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Review Article

The Benefits of Door Open for a Country

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Abstract

In this paper, the amazing and fantastic benefits by taking the door open policy have been presented. It is within (1979-1949) = 30 years, China has become from a very poor country to the second richest country only next to USA. It is anticipated China will become the richest country in 2030.

Keywords: deng xiaoping; mao zedong and buddha; cross the river by feeling the stones; cats able to catch mice are good ones regardless their color; no one is perfect, and no gold is really pure

INTRODUCTION

After the notorious "Cultural Revolution" developed by **Mao Zedong**, the dictator and head of China, had been defeated, China was under the leadership of **Deng Xiaoping**. He adopted the door-opening policy with the philosophy: (**1**) "Cross the river by feeling the stones meaning "**摸著石头过河**", (**2**) "No one is perfect, and no gold is really pure" meaning "**人无完人, 金无足赤**", and (**3**) Cats able to catch mice are certainly good regardless of their color" meaning **"不管白猫黑猫，能够捕捉老鼠就是好猫".** Ever since then, China has been starting economically booming, and has become the second richest country next to USA only. It is anticipated that China will be superior to USA in about 2030.

Growing-up and strongly established

As a consequence of the "door open" theory, Prof. Dr. Chou 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. Deng Xiaoping's policy can stimulate a lot of great creativities, as indicated by a lot of achievements. Listed below are just a few.

    (1)   Proposing graphical rules in molecular biology.
    (2)   Proposing pseudo amino acid composition [1-16].
    (3)   Proposing Pseudo K-Tuple Nucleotide Composition [17-20].
    (4)   Proposing Pseudo-in-one [21, 22].
    (5)   Proposing 5-steps rule [7, 8, 23-63, 64 , 65-95].
    (6)   Proposing "The Biological Functions of Low-Frequency Phonons, [96-105].

III. CONCLUSIVE REMARKS

It is really awesome and amazing to adopt the Door-opening policy to achieve such great achievements during so short period of time, fully indicating "the community with a shared future for mankind" (i.e., "人类

命运共同体") and "Multilateralism" （i.e., "多边主义" by **Xi Jinping** is indeed very correct and wise.

REFERENCES

[1] K.C. Chou, Prediction of protein cellular attributes using pseudo amino acid composition, PROTEINS: Structure, Function, and Genetics (Erratum: ibid., 2001, Vol.44, 60), 43 (2001) 246-255.

[2] K.C. Chou, Y.D. Cai, Predicting protein quaternary structure by pseudo amino acid composition, Proteins: Struct., Funct., Genet., 53 (2003) 282-289.

[3] K.C. Chou, Y.D. Cai, Prediction and classification of protein subcellular location: sequence-order effect and pseudo amino acid composition, Journal of Cellular Biochemistry (Addendum, ibid. 2004, 91, 1085), 90 (2003) 1250-1260.

[4] K.C. Chou, Y.D. Cai, Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo amino acid composition, J. Cell. Biochem., 91 (2004) 1197-1203.

[5] K.C. Chou, Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes, Bioinformatics, 21 (2005) 10-19.

[6] K.C. Chou, Pseudo amino acid composition and its applications in bioinformatics, proteomics and system biology, Current Proteomics, 6 (2009) 262-274.

[7] K.C. Chou, Some remarks on protein attribute prediction and pseudo amino acid composition (50th Anniversary Year Review, 5-steps rule), J. Theor. Biol., 273 (2011) 236-247.

[8] K.C. Chou, Impacts of pseudo amino acid components and 5-steps rule to proteomics and proteome analysis, Current Topics in Medicinak Chemistry (CTMC) (Special Issue ed. G.P Zhou), 19 (2019) 2283-2300.

[9] K.C. Chou, Proposing pseudo amino acid components is an important milestone for proteome and genome analyses (2019),

International Journal for Peptide Research and Therapeutics (IJPRT) 26 (2019) 1085-1098.

[10] K.C. Chou, An Insightful 20-Year Recollection Since the Birth of Pseudo Amino Acid Components, JOURNAL OF MATHEMATICS, STATISTICS AND COMPUTING, 1 (2019) 5-16.

[11] K.C. Chou, How the Artificial Intelligence Tool iRNA-PseU is Working in Predicting the RNA Pseudouridine Sites, Biomed J Sci & Tech Res https://doi.org/10.26717/BJSTR.2020.24.004016, 24 (2020).

[12] K.C. Chou, An insightful 20-year recollection since the birth of pseudo amino acid components, Amino Acids, in press (2020).

[13] K.C. Chou, The Significant and Profound Impacts of Chou's Pseudo Amino Acid Composition or PseAAC, Natural Acience, 12 (2020) 647-658.

[14] K.C. Chou, The Significant and Profound Impacts of Pseudo K-Tuple Nucleotide Composition, Voice of the Publisher (VP), 6 (2020) 91-101.

[15] K.C. Chou, Analyze the Role of "Pseudo Amino Acid Composition" in Stimulating the Drug Development. Annual Cas Rep Rev: ACRR-161, Annals of Case Reports & Reviews (ACRR), (2020).

[16] K.C. Chou, The Significant and Profound Impacts of Pseudo K-Tuple Nucleotide Composition, Archives of Molecular Medicine Journal (Arch Mol Med J), Vol.1 (2020) page 1-4.

[17] H. Lin, E.Z. Deng, H. Ding, W. Chen, K.C. Chou, iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition, Nucleic Acids Res., 42 (2014) 12961-12972.

[18] W. Chen, T.Y. Lei, D.C. Jin, H. Lin, K.C. Chou, PseKNC: a flexible web-server for generating pseudo K-tuple nucleotide composition, Anal. Biochem., 456 (2014) 53-60.

[19] S.H. Guo, E.Z. Deng, L.Q. Xu, H. Ding, H. Lin, W. Chen, K.C. Chou, iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition, Bioinformatics, 30 (2014) 1522-1529.

[20] B. Liu, L. Fang, S. Wang, X. Wang, H. Li, K.C. Chou, Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy, Journal of Theoretical Biology, 385 (2015) 153-159.

[21] B. Liu, F. Liu, X. Wang, J. Chen, L. Fang, K.C. Chou, Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences, Nucleic Acids Res., 43 (2015) W65-W71.

[22] B. Liu, H. Wu, K.C. Chou, 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 (2017) 67-91.

[23] O. Barukab, Y.D. Khan, S.A. Khan, K.C. Chou, iSulfoTyr-PseAAC: Identify tyrosine sulfation sites by incorporating statistical moments via Chou's 5-steps rule and pseudo components Current Genomics, 20 (2019) 306-320.

[24] Y. Chen, X. Fan, Use Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangsheng Pingfei San on Idiopathic Pulmonary Fibrosis, Current Molecular Medicine, 19 (2019) 511-563.

[25] K.C. Chou, Recent progresses in predicting protein subcellular localization with artificial intelligence tools developed via the 5-steps rule, Medicinal Chemistry, Submitted (2019).

[26] K.C. Chou, Artificial intelligence (AI) tools constructed via the 5-steps rule for predicting post-translational modifications, Trends in Artificial Inttelengence (TIA), 3 (2019) 60-74.

[27] K.C. Chou, Recent Progresses in Predicting Protein Subcellular Localization with Artificial Intelligence (AI) Tools Developed Via the 5-Steps Rule, Japanese Journal of Gastroenterology and Hepatology https://www.jjgastrohepto.org/v2issue4.php 2(2019) 1-4.

[28] K.C. Chou, An Insightful 10-year Recollection Since the Emergence of the 5-steps Rule, Current Pharmaceutical Design, 25 (2019) 4223-4234.

[29] X. Du, Y. Diao, H. Liu, S. Li, MsDBP: Exploring DNA-binding Proteins by Integrating Multi-scale Sequence Information via Chou's 5-steps Rule, Journal of Proteome Research, 18 (2019) 3119-3132.

[30] A. Dutta, A. Dalmia, A. R, K.K. Singh, A. Anand, Using the Chou's 5-steps rule to predict splice junctions with interpretable bidirectional long short-term memory networks, Comput Biol Med, 116 (2019) 103558.

[31] W. Hussain, S.D. Khan, N. Rasool, S.A. Khan, K.C. Chou, SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins, Anal. Biochem., 568 (2019) 14-23.

[32] W. Hussain, Y.D. Khan, N. Rasool, S.A. Khan, K.C. Chou, SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins, J. Theor. Biol., 468 (2019) 1-11.

[33] S. Ilyas, W. Hussain, A. Ashraf, Y.D. Khan, S.A. Khan, K.C. Chou, 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, doi: 10.2174/1389202920666190809095206 (2019).

[34] Z. Jun, S.Y. Wang, Identify Lysine Neddylation Sites Using Bi-profile Bayes Feature Extraction via the Chou's 5-steps Rule and General Pseudo Components, Current Genomics, 20 (2019) 592-601.

[35] S. Khan, M. Khan, N. Iqbal, T. Hussain, S.A. Khan, K.C. Chou, A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chou's 5-Steps Rule Human Genetics 19 (2019) 756-799.

[36] J. Lan, J. Liu, C. Liao, D.J. Merkler, Q. Han, J. Li, A Study for Therapeutic Treatment against Parkinson's Disease via Chou's 5-steps Rule, Current Topics in Medicinal Chemistry, 19 (2019) 2318-2333.

[37] R. Liang, J. Xie, C. Zhang, M. Zhang, H. Huang, H. Huo, X. Cao, B. Niu, Identifying Cancer Targets Based on Machine Learning Methods via Chou's 5-steps Rule and General Pseudo Components, Current Topics in Medicnal Chemistry, 19 (2019) 2301-2317.

[38] Y. Liang, S. Zhang, Identifying DNase I hypersensitive sites using multi-features fusion and F-score features selection via Chou's 5-steps rule, Biophys Chem, 253 (2019) 106227.

[39] A. Wiktorowicz, A. Wit, A. Dziewierz, L. Rzeszutko, D. Dudek, P. Kleczynski, Calcium Pattern Assessment in Patients with

Severe Aortic Stenosis Via the Chou's 5-Steps Rule, Current Pharmaceutical Design 25 (2019) 6-31.

[40] L. Yang, Y. Lv, S. Wang, Q. Zhang, Y. Pan, D. Su, Q. Lu, Y. Zuo, Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule, Genomics, 112 (2019) 1500-1515.

[41] M.A. Akmal, W. Hussain, N. Rasool, Y.D. Khan, S.A. Khan, K.C. Chou, Using Chou's 5-steps rule to predict O-linked serine glycosylation sites by blending position relative features and statistical moment, IEEE/ACM Trans Comput Biol Bioinform, PP (2020).

[42] H. Bouziane, A. Chouarfia, Use of Chou's 5-steps rule to predict the subcellular localization of gram-negative and gram-positive bacterial proteins by multi-label learning based on gene ontology annotation and profile alignment, J Integr Bioinform, (2020).

[43] P. Charoenkwan, N. Schaduangrat, C. Nantasenamat, T. Piacham, W. Shoombuatong, 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. , 21 (2020) 75.

[44] P. Charoenkwan, N. Schaduangrat, C. Nantasenamat, T. Piacham, W. Shoombuatong, 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, Int J Mol Sci, 21 (2020).

[45] Y. Chen, X. Fan, Use of Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangshen Pingfei San on Idiopathic Pulmonary Fibrosis, Curr Mol Med, 20 (2020) 220-230.

[46] K.C. Chou, Proposing 5-Steps Rule Is a Notable Milestone for Studying Molecular Biology, Natural Science, 12 (2020) 74-79.

[47] K.C. Chou, The Significant and Profound Impacts of Chou's 5-Steps Rule, Natural Science, 12 (2020) 633-637.

[48] K.C. Chou, Analyze the Role of the "5-Steps Rule" Guidelines in Stimulating the Drug Development (Short Communication), Scholarly Journal of Food and Nutrition (SJFN), 3 (2020) 385-386.

[49] L. Du, Q. Meng, H. Jiang, Y. Li, 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 (2020) 56452-56461.

[50] A. Dutta, A. Dalmia, A. R, K.K. Singh, A. Anand, Using the Chou's 5-steps rule to predict splice junctions with interpretable bidirectional long short-term memory networks, Comput Biol Med, 116 (2020) 103558.

[51] