The Implication of "I Am the Alpha and the Omega" to Internet Institutes

Kuo-Chen Chou

Gordon Life Science Institute, Boston, Massachusetts 02478, United States of America

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

Keywords: Pandemic COVID-19, Coronavirus, Atheists, Fiery Furnace, Evil and Righteous, Internet Institutes

Received: July 4, 2020 **Accepted:** July 12, 2020 **Published:** July 15, 2020

ABSTRACT

It is extremely fearful for the pestilences covering our Earth. Does that mean the "World End" is around the corner? For the so-called "Atheists" originally proposed by Karl Max and Friedrich Engels, "there is a Beginning, there must be an End", meaning our Earth will finally no longer exist in the entire Universe by colliding with the other planet. According to Holly Bible, however, Jesus, will send out his angels to separate the wicked from the righteous and throw the former into the fiery furnace. For such a special time-period, many useful ideas or outcomes can be acquired by the Internet Institutes.

1. INTRODUCTION

As of July-03-2020, more than 230 countries on the Earth have been attacked by the coronavirus disease 2019 (COVID-19): for USA alone with reported 2,803,454 cases of which 130,995 result in deaths; for United Kingdom with 283,757 cases and 43,995 to deaths.

2. FACTS AND DISCUSSIONS

It is much more fearful than the "atomic bombs" (2nd World War, 1945) or any kind of terrorists ("911", 2001). The death number has also far beyond the reach of the death of military persons killed in any of war involved with USA.

For the so-called "Atheists", typically represented by "Karl Max" and "Friedrich Engels", claiming "there is a Beginning, there must be an End", meaning our Earth will finally no longer exist in the entire Universe by colliding with the other planet.

According to Bible, however, close to the "World-End", nation will rise against nation, and kingdom against kingdom. There will be great earthquakes, famines and pestilences in various places, and fearful events and great signs from Heaven."

Jesus will send out his angels to weed out those who are sin, evil and wicked. They will be thrown by the angels into the fiery furnace, where they will be weeping and gnashing of teeth. In contrast to this, the righteous will be raised to the Heaven.

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome, which was first identified in December 2019 in Wuhan, Hubei, China. After April 2020 and causing about 4000 deaths, although no remarkable infectious cases reported in Wuhan. Nevertheless and unfortunately, the 2nd-wave coronavirus diseases have been also identified on Beijing during May 2020. This kind of originally from "East-Globe" or "Eastern hemisphere" to "West "Globe" or "Hemisphere" and then kicked back from the West to the East, very much like playing "Tennis", "ping-pong" or "Badminton", "ball". The extremely dangerous ball is none but "Coronavirus".

Since all the scientists working in a sharing laboratory of the Universities or most conversional Institutes must wear masks except those working in the "Internet Institute" such as the "Gordon Life Scient Institute" [1, 2]. And the results thus obtained will be of real usage for the other planet as indicated in [3] as well as widely and increasingly agreeable as supported by many papers from different angles or aspects, particularly for the idea of "Pseudo Amino Acid Composition" or "PseAAC" [4-74], the "5-steps Rule" [75-96], the "Wenxiang Diagram" [98-100], the "HIV protease inhibitor prediction" [101-106], and the "Graphic Rules" [107-115]. Using graphic approaches to study biological and medical systems can provide an intuitive vision and useful insights for helping analyze complicated relations therein as shown by the eight master pieces of pioneering papers from the then Chairman of Nobel Prize Committee Sture Forsen [107, 109, 110, 116-120] and many follow-up papers [67, 98, 99, 113, 115, 121-163], and a series of recent papers [164-180].

3. CONCLUSIONS

For our Earth, after several waves of the killings as described in the Section 2, the time of its "End" will become much faster according to the exponential mode. Before its "End", it will provide the most useful knowledge to do the science with the "Internet Institutes".

