j.jtbi.2019.02.007

258. Jia, J., Li, X., Qiu, W., Xiao, X. and Chou, K.C. (2019) iPPI-PseAAC (CGR): Identify Protein-Protein Interac-

tions by Incorporating Chaos Game Representation into PseAAC. *Journal of Theoretical Biology*, **460**, 195-203. https://doi.org/10.1016/j.jtbi.2018.10.021

259. Kabir, M., Ahmad, S., Iqbal, M. and Hayat, M. (2020) iNR-2L: A Two-Level Sequence-Based Predictor Developed via Chou's 5-Steps Rule and General PseAAC for Identifying Nuclear Receptors and Their Families. *Genomics*, **112**, 276-285. https://doi.org/10.1016/j.ygeno.2019.02.006
260. Khan, Y.D., Jamil, M., Hussain, W., Rasool, N., Khan, S.A. and Chou, K.C. (2019) pSSbond-PseAAC: Prediction of Disulfide Bonding Sites by Integration of PseAAC and Statistical Moments. *Journal of Theoretical Biology*, **463**, 47-55. https://doi.org/10.1016/j.jtbi.2018.12.015
261. Ning, Q., Ma, Z. and Zhao, X. (2019) dForml(KNN)-PseAAC: Detecting Formylation Sites from Protein Sequences Using K-Nearest Neighbor Algorithm via Chou's 5-Step Rule and Pseudo Components. *Journal of Theoretical Biology*, **470**, 43-49. https://doi.org/10.1016/j.jtbi.2019.03.011
262. Shen, Y., Tang, J. and Guo, F. (2019) Identification of Protein Subcellular Localization via Integrating Evolutionary and Physicochemical Information into Chou's General PseAAC. *Journal of Theoretical Biology*, **462**, 230-239. https://doi.org/10.1016/j.jtbi.2018.11.012
263. Tahir, M., Hayat, M. and Khan, S.A. (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**, 199-210. https://doi.org/10.1007/s00438-018-1498-2
264. Wang, L., Zhang, R. and Mu, Y. (2019) Fu-SulfPred: Identification of Protein S-Sulfenylation Sites by Fusing Forests via Chou's General PseAAC. *Journal of Theoretical Biology*, **461**, 51-58. https://doi.org/10.1016/j.jtbi.2018.10.046
265. Xiao, X., Cheng, X., Chen, G., Mao, Q. and Chou, K.C. (2019) pLoc_bal-mGpos: Predict Subcellular Localization of Gram-Positive Bacterial Proteins by Quasi-Balancing Training Dataset and PseAAC. *Genomics*, **111**, 886-892. https://doi.org/10.1016/j.ygeno.2018.05.017
266. Xiao, X., Cheng, X., Chen, G., Mao, Q. and Chou, K.C. (2019) pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. *Medicinal Chemistry*, **15**, 496-509. https://doi.org/10.2174/1573406415666181217114710
267. Al Maruf, M.A. and Shatabda, S. (2019) iRSpot-SF: Prediction of Recombination Hotspots by Incorporating Sequence Based Features into Chou's Pseudo Components. *Genomics*, **111**, 966-972. https://doi.org/10.1016/j.ygeno.2018.06.003
268. Tahir, M., Tayara, H. and Chong, K.T. (2019) iRNA-PseKNC(2methyl): Identify RNA 2'-O-Methylation Sites by Convolution Neural Network and Chou's Pseudo Components. *Journal of Theoretical Biology*, **465**, 1-6. https://doi.org/10.1016/j.jtbi.2018.12.034
269. Tian, B., Wu, X., Chen, C., Qiu, W., Ma, Q. and Yu, B. (2019) Predicting Protein-Protein Interactions by Fusing Various Chou's Pseudo Components and Using Wavelet Denoising Approach. *Journal of Theoretical Biology* **462**, 329-346. https://doi.org/10.1016/j.jtbi.2018.11.011
270. Zhang, L. and Kong, L. (2019) iRSpot-PDI: Identification of Recombination Spots by Incorporating Dinucleotide Property Diversity Information into Chou's Pseudo Components. *Genomics*, **111**, 457-464. https://doi.org/10.1016/j.ygeno.2018.03.003
271. Zhang, S., Yang, K., Lei, Y. and 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. https://doi.org/10.1016/j.ygeno.2018.11.031
272. Nosrati, M., Mohabatkar, H. and 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. *International Immunopharmacology*, **78**, Article ID: 106020. https://doi.org/10.1016/j.intimp.2019.106020

273. Shen, H.B. and Chou, K.C. (2008) PseAAC: A Flexible Web-Server for Generating Various Kinds of Protein Pseudo Amino Acid Composition. *Analytical Biochemistry*, **373**, 386-388. https://doi.org/10.1016/j.ab.2007.10.012
274. Du, P., Wang, X., Xu, C. and 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. https://doi.org/10.1016/j.ab.2012.03.015
275. Cao, D.S., Xu, Q.S. and Liang, Y.Z. (2013) Propy: A Tool to Generate Various Modes of Chou's PseAAC. *Bioinformatics*, **29**, 960-962. https://doi.org/10.1093/bioinformatics/btt072
276. Du, P., Gu, S. and 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. https://doi.org/10.3390/ijms15033495
277. Chou, K.C. (2009) Pseudo Amino Acid Composition and Its Applications in Bioinformatics, Proteomics and System Biology. *Current Proteomics*, **6**, 262-274. https://doi.org/10.2174/157016409789973707
278. Chou, K.C. (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. https://doi.org/10.1016/j.jtbi.2010.12.024
279. Chen, W., Lei, T.Y., Jin, D.C., Lin, H. and Chou, K.C. (2014) PseKNC: A Flexible Web-Server for Generating Pseudo K-Tuple Nucleotide Composition. *Analytical Biochemistry*, **456**, 53-60. https://doi.org/10.1016/j.ab.2014.04.001
280. Chen, W., Lin, H. and Chou, K.C. (2015) Pseudo Nucleotide Composition or PseKNC: An Effective Formulation for Analyzing Genomic Sequences. *Molecular BioSystems*, **11**, 2620-2634. https://doi.org/10.1039/C5MB00155B
281. Liu, B., Yang, F., Huang, D.S. and Chou, K.C. (2018) iPromoter-2L: A Two-Layer Predictor for Identifying Promoters and Their Types by Multi-Window-Based PseKNC. *Bioinformatics*, **34**, 33-40. https://doi.org/10.1093/bioinformatics/btx579
282. Guo, S.H., Deng, E.Z., Xu, L.Q., Ding, H., Lin, H., Chen, W. and Chou, K.C. (2014) iNuc-PseKNC: A Sequence-Based Predictor for Predicting Nucleosome Positioning in Genomes with Pseudo k-Tuple Nucleotide Composition. *Bioinformatics*, **30**, 1522-1529. https://doi.org/10.1093/bioinformatics/btu083
283. Lin, H., Deng, E.Z., Ding, H., Chen, W. and Chou, K.C. (2014) iPro54-PseKNC: A Sequence-Based Predictor for Identifying Sigma-54 Promoters in Prokaryote with Pseudo k-Tuple Nucleotide Composition. *Nucleic Acids Research*, **42**, 12961-12972. https://doi.org/10.1093/nar/gku1019
284. Chen, W., Zhang, X., Brooker, J., Lin, H., Zhang, L. and Chou, K.C. (2015) PseKNC-General: A Cross-Platform Package for Generating Various Modes of Pseudo Nucleotide Compositions. *Bioinformatics*, **31**, 119-120. https://doi.org/10.1093/bioinformatics/btu602
285. Liu, B., Fang, L., Long, R., Lan, X. and Chou, K.C. (2016) iEnhancer-2L: A Two-Layer Predictor for Identifying Enhancers and Their Strength by Pseudo k-Tuple Nucleotide Composition. *Bioinformatics*, **32**, 362-369. https://doi.org/10.1093/bioinformatics/btv604
286. Xiao, X., Ye, H.X., Liu, Z., Jia, J.H. and Chou, K.C. (2016) iROS-gPseKNC: Predicting Replication Origin Sites in DNA by Incorporating Dinucleotide Position-Specific Propensity into General Pseudo Nucleotide Composition. *Oncotarget*, **7**, 34180-34189. https://doi.org/10.18632/oncotarget.9057
287. Feng, P., Ding, H., Yang, H., Chen, W., Lin, H. and Chou, K.C. (2017) iRNA-PseColl: Identifying the Occur-

rence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. *Molecular Therapy—Nucleic Acids*, **7**, 155-163. https://doi.org/10.1016/j.omtn.2017.03.006

288. Qiu, W.R., Jiang, S.Y., Sun, B.Q., Xiao, X., Cheng, X. and Chou, K.C. (2017) iRNA-2methyl: Identify RNA 2'-O-Methylation Sites by Incorporating Sequence-Coupled Effects into General PseKNC and Ensemble Classifier. *Medicinal Chemistry*, **13**, 734-743. https://doi.org/10.2174/1573406413666170623082245
289. Liu, B., Weng, F., Huang, D.S. and Chou, K.C. (2018) iRO-3wPseKNC: Identify DNA Replication Origins by Three-Window-Based PseKNC. *Bioinformatics*, **34**, 3086-3093. https://doi.org/10.1093/bioinformatics/bty312
290. Sabooh, M.F., Iqbal, N., Khan, M., Khan, M. and Maqbool, H.F. (2018) Identifying 5-Methylcytosine Sites in RNA Sequence Using Composite Encoding Feature into Chou's PseKNC. *Journal of Theoretical Biology*, **452**, 1-9. https://doi.org/10.1016/j.jtbi.2018.04.037
291. Su, Z.D., Huang, Y., Zhang, Z.Y., Zhao, Y.W., Wang, D., Chen, W., Chou, K.C. and Lin, H. (2018) iLoc-lncRNA: Predict the Subcellular Location of lncRNAs by Incorporating Octamer Composition into General PseKNC. *Bioinformatics*, **34**, 4196-4204. https://doi.org/10.1093/bioinformatics/bty508
292. Xiao, X., Xu, Z.C., Qiu, W.R., Wang, P., Ge, H.T. and Chou, K.C. (2019) iPSW(2L)-PseKNC: A Two-Layer Predictor for Identifying Promoters and Their Strength by Hybrid Features via Pseudo K-Tuple Nucleotide Composition. *Genomics*, **111**, 1785-1793. https://doi.org/10.1016/j.ygeno.2018.12.001
293. Yang, H., Qiu, W.R., Liu, G., Guo, F.B., Chen, W., Chou, K.C. and Lin, H. (2018) iRSpot-Pse6NC: Identifying Recombination Spots in *Saccharomyces cerevisiae* by Incorporating Hexamer Composition into General PseKNC. *International Journal of Biological Sciences*, **14**, 883-891. https://doi.org/10.7150/ijbs.24616
294. Feng, P., Yang, H., Ding, H., Lin, H., Chen, W. and Chou, K.C. (2019) iDNA6mA-PseKNC: Identifying DNA N^6-Methyladenosine Sites by Incorporating Nucleotide Physicochemical Properties into PseKNC. *Genomics*, **111**, 96-102. https://doi.org/10.1016/j.ygeno.2018.01.005
295. Nazari, I., Tahir, M., Tayari, H. and Chong, K.T. (2019) iN6-Methyl (5-Step): Identifying RNA N6-Methyladenosine Sites Using Deep Learning Mode via Chou's 5-Step Rules and Chou's General PseKNC. *Chemometrics and Intelligent Laboratory Systems*, **193**, Article ID: 103811. https://doi.org/10.1016/j.chemolab.2019.103811
296. Liu, B., Liu, F., Wang, X., Chen, J., Fang, L. and Chou, K.C. (2015) Pse-in-One: A Web Server for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. *Nucleic Acids Research*, **43**, W65-W71. https://doi.org/10.1093/nar/gkv458
297. Liu, B., Wu, H. and Chou, K.C. (2017) Pse-in-One 2.0: An Improved Package of Web Servers for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. *Natural Science*, **9**, 67-91. https://doi.org/10.4236/ns.2017.94007
298. Voet, D., Voet, J.G. and Pratt, C.W. (2002) Fundamentals of Biochemistry. John Wiley & Sons, New York.
299. Chou, K.C. and Chen, N.Y. (1977) The Biological Functions of Low-Frequency Phonons. *Scientia Sinica*, **20**, 447-457.
300. Du, Q.S., Wang, S.Q., Wei, D.Q., Zhu, Y., Guo, H., Sirois, S. and Chou, K.C. (2004) Polyprotein Cleavage Mechanism of SARS CoV Mpro and Chemical Modification of Octapeptide. *Peptides*, **25**, 1857-1864. https://doi.org/10.1016/j.peptides.2004.06.018
301. Chou, K.C. (1996) Review: Prediction of Human Immunodeficiency Virus Protease Cleavage Sites in Proteins. *Analytical Biochemistry*, **233**, 1-14. https://doi.org/10.1006/abio.1996.0001
302. Liang, G.Z. and Li, S.Z. (2007) A New Sequence Representation as Applied in Better Specificity Elucidation for Human Immunodeficiency Virus Type 1 Protease. *Biopolymers*, **88**, 401-412. https://doi.org/10.1002/bip.20669
303. Nanni, L. and Lumini, A. (2009) Using Ensemble of Classifiers for Predicting HIV Protease Cleavage Sites in Proteins. *Amino Acids*, **36**, 409-416. https://doi.org/10.1007/s00726-008-0076-z

304. Shen, H.B. and Chou, K.C. (2008) HIVcleave: A Web-Server for Predicting HIV Protease Cleavage Sites in Proteins. *Analytical Biochemistry*, **375**, 388-390. https://doi.org/10.1016/j.ab.2008.01.012

305. Du, Q.S., Sun, H. and Chou, K.C. (2007) Inhibitor Design for SARS Coronavirus Main Protease Based on "Distorted Key Theory". *Medicinal Chemistry*, **3**, 1-6. https://doi.org/10.2174/157340607779317616

306. Du, Q.S., Wang, S., Wei, D.Q., Sirois, S. and Chou, K.C. (2005) Molecular Modelling and Chemical Modification for Finding Peptide Inhibitor against SARS CoV Mpro. *Analytical Biochemistry*, **337**, 262-270. https://doi.org/10.1016/j.ab.2004.10.003

307. Gan, Y.R., Huang, H., Huang, Y.D., Rao, C.M., Zhao, Y., Liu, J.S., Wu, L. and Wei, D.Q. (2006) Synthesis and Activity of an Octapeptide Inhibitor Designed for SARS Coronavirus Main Proteinase. *Peptides*, **27**, 622-625. https://doi.org/10.1016/j.peptides.2005.09.006

308. Chou, K.C., Jiang, S.P., Liu, W.M. and Fee, C.H. (1979) Graph Theory of Enzyme Kinetics: 1. Steady-State Reaction System. *Scientia Sinica*, **22**, 341-358.

309. Chou, K.C., Zhang, C.T. and Maggiora, G.M. (1997) Disposition of Amphiphilic Helices in Heteropolar Environments. *PROTEINS*: *Structure*, *Function*, *and Genetics*, **28**, 99-108. https://doi.org/10.1002/(SICI)1097-0134(199705)28:1<99::AID-PROT10>3.0.CO;2-C

310. Chou, K.C., Lin, W.Z. and Xiao, X. (2011) Wenxiang: A Web-Server for Drawing Wenxiang Diagrams. *Natural Science*, **3**, 862-865. https://doi.org/10.4236/ns.2011.310111

311. Zhou, G.P. (2011) The Disposition of the LZCC Protein Residues in Wenxiang Diagram Provides New Insights into the Protein-Protein Interaction Mechanism. *Journal of Theoretical Biology*, **284**, 142-148. https://doi.org/10.1016/j.jtbi.2011.06.006

312. Zhou, G.P., Chen, D., Liao, S. and Huang, R.B. (2016) Recent Progresses in Studying Helix-Helix Interactions in Proteins by Incorporating the Wenxiang Diagram into the NMR Spectroscopy. *Current Topics in Medicinal Chemistry*, **16**, 581-590. https://doi.org/10.2174/1568026615666150819104617

313. Zhong, W.Z., Lalovic, B. and Ahan, J. (2009) Characterization of *in Vitro* and *in Vivo* Metabolism of AG-024322, a Novel Cyclin-Dependent Kinase (CDK) Inhibitor. *Health*, **1**, 249-262. https://doi.org/10.4236/health.2009.14041

314. Andrade, M.A., O'Donoghue, S.I. and Rost, B. (1998) Adaptation of Protein Surfaces to Subcellular Location. *Journal of Molecular Biology*, **276**, 517-525. https://doi.org/10.1006/jmbi.1997.1498

315. Reinhardt, A. and Hubbard, T. (1998) Using Neural Networks for Prediction of the Subcellular Location of Proteins. *Nucleic Acids Research*, **26**, 2230-2236. https://doi.org/10.1093/nar/26.9.2230

316. Yuan, Z. (1999) Prediction of Protein Subcellular Locations Using Markov Chain Models. *FEBS Letters*, **451**, 23-26. https://doi.org/10.1016/S0014-5793(99)00506-2

317. Emanuelsson, O., Nielsen, H., Brunak, S. and von Heijne, G. (2000) Predicting Subcellular Localization of Proteins Based on Their N-Terminal Amino Acid Sequence. *Journal of Molecular Biology*, **300**, 1005-1016. https://doi.org/10.1006/jmbi.2000.3903

318. Nakai, K. (2000) Protein Sorting Signals and Prediction of Subcellular Localization. *Advances in Protein Chemistry*, **54**, 277-344. https://doi.org/10.1016/S0065-3233(00)54009-1

319. Chou, K.C. and Shen, H.B. (2007) Recent Progresses in Protein Subcellular Location Prediction. *Analytical Biochemistry*, **370**, 1-16. https://doi.org/10.1016/j.ab.2007.07.006

320. Chou, K.C. and Shen, H.B. (2008) Cell-PLoc: A Package of Web Servers for Predicting Subcellular Localization of Proteins in Various Organisms. *Nature Protocols*, **3**, 153-162. https://doi.org/10.1038/nprot.2007.494

321. Zhong, W.Z. and Zhou, S.F. (2014) Molecular Science for Drug Development and Biomedicine. *International*

Journal of Molecular Sciences, **15**, 20072-20078. https://doi.org/10.3390/ijms151120072

322. Du, Q.S., Huang, R.B., Wang, S.Q. and Chou, K.C. (2010) Designing Inhibitors of M2 Proton Channel against H1N1 Swine Influenza Virus. *PLoS ONE*, **5**, e9388. https://doi.org/10.1371/journal.pone.0009388
323. Wang, S.Q., Cheng, X.C., Dong, W.L., Wang, R.L. and Chou, K.C. (2010) Three New Powerful Oseltamivir Derivatives for Inhibiting the Neuraminidase of Influenza Virus. *Biochemical and Biophysical Research Communications* (*BBRC*), **401**, 188-191. https://doi.org/10.1016/j.bbrc.2010.09.020
324. Li, X.B., Wang, S.Q., Xu, W.R., Wang, R.L. and Chou, K.C. (2011) Novel Inhibitor Design for Hemagglutinin against H1N1 Influenza Virus by Core Hopping Method. *PLoS ONE*, **6**, e28111. https://doi.org/10.1371/journal.pone.0028111
325. Ma, Y., Wang, S.Q., Xu, W.R., Wang, R.L. and Chou, K.C. (2012) Design Novel Dual Agonists for Treating Type-2 Diabetes by Targeting Peroxisome Proliferator-Activated Receptors with Core Hopping Approach. *PLoS ONE*, **7**, e38546. https://doi.org/10.1371/journal.pone.0038546
326. Liu, L., Ma, Y., Wang, R.L., Xu, W.R., Wang, S.Q. and Chou, K.C. (2013) Find Novel Dual-Agonist Drugs for Treating Type 2 Diabetes by Means of Cheminformatics. *Drug Design, Development and Therapy*, **7**, 279-287. https://doi.org/10.2147/DDDT.S42113
327. Chou, K.C. and Shen, H.B. (2006) Hum-PLoc: A Novel Ensemble Classifier for Predicting Human Protein Subcellular Localization. *Biochemical and Biophysical Research Communications* (*BBRC*), **347**, 150-157. https://doi.org/10.1016/j.bbrc.2006.06.059
328. Chou, K.C. and Shen, H.B. (2006) Addendum to "Hum-PLoc: A Novel Ensemble Classifier for Predicting Human Protein Subcellular Localization". *Biochemical and Biophysical Research Communications* (*BBRC*), **348**, 1479. https://doi.org/10.1016/j.bbrc.2006.08.030
329. Shen, H.B. and Chou, K.C. (2007) Gpos-PLoc: An Ensemble Classifier for Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. *Protein Engineering, Design, and Selection*, **20**, 39-46. https://doi.org/10.1093/protein/gzl053
330. Shen, H.B. and Chou, K.C. (2007) Virus-PLoc: A Fusion Classifier for Predicting the Subcellular Localization of Viral Proteins within Host and Virus-Infected Cells. *Biopolymers*, **85**, 233-240. https://doi.org/10.1002/bip.20640
331. Shen, H.B. and Chou, K.C. (2007) Nuc-PLoc: A New Web-Server for Predicting Protein Subnuclear Localization by Fusing PseAA Composition and PsePSSM. *Protein Engineering, Design & Selection*, **20**, 561-567. https://doi.org/10.1093/protein/gzm057
332. Shen, H.B., Yang, J. and Chou, K.C. (2007) Euk-PLoc: An Ensemble Classifier for Large-Scale Eukaryotic Protein Subcellular Location Prediction. *Amino Acids*, **33**, 57-67. https://doi.org/10.1007/s00726-006-0478-8
333. Chou, K.C. and Shen, H.B. (2010) Cell-PLoc 2.0: An Improved Package of Web-Servers for Predicting Subcellular Localization of Proteins in Various Organisms. *Natural Science*, **2**, 1090-1103. https://doi.org/10.4236/ns.2010.210136
334. Chou, K.C., Wu, Z.C. and Xiao, X. (2011) iLoc-Euk: A Multi-Label Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Eukaryotic Proteins. *PLoS ONE*, **6**, e18258. https://doi.org/10.1371/journal.pone.0018258
335. Wu, Z.C., Xiao, X. and Chou, K.C. (2011) iLoc-Plant: A Multi-Label Classifier for Predicting the Subcellular Localization of Plant Proteins with Both Single and Multiple Sites. *Molecular BioSystems*, **7**, 3287-3297. https://doi.org/10.1039/c1mb05232b
336. Xiao, X., Wu, Z.C. and Chou, K.C. (2011) iLoc-Virus: A Multi-Label Learning Classifier for Identifying the Subcellular Localization of Virus Proteins with Both Single and Multiple Sites. *Journal of Theoretical Biology*,

284, 42-51. https://doi.org/10.1016/j.jtbi.2011.06.005

337. Chou, K.C., Wu, Z.C. and Xiao, X. (2012) iLoc-Hum: Using Accumulation-Label Scale to Predict Subcellular Locations of Human Proteins with Both Single and Multiple Sites. *Molecular BioSystems*, **8**, 629-641. https://doi.org/10.1039/C1MB05420A

338. Wu, Z.C., Xiao, X. and Chou, K.C. (2012) iLoc-Gpos: A Multi-Layer Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Gram-Positive Bacterial Proteins. *Protein & Peptide Letters*, **19**, 4-14. https://doi.org/10.2174/092986612798472839

339. Lin, W.Z., Fang, J.A., Xiao, X. and Chou, K.C. (2013) iLoc-Animal: A Multi-Label Learning Classifier for Predicting Subcellular Localization of Animal Proteins. *Molecular BioSystems*, **9**, 634-644. https://doi.org/10.1039/c3mb25466f

340. Cheng, X., Zhao, S.G., Lin, W.Z., Xiao, X. and Chou, K.C. (2017) pLoc-mAnimal: Predict Subcellular Localization of Animal Proteins with Both Single and Multiple Sites. *Bioinformatics*, **33**, 3524-3531. https://doi.org/10.1093/bioinformatics/btx476

341. Chou, K.C. (2019) Advance in Predicting Subcellular Localization of Multi-Label Proteins and Its Implication for Developing Multi-Target Drugs. *Current Medicinal Chemistry*, **26**, 4918-4943. https://doi.org/10.2174/0929867326666190507082559 http://www.eurekaselect.com/172010/article

342. Chou, K.C. (2019) An Insightful Recollection for Predicting Protein Subcellular Locations in Multi-Label Systems. *Genomics*, in press. https://www.sciencedirect.com/science/article/pii/S0888754319304604?via%3Dihub

343. Chen, W., Feng, P.M., Lin, H. and Chou, K.C. (2013) iRSpot-PseDNC: Identify Recombination Spots with Pseudo Dinucleotide Composition. *Nucleic Acids Research*, **41**, e68. https://doi.org/10.1093/nar/gks1450

344. Feng, P.M., Chen, W., Lin, H. and Chou, K.C. (2013) iHSP-PseRAAAC: Identifying the Heat Shock Protein Families Using Pseudo Reduced Amino Acid Alphabet Composition. *Analytical Biochemistry*, **442**, 118-125. https://doi.org/10.1016/j.ab.2013.05.024

345. Chen, W., Feng, P.M., Deng, E.Z., Lin, H. and Chou, K.C. (2014) iTIS-PseTNC: A Sequence-Based Predictor for Identifying Translation Initiation Site in Human Genes Using Pseudo Trinucleotide Composition. *Analytical Biochemistry*, **462**, 76-83. https://doi.org/10.1016/j.ab.2014.06.022

346. Ding, H., Deng, E.Z., Yuan, L.F., Liu, L., Lin, H., Chen, W. and Chou, K.C. (2014) iCTX-Type: A Sequence-Based Predictor for Identifying the Types of Conotoxins in Targeting Ion Channels. *BioMed Research International* (*BMRI*), **2014**, Article ID: 286419. https://doi.org/10.1155/2014/286419

347. Liu, B., Fang, L., Liu, F., Wang, X., Chen, J. and Chou, K.C. (2015) Identification of Real microRNA Precursors with a Pseudo Structure Status Composition Approach. *PLoS ONE*, **10**, e0121501. https://doi.org/10.1371/journal.pone.0121501

348. Liu, Z., Xiao, X., Qiu, W.R. and Chou, K.C. (2015) iDNA-Methyl: Identifying DNA Methylation Sites via Pseudo Trinucleotide Composition. *Analytical Biochemistry*, **474**, 69-77. https://doi.org/10.1016/j.ab.2014.12.009

349. Xiao, X., Min, J.L., Lin, W.Z., Liu, Z., Cheng, X. and Chou, K.C. (2015) iDrug-Target: Predicting the Interactions between Drug Compounds and Target Proteins in Cellular Networking via the Benchmark Dataset Optimization Approach. *Journal of Biomolecular Structure and Dynamics* (*JBSD*), **33**, 2221-2233. https://doi.org/10.1080/07391102.2014.998710

350. Jia, J., Liu, Z., Xiao, X., Liu, B. and Chou, K.C. (2016) iSuc-PseOpt: Identifying Lysine Succinylation Sites in Proteins by Incorporating Sequence-Coupling Effects into Pseudo Components and Optimizing Imbalanced Training Dataset. *Analytical Biochemistry*, **497**, 48-56. https://doi.org/10.1016/j.ab.2015.12.009

351. Chen, W., Feng, P., Yang, H., Ding, H., Lin, H. and Chou, K.C. (2017) iRNA-AI: Identifying the Adenosine to

Inosine Editing Sites in RNA Sequences. *Oncotarget*, **8**, 4208-4217. https://doi.org/10.18632/oncotarget.13758

352. Chen, W., Ding, H., Zhou, X., Lin, H. and Chou, K.C. (2018) iRNA(m6A)-PseDNC: Identifying N6-Methyladenosine Sites Using Pseudo Dinucleotide Composition. *Analytical Biochemistry*, **561-562**, 59-65. https://doi.org/10.1016/j.ab.2018.09.002
353. Chen, W., Feng, P., Yang, H., Ding, H., Lin, H. and Chou, K.C. (2018) iRNA-3typeA: Identifying 3-Types of Modification at RNA's Adenosine sites. *Molecular Therapy*: *Nucleic Acid*, **11**, 468-474. https://doi.org/10.1016/j.omtn.2018.03.012
354. Li, J.X., Wang, S.Q., Du, Q.S., Wei, H., Li, X.M., Meng, J.Z., Wang, Q.Y., Xie, N.Z., Huang, R.B. and Chou, K.C. (2018) Simulated Protein Thermal Detection (SPTD) for Enzyme Thermostability Study and an Application Example for Pullulanase from Bacillus Deramificans. *Current Pharmaceutical Design*, **24**, 4023-4033. https://doi.org/10.2174/1381612824666181113120948
355. Qiu, W.R., Sun, B.Q., Xiao, X., Xu, Z.C., Jia, J.H. and Chou, K.C. (2018) iKcr-PseEns: Identify Lysine Crotonylation Sites in Histone Proteins with Pseudo Components and Ensemble Classifier. *Genomics*, **110**, 239-246. https://doi.org/10.1016/j.ygeno.2017.10.008
356. Chou, K.C. (2019) Progresses in Predicting Post-Translational Modification. *International Journal of Peptide Research and Therapeutics*. https://doi.org/10.1007/s10989-019-09893-5 https://link.springer.com/article/10.1007%2Fs10989-019-09893-5
357. Du, X., Diao, Y., Liu, H. and Li, S. (2019) MsDBP: Exploring DNA-Binding Proteins by Integrating Multi-Scale Sequence Information via Chou's 5-Steps Rule. *Journal of Proteome Research*, **18**, 3119-3132. https://doi.org/10.1021/acs.jproteome.9b00226
358. Ju, Z. and Wang, S.Y. (2020) Prediction of Lysine Formylation Sites Using the Composition of k-Spaced Amino Acid Pairs via Chou's 5-Steps Rule and General Pseudo Components. *Genomics*, **112**, 859-866. https://doi.org/10.1016/j.ygeno.2019.05.027
359. Khan, Y.D., Batool, A., Rasool, N., Khan, A. and Chou, K.C. (2019) Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. *Letters in Organic Chemistry*, **16**, 283-293. https://doi.org/10.2174/1570178615666180802122953
360. Le, N.Q.K. (2019) iN6-Methylat (5-Step): Identifying DNA N(6)-Methyladenine Sites in Rice Genome Using Continuous Bag of Nucleobases via Chou's 5-Step Rule. *Molecular Genetics and Genomics*, **294**, 1173-1182. https://doi.org/10.1007/s00438-019-01570-y
361. Le, N.Q.K., Yapp, E.K.Y., Ho, Q.T., Nagasundaram, N., Ou, Y.Y. and Yeh, H.Y. (2019) iEnhancer-5Step: Identifying Enhancers Using Hidden Information of DNA Sequences via Chou's 5-Step Rule and Word Embedding. *Analytical Biochemistry*, **571**, 53-61. https://doi.org/10.1016/j.ab.2019.02.017
362. Lu, Y., Wang, S., Wang, J., Zhou, G., Zhang, Q., Zhou, X., Niu, B., Chen, Q. and Chou, K.C. (2019) An Epidemic Avian Influenza Prediction Model Based on Google Trends. *Letters in Organic Chemistry*, **16**, 303-310. https://doi.org/10.2174/1570178615666180724103325
363. Romero-Molina, S., Ruiz-Blanco, Y.B., Harms, M., J. Münch and E. Sanchez-Garcia (2019) PPI-Detect: A Support Vector Machine Model for Sequence-Based Prediction of Protein-Protein Interactions. *Journal of Computational Chemistry*, **40**, 1233-1242. https://doi.org/10.1002/jcc.25780
364. Tahir, M., Tayara, H. and Chong, K.T. (2019) iDNA6mA (5-Step Rule): Identification of DNA N6-Methyladenine Sites in the Rice Genome by Intelligent Computational Model via Chou's 5-Step Rule. *Chemometrics and Intelligent Laboratory Systems*, **189**, 96-101. https://doi.org/10.1016/j.chemolab.2019.04.007
365. Song, J., Li F., Takemoto, K., Haffari, G., Akutsu, T., Chou, K.C. and Webb, G.I. (2018) PREvaIL, an Integrative Approach for Inferring Catalytic Residues Using Sequence, Structural and Network Features in a Machine

Learning Framework. *Journal of Theoretical Biology*, **443**, 125-137. https://doi.org/10.1016/j.jtbi.2018.01.023

366. Chen, Z., Liu, X., Li, F., Li, C., Marquez-Lago, T., Leier, A., Akutsu, T., Webb, G.I., Xu, D., Smith, A.I., Li, L., Chou, K.C. and Song, J. (2019) Large-Scale Comparative Assessment of Computational Predictors for Lysine Post-Translational Modification Sites. *Briefings in Bioinformatics*, **20**, 2267-2290. https://doi.org/10.1093/bib/bby089

367. Chen, Z., Zhao, P.Y., Li, F., Leier, A., Marquez-Lago, T.T., Wang, Y., Webb, G.I., Smith, A.I., Daly, R.J., Chou, K.C. and Song, J. (2018) iFeature: A Python Package and Web Server for Features Extraction and Selection from Protein and Peptide Sequences. *Bioinformatics*, **34**, 2499-2502. https://doi.org/10.1093/bioinformatics/bty140

368. Li, F., Li, C., Marquez-Lago, T.T., Leier, A., Akutsu, T., Purcell, A.W., Smith, A.I., Lightow, T., Daly, R.J., Song, J. and Chou, K.C. (2018) Quokka: A Comprehensive Tool for Rapid and Accurate Prediction of Kinase Family-Specific Phosphorylation Sites in the Human Proteome. *Bioinformatics*, **34**, 4223-4231. https://doi.org/10.1093/bioinformatics/bty522

369. Li, F., Wang, Y., Li, C., Marquez-Lago, T.T., Leier, A., Rawlings, N.D., Haffari, G., Revote, J., Akutsu, T., Chou, K.C., Purcell, A.W., Pike, R.N., Webb, G.I., Ian Smith, A., Lithgow, T., Daly, R.J., Whisstock, J.C. and Song, J. (2019) Twenty Years of Bioinformatics Research for Protease-Specific Substrate and Cleavage Site Prediction: A Comprehensive Revisit and Benchmarking of Existing Methods. *Briefings in Bioinformatics*, **20**, 2150-2166. https://doi.org/10.1093/bib/bby077

370. Song, J., Li, F., Leier, A., Marquez-Lago, T.T., Akutsu, T., Haffari, G., Chou, K.C., Webb, G.I. and Pike, R.N. (2018) PROSPERous: High-Throughput Prediction of Substrate Cleavage Sites for 90 Proteases with Improved Accuracy. *Bioinformatics*, **34**, 684-687. https://doi.org/10.1093/bioinformatics/btx670

371. Song, J., Wang, Y., Li, F., Akutsu, T., Rawlings, N.D., Webb, G.I. and Chou, K.C. (2018) iProt-Sub: A Comprehensive Package for Accurately Mapping and Predicting Protease-Specific Substrates and Cleavage Sites. *Briefings in Bioinformatics*, **20**, 638-658. https://doi.org/10.1093/bib/bby028

372. Wang, J., Li, J., Yang, B., Xie, R., Marquez-Lago, T.T., Leier, A., Hayashida, M., Akutsu, T., Zhang, Y., Chou, K.C., Selkrig, J., Zhou, T., Song, J. and Lithgow, T. (2018) Bastion3: A Two-Layer Approach for Identifying Type III Secreted Effectors Using Ensemble Learning. *Bioinformatics*, **35**, 2017-2028. https://doi.org/10.1093/bioinformatics/bty914

373. Wang, J., Yang, B., Leier, A., Marquez-Lago, T.T., Hayashida, M., Rocker, A., Yanju, Z., Akutsu, T., Chou, K.C., Strugnell, R.A., Song, J. and Lithgow, T. (2018) Bastion6: A Bioinformatics Approach for Accurate Prediction of Type VI Secreted Effectors. *Bioinformatics*, **34**, 2546-2555. https://doi.org/10.1093/bioinformatics/bty155

374. Zhang, S., Yang, K., Lei, Y. and 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.

375. Zhang, Y., Xie, R., Wang, J., Leier, A., Marquez-Lago, T.T., Akutsu, T., Webb, G.I., Chou, K.C. and Song, J. (2019) Computational Analysis and Prediction of Lysine Malonylation Sites by Exploiting Informative Features in an Integrative Machine-Learning Framework. *Briefings in Bioinformatics*, **20**, 2185-2199. https://doi.org/10.1093/bib/bby079

376. Ilyas, S., Hussain, W., Ashraf, A., Khan, Y.D., Khan, S.A. and Chou, K.C. (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*, **20**, 275-292. https://doi.org/10.2174/1389202920666190809095206

377. Dutta, A., Dalmia, A., Athul R, Singh, K.K. and Anand, A. (2019) Using the Chou's 5-Steps Rule to Predict Splice Junctions with Interpretable Bidirectional Long Short-Term Memory Networks. *Computers in Biology and Medicine*, **116**, Article ID: 103558. https://doi.org/10.1016/j.compbiomed.2019.103558

378. Wiktorowicz, A., Wit, A., Dziewierz, A., Rzeszutko, L., Dudek, D. and Kleczynski, P. (2019) Calcium Pattern Assessment in Patients with Severe Aortic Stenosis via the Chou's 5-Steps Rule. *Current Pharmaceutical Design*, **25**, 3769-3775. https://doi.org/10.2174/1381612825666190930101258

379. Vundavilli, H., Datta, A., Sima, C., Hua, J., Lopes, R. and Bittner, M. (2020) Using Chou's 5-Steps Rule to Model Feedback in Lung Cancer. *IEEE Journal of Biomedical and Health Informatics*, in press. https://doi.org/10.1109/JBHI.2019.2958042

380. Charoenkwan, P., Schaduangrat, N., Nantasenamat, C., Piacham, T. and Shoombuatong, W. (2020) iQSP: A Sequence-Based Tool for the Prediction and Analysis of Quorum Sensing Peptides via Chou's 5-Steps Rule and Informative Physicochemical Properties. *International Journal of Molecular Sciences*, **21**, 75. https://doi.org/10.3390/ijms21010075

381. Vishnoi, S., Garg, P. and Arora, P. (2020) Physicochemical n-Grams Tool: A Tool for Protein Physicochemical Descriptor Generation via Chou's 5-Step Rule. *Chemical Biology & Drug Design*, **95**, 79-86. https://doi.org/10.1111/cbdd.13617

382. Dobosz, R., Mucko, J. and Gawinecki, R. (2020) Using Chou's 5-Step Rule to Evaluate the Stability of Tautomers: Susceptibility of 2-[(Phenylimino)-methyl]-cyclohexane-1,3-diones to Tautomerization Based on the Calculated Gibbs Free Energies. *Energies*, **13**, 183. https://doi.org/10.3390/en13010183

383. Zhai, X., Chen, M. and Lu, W. (2018) Accelerated Search for Perovskite Materials with Higher Curie Temperature Based on the Machine Learning Methods. *Computational Materials Science*, **151**, 41-48. https://doi.org/10.1016/j.commatsci.2018.04.031

384. Chou, K.C. and Forsen, S. (1980) Diffusion-Controlled Effects in Reversible Enzymatic Fast Reaction System: Critical Spherical Shell and Proximity Rate Constants. *Biophysical Chemistry*, **12**, 255-263. https://doi.org/10.1016/0301-4622(80)80002-0

385. Chou, K.C. and Forsen, S. (1980) Graphical Rules for Enzyme-Catalyzed Rate Laws. *Biochemical Journal*, **187**, 829-835. https://doi.org/10.1042/bj1870829

386. Chou, K.C., Forsen, S. and Zhou, G.Q. (1980) Three Schematic Rules for Deriving Apparent Rate Constants. *Chemica Scripta*, **16**, 109-113.

387. Chou, K.C., Li, T.T. and Forsen, S. (1980) The Critical Spherical Shell in Enzymatic Fast Reaction Systems. *Biophysical Chemistry*, **12**, 265-269. https://doi.org/10.1016/0301-4622(80)80003-2

388. Li, T.T., Chou, K.C. and Forsen, S. (1980) The Flow of Substrate Molecules in Fast Enzyme-Catalyzed Reaction Systems. *Chemica Scripta*, **16**, 192-196.

389. Chou, K.C., Carter, R.E. and Forsen, S. (1981) A New Graphical Method for Deriving Rate Equations for Complicated Mechanisms. *Chemica Scripta*, **18**, 82-86.

390. Chou, K.C., Chen, N.Y. and Forsen, S. (1981) The Biological Functions of Low-Frequency Phonons: 2. Cooperative Effects. *Chemica Scripta*, **18**, 126-132.

391. Chou, K.C. and Forsen, S. (1981) Graphical Rules of Steady-State Reaction Systems. *Canadian Journal of Chemistry*, **59**, 737-755. https://doi.org/10.1139/v81-107

392. Chou, K.C. (1983) Low-Frequency Vibrations of Helical Structures in Protein Molecules. *Biochemical Journal*, **209**, 573-580. https://doi.org/10.1042/bj2090573

393. Chou, K.C. (1983) Identification of Low-Frequency Modes in Protein Molecules. *Biochemical Journal*, **215**, 465-469. https://doi.org/10.1042/bj2150465

394. Zhou, G.P. and Deng, M.H. (1984) An Extension of Chou's Graphic Rules for Deriving Enzyme Kinetic Equations to Systems Involving Parallel Reaction Pathways. *Biochemical Journal*, **222**, 169-176. https://doi.org/10.1042/bj2220169

395. Chou, K.C. (1984) Biological Functions of Low-Frequency Vibrations (Phonons). 3. Helical Structures and Microenvironment. *Biophysical Journal*, **45**, 881-889. https://doi.org/10.1016/S0006-3495(84)84234-4

396. Chou, K.C. (1984) The Biological Functions of Low-Frequency Phonons. 4. Resonance Effects and Allosteric Transition. *Biophysical Chemistry*, **20**, 61-71. https://doi.org/10.1016/0301-4622(84)80005-8

397. Chou, K.C. (1984) Low-Frequency Vibrations of DNA Molecules. *Biochemical Journal*, **221**, 27-31. https://doi.org/10.1042/bj2210027

398. Chou, K.C. (1985) Low-Frequency Motions in Protein Molecules: Beta-Sheet and Beta-Barrel. *Biophysical Journal*, **48**, 289-297. https://doi.org/10.1016/S0006-3495(85)83782-6

399. Chou, K.C. (1985) Prediction of a Low-Frequency Mode in Bovine Pancreatic Trypsin Inhibitor Molecule. *International Journal of Biological Macromolecules*, **7**, 77-80. https://doi.org/10.1016/0141-8130(85)90035-2

400. Chou, K.C. and Kiang, Y.S. (1985) The Biological Functions of Low-Frequency Phonons: 5. A Phenomenological Theory. *Biophysical Chemistry*, **22**, 219-235. https://doi.org/10.1016/0301-4622(85)80045-4

401. Chou, K.C. (1986) Origin of Low-Frequency Motion in Biological Macromolecules: A View of Recent Progress of Quasi-Continuity Model. *Biophysical Chemistry*, **25**, 105-116. https://doi.org/10.1016/0301-4622(86)87001-6

402. Chou, K.C. (1987) The Biological Functions of Low-Frequency Phonons: 6. A Possible Dynamic Mechanism of Allosteric Transition in Antibody Molecules. *Biopolymers*, **26**, 285-295. https://doi.org/10.1002/bip.360260209

403. Chou, K.C. (1988) Review: Low-Frequency Collective Motion in Biomacromolecules and Its Biological Functions. *Biophysical Chemistry*, **30**, 3-48. https://doi.org/10.1016/0301-4622(88)85002-6

404. Chou, K.C. and Maggiora, G.M. (1988) The Biological Functions of Low-Frequency Phonons: 7. The Impetus for DNA to Accommodate Intercalators. *British Polymer Journal*, **20**, 143-148. https://doi.org/10.1002/pi.4980200209

405. Chou, K.C. (1989) Low-Frequency Resonance and Cooperativity of Hemoglobin. Trends in Biochemical Sciences, **14**, 212-213. https://doi.org/10.1016/0968-0004(89)90026-1

406. Chou, K.C., Maggiora, G.M. and Mao, B. (1989) Quasi-Continuum Models of Twist-Like and Accordion-Like Low-Frequency Motions in DNA. *Biophysical Journal*, **56**, 295-305. https://doi.org/10.1016/S0006-3495(89)82676-1

407. Chou, K.C. (1989) Graphic Rules in Steady and Non-Steady Enzyme Kinetics. *Journal of Biological Chemistry*, **264**, 12074-12079.

408. Chou, K.C. (1990) Review: Applications of Graph Theory to Enzyme Kinetics and Protein Folding Kinetics. Steady and Non-Steady State Systems. *Biophysical Chemistry*, **35**, 1-24. https://doi.org/10.1016/0301-4622(90)80056-D

409. Althaus, I.W., Chou, J.J., Gonzales, A.J., Diebel, M.R., Chou, K.C., Kezdy, F.J., Romero, D.L., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1993) Steady-State Kinetic Studies with the Non-Nucleoside HIV-1 Reverse Transcriptase Inhibitor U-87201E. *Journal of Biological Chemistry*, **268**, 6119-6124.

410. Althaus, I.W., Gonzales, A.J., Chou, J.J., Diebel, M.R., Chou, K.C., Kezdy, F.J., Romero, D.L., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1993) The Quinoline U-78036 Is a Potent Inhibitor of HIV-1 Reverse Transcriptase. *Journal of Biological Chemistry*, **268**, 14875-14880.

411. Althaus, I.W., Chou, J.J., Gonzales, A.J., Diebel, M.R., Chou, K.C., Kezdy, F.J., Romero, D.L., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1993) Kinetic Studies with the Nonnucleoside HIV-1 Reverse Transcriptase Inhibitor U-88204E. *Biochemistry*, **32**, 6548-6554. https://doi.org/10.1021/bi00077a008

412. Althaus, I.W., Chou, J.J., Gonzales, A.J., Diebel, M.R., Chou, K.C., Kezdy, F.J., Romero, D.L., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1994) Steady-State Kinetic Studies with the Polysulfonate U-9843, an HIV Re-

verse Transcriptase Inhibitor. *Cellular and Molecular Life Science* (*Experientia*), **50**, 23-28. https://doi.org/10.1007/BF01992044

413. Althaus, I.W., Chou, J.J., Gonzales, A.J., Diebel, M.R., Chou, K.C., Kezdy, F.J., Romero, D.L., Thomas, R.C., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1994) Kinetic Studies with the Non-Nucleoside Human Immunodeficiency Virus Type-1 Reverse Transcriptase Inhibitor U-90152e. *Biochemical Pharmacology*, **47**, 2017-2028. https://doi.org/10.1016/0006-2952(94)90077-9
414. Chou, K.C., Kezdy, F.J. and Reusser, F. (1994) Review: Kinetics of Processive Nucleic Acid Polymerases and Nucleases. *Analytical Biochemistry*, **221**, 217-230. https://doi.org/10.1006/abio.1994.1405
415. Chou, K.C., Zhang, C.T. and Maggiora, G.M. (1994) Solitary Wave Dynamics as a Mechanism for Explaining the Internal Motion during Microtubule Growth. *Biopolymers*, **34**, 143-153. https://doi.org/10.1002/bip.360340114
416. Althaus, I.W., Chou, K.C., Franks, K.M., Diebel, M.R., Kezdy, F.J., Romero, D.L., Thomas, R.C., Aristoff, P.A., Tarpley, W.G. and Reusser, F. (1996) The Benzylthio-Pyrididine U-31,355, a Potent Inhibitor of HIV-1 Reverse Transcriptase. *Biochemical Pharmacology*, **51**, 743-750. https://doi.org/10.1016/0006-2952(95)02390-9
417. Liu, H., Wang, M. and Chou, K.C. (2005) Low-Frequency Fourier Spectrum for Predicting Membrane Protein Types. *Biochemical and Biophysical Research Communications* (*BBRC*), **336**, 737-739. https://doi.org/10.1016/j.bbrc.2005.08.160
418. Gordon, G. (2007) Designed Electromagnetic Pulsed Therapy: Clinical Applications. *Journal of Cellular Physiology*, **212**, 579-582. https://doi.org/10.1002/jcp.21025
419. Andraos, J. (2008) Kinetic Plasticity and the Determination of Product Ratios for Kinetic Schemes Leading to Multiple Products without Rate Laws: New Methods Based on Directed Graphs. *Canadian Journal of Chemistry*, **86**, 342-357. https://doi.org/10.1139/v08-020
420. Chou, K.C. and Shen, H.B. (2009) FoldRate: A Web-Server for Predicting Protein Folding Rates from Primary Sequence. *The Open Bioinformatics Journal*, **3**, 31-50. https://doi.org/10.2174/1875036200903010031
421. Shen, H.B., Song, J.N. and Chou, K.C. (2009) Prediction of Protein Folding Rates from Primary Sequence by Fusing Multiple Sequential Features. *Journal of Biomedical Science and Engineering* (*JBiSE*), **2**, 136-143. https://doi.org/10.4236/jbise.2009.23024
422. Wang, J.F. and Chou, K.C. (2009) Insight into the Molecular Switch Mechanism of Human Rab5a from Molecular Dynamics Simulations. *Biochemical and Biophysical Research Communications* (*BBRC*), **390**, 608-612. https://doi.org/10.1016/j.bbrc.2009.10.014
423. Gordon, G. (2008) Extrinsic Electromagnetic Fields, Low Frequency (Phonon) Vibrations, and Control of Cell Function: A Non-Linear Resonance System. *Journal of Biomedical Science and Engineering* (*JBiSE*), **1**, 152-156. https://doi.org/10.4236/jbise.2008.13025
424. Madkan, A., Blank, M., Elson, E., Chou, K.C., Geddis, M.S. and Goodman, R. (2009) Steps to the Clinic with ELF EMF. *Natural Science*, **1**, 157-165. https://doi.org/10.4236/ns.2009.13020
425. Chou, K.C. (2010) Graphic Rule for Drug Metabolism Systems. *Current Drug Metabolism*, **11**, 369-378. https://doi.org/10.2174/138920010791514261
426. Lian, P., Wei, D.Q., Wang, J.F. and Chou, K.C. (2011) An Allosteric Mechanism Inferred from Molecular Dynamics Simulations on Phospholamban Pentamer in Lipid Membranes. *PLoS ONE*, **6**, e18587. https://doi.org/10.1371/journal.pone.0018587
427. Liao, Q.H., Gao, Q.Z., Wei, J. and Chou, K.C. (2011) Docking and Molecular Dynamics Study on the Inhibitory Activity of Novel Inhibitors on Epidermal Growth Factor Receptor (EGFR). *Medicinal Chemistry*, **7**, 24-31. https://doi.org/10.2174/157340611794072698

428. Li, J., Wei, D.Q., Wang, J.F., Yu, Z.T. and Chou, K.C. (2012) Molecular Dynamics Simulations of CYP2E1. *Medicinal Chemistry*, **8**, 208-221. https://doi.org/10.2174/157340612800493692

429. Wang, J.F. and Chou, K.C. (2012) Recent Advances in Computational Studies on Influenza a Virus M2 Proton Channel. *Mini-Reviews in Medicinal Chemistry*, **12**, 971-978. https://doi.org/10.2174/138955712802762275

430. Zhang, T., Wei, D.Q. and Chou, K.C. (2012) A Pharmacophore Model Specific to Active Site of CYP1A2 with a Novel Molecular Modeling Explorer and CoMFA. *Medicinal Chemistry*, **8**, 198-207. https://doi.org/10.2174/157340612800493601

431. Chou, K.C. (2019) Showcase to Illustrate How the Web-Server iDNA6mA-PseKNC Is Working. *Journal of Pathology Research Reviews & Reports*, **1**, 1-15.

432. Chou, K.C. (2019) The pLoc_bal-mPlant Is a Powerful Artificial Intelligence Tool for Predicting the Subcellular Localization of Plant Proteins Purely Based on Their Sequence Information. *International Journal of Nutritional Sciences*, **4**, 1037.

433. Chou, K.C. (2019) Showcase to Illustrate How the Web-Server iNitro-Tyr Is Working. *Glo J of Com Sci and Infor Tec*, **2**, 1-16.

434. Chou, K.C. (2019) The pLoc_bal-mAnimal Is a Powerful Artificial Intelligence Tool for Predicting the Subcellular Localization of Animal Proteins Based on Their Sequence Information Alone. *Scientific Journal of Biometrics & Biostatistics* (*Sci J Biome and Biost*), **2**, 1-13.

435. Chou, K.C. (2020) Showcase to Illustrate How the Webserver pLoc_bal-mEuk Is Working. *Biomedical Journal of Scientific & Technical Research*, **24**, 18156-18160.

436. Chou, K.C. (2020) The pLoc_bal-mGneg Predictor Is a Powerful Web-Server for Identifying the Subcellular Localization of Gram-Negative Bacterial Proteins Based on their Sequences Information Alone. *International Journal of Sciences*, **9**, 27-34. https://doi.org/10.18483/ijSci.2248

437. Chou, K.C. (2020) How the Artificial Intelligence Tool iRNA-2methyl Is Working for RNA 2'-Omethylation sites. *Journal of Medical Care Research and Review*, **3**, 348-366.

438. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server iKcr-PseEns Is Working. *Journal of Medical Care Research and Review*, **3**, 331-347. https://doi.org/10.18483/ijSci.2247

439. Shen, H.B. and Chou, K.C. (2007) Hum-mPLoc: An Ensemble Classifier for Large-Scale Human Protein Subcellular Location Prediction by Incorporating Samples with Multiple Sites. *Biochemical and Biophysical Research Communications* (*BBRC*), **355**, 1006-1011. https://doi.org/10.1016/j.bbrc.2007.02.071