CONFLICTS OF INTEREST

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

REFERENCES

1. Chou, K.C. (2019) The Cradle of Gordon Life Science Institute and Its Development and Driving Force. *Biomedical Journal of Scientific & Technical Research*, **23**, Article ID: 17848.
2. Chou, K.C. (2019) Intriguing Story about the Birth of Gordon Life Science Institute and Its Development and Driving Force. *Journal of Retro Virology and Anti Retro Virology*, **1**, Article ID: 180002.
3. Chou, K.C. (2020) The Development of Gordon Life Science Institute: Its Driving Force and Accomplishments. *Natural Science*, **12**, 202-217. https://doi.org/10.4236/ns.2020.124018
4. 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
5. 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
6. 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
7. 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

8. 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

9. 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

10. 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

11. 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

12. 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

13. 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

14. 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

15. 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

16. 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

17. 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

18. 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

19. 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

20. 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

21. 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

22. Tahir, M. and Hayat, M. (2016) iNuc-STNC: A Sequence-Based Predictor for Identification of Nucleosome Po-

sitioning in Genomes by Extending the Concept of SAAC and Chou's PseAAC. *Molecular BioSystems*, **12**, 2587-2593. https://doi.org/10.1039/C6MB00221H

23. 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
24. 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
25. 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
26. 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
27. 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
28. 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*, **6**, 66545-66556. https://doi.org/10.1109/ACCESS.2018.2876656
29. Javed, F. and Hayat, M. (2018) 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
30. 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
31. 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
32. 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
33. 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
34. Javed, F. and Hayat, M. (2019) Predicting Subcellular Localization 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
35. 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
36. 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
37. 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

38. 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
39. 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
40. 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*, **146**, 232-240. https://doi.org/10.1016/j.chemolab.2015.05.028
41. 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*, **142**, 28-35. https://doi.org/10.1016/j.chemolab.2015.01.004
42. 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
43. 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
44. 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
45. 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
46. 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
47. 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
48. 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**, 551-557. https://doi.org/10.1007/s00232-016-9904-3
49. Jiao, Y.S. and Du, P.F. (2017) Predicting Protein Submitochondrial Locations by Incorporating the Positional-Specific Physicochemical Properties into Chou's General Pseudo-Amino Acid Compositions. *Journal of Theoretical Biology*, **416**, 81-87. https://doi.org/10.1016/j.jtbi.2016.12.026
50. 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
51. 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

52. 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
53. 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
54. 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**, Article ID: 1600085. https://doi.org/10.1002/minf.201600085
55. 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.
56. 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
57. 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
58. 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
59. 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
60. 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
61. 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
62. 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
63. 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
64. 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
65. 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
66. 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

67. 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
68. Behbahani, M., Nosrati, M., Moradi, M. and Mohabatkar, H. (2019) Using Chou's General Pseudo Amino Acid Composition to Classify Laccases from Bacterial and Fungal Sources via Chou's Five-Step Rule. *Applied Biochemistry and Biotechnology*, **190**, 1035-1048. https://doi.org/10.1007/s12010-019-03141-8
69. 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
70. 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
71. 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
72. 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
73. 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
74. Behbahani, M., Nosrati, M., Moradi, M. and Mohabatkar, H. (2020) Using Chou's General Pseudo Amino Acid Composition to Classify Laccases from Bacterial and Fungal Sources via Chou's Five-Step Rule. *Applied Biochemistry and Biotechnology*, **190**, 1035-1048. https://doi.org/10.1007/s12010-019-03141-8
75. Chen, Y. and Fan, X. (2019) Use Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangsheng Pingfei San on Idiopathic Pulmonary Fibrosis. *Current Molecular Medicine*, **20**, 220-230. https://doi.org/10.2174/1566524019666191011160543
76. 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
77. Dutta, A., Dalmia, A., A. 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
78. 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
79. 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
80. Jun, Z. and Wang, S.Y. (2019) Identify Lysine Neddylation Sites Using Bi-Profile Bayes Feature Extraction via the Chou's 5-Steps Rule and General Pseudo Components. *Current Genomics*, **20**, 592-601. https://doi.org/10.2174/1389202921666191223154629

81. Khan, S., Khan, M., Iqbal, N., Hussain, T., Khan, S.A. and Chou, K.C. (2020) A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chou's 5-Steps Rule. *International Journal of Peptide Research and Therapeutics*, **26**, 795-809. https://doi.org/10.1007/s10989-019-09887-3

82. Lan, J., Liu, J., Liao, C., Merkler, D.J., Han, Q. and Li, J. (2019) A Study for Therapeutic Treatment against Parkinson's Disease via Chou's 5-Steps Rule. *Current Topics in Medicinal Chemistry*, **19**, 2318-2333. http://www.eurekaselect.com/175887/article https://doi.org/10.2174/1568026619666191019111528

83. Liang, R., Xie, J., Zhang, C., Zhang, M., Huang, H., Huo, H., Cao, X. and Niu, B. (2019) Identifying Cancer Targets Based on Machine Learning Methods via Chou's 5-Steps Rule and General Pseudo Components. *Current Topics in Medicinal Chemistry*, **19**, 2301-2317. https://doi.org/10.2174/1568026619666191016155543

84. Liang, Y. and Zhang, S. (2019) Identifying DNase I Hypersensitive Sites Using Multi-Features Fusion and F-Score Features Selection via Chou's 5-Steps Rule. *Biophysical Chemistry*, **253**, Article ID: 106227. https://doi.org/10.1016/j.bpc.2019.106227

85. 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

86. Yang, L., Lv, Y., Wang, S., Zhang, Q., Pan, Y., Su, D., Lu, Q. and Zuo, Y. (2019) Identifying FL11 Subtype by Characterizing Tumor Immune Microenvironment in Prostate Adenocarcinoma via Chou's 5-Steps Rule. *Genomics*, **112**, 1500-1515. https://doi.org/10.1016/j.ygeno.2019.08.021

87. Akmal, M.A., Hussain, W., Rasool, N., Khan, Y.D., Khan, S.A. and Chou, K.C. (2020) Using Chou's 5-Steps Rule to Predict O-Linked Serine Glycosylation Sites by Blending Position Relative Features and Statistical Moment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, in press. https://doi.org/10.1109/TCBB.2020.2968441

88. 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

89. Charoenkwan, P., Schaduangrat, N., Nantasenamat, C., Piacham, T. and Shoombuatong, W. (2020) Correction: Shoombuatong, W., *et al.* iQSP: A Sequence-Based Tool for the Prediction and Analysis of Quorum Sensing Peptides via Chou's 5-Steps Rule and Informative Physicochemical Properties. Int. J. Mol. Sci. 2020, 21, 75. *International Journal of Molecular Sciences*, **21**, 2629. https://doi.org/10.3390/ijms21072629

90. Chen, Y. and Fan, X. (2020) Use of Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangshen Pingfei San on Idiopathic Pulmonary Fibrosis. *Current Molecular Medicine*, **20**, 220-230. https://doi.org/10.2174/1566524019666191011160543

91. Du, L., Meng, Q., Jiang, H. and Li, Y. (2020) Using Evolutionary Information and Multi-Label Linear Discriminant Analysis to Predict the Subcellular Location of Multi-Site Bacterial Proteins via Chou's 5-Steps Rule. *IEEE Access*, **8**, 56452-56461. https://doi.org/10.1109/ACCESS.2020.2982160

92. Dutta, A., Dalmia, A., A. R, Singh, K.K. and Anand, A. (2020) 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

93. 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

94. 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

95. Lin, W., Xiao, X., Qiu, W. and Chou, K.C. (2020) Use Chou's 5-Steps Rule to Predict Remote Homology Proteins by Merging Grey Incidence Analysis and Domain Similarity Analysis. *Natural Science*, **12**, 181-198. https://doi.org/10.4236/ns.2020.123016

96. Yang, L., Lv, Y., Wang, S., Zhang, Q., Pan, Y., Su, D., Lu, Q. and Zuo, Y. (2020) Identifying FL11 Subtype by Characterizing Tumor Immune Microenvironment in Prostate Adenocarcinoma via Chou's 5-Steps Rule. *Genomics*, **112**, 1500-1515. https://doi.org/10.1016/j.ygeno.2019.08.021

97. 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

98. 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

99. 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

100. Chou, K.C. (1993) A Vectorized Sequence-Coupling Model for Predicting HIV Protease Cleavage Sites in Proteins. *The Journal of Biological Chemistry*, **268**, 16938-16948.

101. Chou, K.C. and Zhang, C.T. (1992) Diagrammatization of Codon Usage in 339 HIV Proteins and Its Biological Implication. *AIDS Research and Human Retroviruses*, **8**, 1967-1976. https://doi.org/10.1089/aid.1992.8.1967

102. Chou, J.J. (1993) Predicting Cleavability of Peptide Sequences by HIV Protease via Correlation-Angle Approach. *Journal of Protein Chemistry*, **12**, 291-302. https://doi.org/10.1007/BF01028191

103. Chou, K.C., Tomasselli, A.L., Reardon, I.M. and Heinrikson, R.L. (1996) Predicting HIV Protease Cleavage Sites in Proteins by a Discriminant Function Method. *Proteins: Structure, Function, and Bioinformatics*, **24**, 51-72. https://doi.org/10.1002/(SICI)1097-0134(199601)24:1<51::AID-PROT4>3.0.CO;2-R

104. Chou, K.C. and Zhang, C.T. (1993) Studies on the Specificity of HIV Protease: An Application of Markov Chain Theory. *Journal of Protein Chemistry*, **12**, 709-724. https://doi.org/10.1007/BF01024929

105. Chou, K.C., Zhang, C.T. and Kezdy, F.J. (1993) A Vector Approach to Predicting HIV Protease Cleavage Sites in Proteins. *Proteins: Structure, Function, and Bioinformatics*, **16**, 195-204. https://doi.org/10.1002/prot.340160206

106. 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

107. Chou, K.C. (1981) A New Graphical Rule for Rate Laws of Enzyme Reactions with Branched Pathways. *Canadian Journal of Biochemistry*, **59**, 757-761. https://doi.org/10.1139/o81-105

108. 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.

109. 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

110. Chou, K.C. and Liu, W.M. (1981) Graphical Rules for Non-Steady State Enzyme Kinetics. *Journal of Theoretical Biology*, **91**, 637-654. https://doi.org/10.1016/0022-5193(81)90215-0

111. Chou, K.C. (1983) Advances in Graphical Methods of Enzyme Kinetics. *Biophysical Chemistry*, **17**, 51-55. https://doi.org/10.1016/0301-4622(83)87013-6

112. Chou, K.C. (1989) Graphic Rules in Steady and Non-Steady Enzyme Kinetics. *The Journal of Biological Chemi-*

stry, **264**, 12074-12079.

113. Chou, K.C. (1993) Graphic Rule for Non-Steady-State Enzyme Kinetics and Protein Folding Kinetics. *Journal of Mathematical Chemistry*, **12**, 97-108. https://doi.org/10.1007/BF01164628
114. Chou, K.C. (2010) Graphic Rule for Drug Metabolism Systems. *Current Drug Metabolism*, **11**, 369-378. https://doi.org/10.2174/138920010791514261
115. 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.
116. 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
117. 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
118. 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.
119. Chou, K.C., Forsen, S. and Zhou, G.Q. (1980) Three Schematic Rules for Deriving Apparent Rate Constants. *Chemica Scripta*, **16**, 109-113.
120. Chou, K.C. (1983) Low-Frequency Vibrations of Helical Structures in Protein Molecules. *Biochemical Journal*, **209**, 573-580. https://doi.org/10.1042/bj2090573
121. Chou, K.C. (1983) Identification of Low-Frequency Modes in Protein Molecules. *Biochemical Journal*, **215**, 465-469. https://doi.org/10.1042/bj2150465
122. 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
123. Chou, K.C. (1984) Biological Functions of Low-Frequency Vibrations (Phonons). III. Helical Structures and Microenvironment. *Biophysical Journal*, **45**, 881-889. https://doi.org/10.1016/S0006-3495(84)84234-4
124. 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
125. Chou, K.C. (1984) Low-Frequency Vibrations of DNA Molecules. *Biochemical Journal*, **221**, 27-31. https://doi.org/10.1042/bj2210027
126. 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
127. 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
128. 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
129. 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
130. 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
131. 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
132. 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

133. 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
134. 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
135. 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
136. 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. *The Journal of Biological Chemistry*, **268**, 6119-6124.
137. 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. *The Journal of Biological Chemistry*, **268**, 14875-14880.
138. 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
139. 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 Reverse Transcriptase Inhibitor. *Experientia*, **50**, 23-28. https://doi.org/10.1007/BF01992044
140. 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
141. 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
142. 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
143. 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
144. 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
145. Gordon, G. (2007) Designed Electromagnetic Pulsed Therapy: Clinical Applications. *Journal of Cellular Physiology*, **212**, 579-582. https://doi.org/10.1002/jcp.21025
146. 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
147. 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

148. 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
149. 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
150. 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
151. 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
152. 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
153. 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
154. 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
155. 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
156. 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
157. 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
158. 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 Compo sition (iPPBS-PseAAC). *Journal of Biomolecular Structure and Dynamics* (*JBSD*), **34**, 1946-1961. https://doi.org/10.1080/07391102.2015.1095116
159. Chou, K.C. (2019) Proposing Pseudo Amino Acid Components Is an Important Milestone for Proteome and Genome Analyses. *International Journal for Peptide Research and Therapeutics* (*IJPRT*), **26**, 1085-1098. https://doi.org/10.1007/s10989-019-09910-7
160. Chou, K.C. (2019) Artificial Intelligence (AI) Tools Constructed via the 5-Steps Rule for Predicting Post-Translational Modifications. *Trends in Artificial Intelligence* (*TIA*), **3**, 60-74. https://doi.org/10.36959/643/304
161. Chou, K.C. (2019) Impacts of Pseudo Amino Acid Components and 5-Steps Rule to Proteomics and Proteome Analysis. *Current Topics in Medicinal Chemistry*, **19**, 2283-2300. https://doi.org/10.2174/1568026619666191018100141
162. Chou, K.C. (2019) An Insightful Recollection for Predicting Protein Subcellular Locations in Multi-Label Systems. *Genomics*. (In Press) https://doi.org/10.1016/j.ygeno.2019.08.022

163. 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

164. Shao, Y.T. and Chou, K.C. (2020) pLoc_Deep-mAnimal: A Novel Deep CNN-BLSTM Network to Predict Subcellular Localization of Animal Proteins. *Natural Science*, **12**, 281-291. https://doi.org/10.4236/ns.2020.125024

165. Shao, Y.T. and Chou, K.C. (2020) pLoc_Deep-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by Deep Learning. *Natural Science*, **12**, 400-428. https://doi.org/10.4236/ns.2020.126034

166. Liu, X.X. and Chou, K.C. (2020) pLoc_Deep-mGneg: Predict Subcellular Localization of Gram Negative Bacterial Proteins by Deep Learning. *Advances in Bioscience and Biotechnology* (*ABB*), **11**, 141-152. https://doi.org/10.4236/abb.2020.115011

167. Shao, Y.T., Liu, X.X., Lu, Z. and Chou, K.C. (2020) pLoc_Deep-mHum: Predict Subcellular Localization of Human Proteins by Deep Learning. *Natural Science*, in press, 1-31.

168. Shao, Y.T., Liu, X.X., Lu, Z. and Chou, K.C. (2020) pLoc_Deep-mPlant: Predict Subcellular Localization of Plant Proteins by Deep Learning. *Natural Science*, **12**, 237-247. https://doi.org/10.4236/ns.2020.125021

169. Shao, Y.H. and Chou, K.C. (2020) pLoc_Deep-mVirus: A CNN Model for Predicting Subcellular Localization of Virus Proteins by Deep Learning. *Natural Science*, **12**, 388-399. https://doi.org/10.4236/ns.2020.126033

170. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server iATC_Deep-mISF Is Working. *Global Journal of Science Frontier Research*: *G Bio-Tech & Genetics*, **20**, 1-3.

171. K.-C. Chou (2020), Showcase to Illustrate How the Web-Server iKcr-PseEns Is Working. *Journal of Medical Care Research and Review*, **3**, 331-347.

172. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server iPTM-mLys Is Working. *Infotext Journal of Infectious Diseases and Therapy* (*IJID*), **1**, 1-16.

173. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server iRNA-Methyl Is Working. *Journal of Molecular Genetics*, **3**, 1-7.

174. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server iSNO-AAPair Is Working. *Journal of Genetics and Genomics*, **24**, 18156-18160.

175. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server pLoc_Deep-mAnimal Is Working. *American Journal of Virology & Disease*, **2**, 1-2.

176. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server pLoc_Deep-mGneg Is Working. *Clinical and Medical Case Report Journal*, **1**, 1-2.

177. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server pLoc_Deep-mPlant Is Working. *Integrative Molecular Biology and Biotechnology*, **1**, 1-2.

178. Chou, K.C. (2020) Showcase to Illustrate How the Web-Server pLoc_Deep-mVirus Is Working. *Clinical Research and Trials*, **6**, 1-2.

179. K.-C. Chou (2020) Showcase to Illustrate How the Web-Server pSuc-Lys Is Working. *Social Sciences and Humanities Open Access Journal*, **1**, 1-3.

180. Chou, K.C. (2020) Showcase to Illustrate How the Webserver pLoc_bal-mEuk Is Working. *Biomedical Journal of Scientific & Technical Research*, **24**, Article ID: 18156. https://doi.org/10.26717/BJSTR.2020.24.004033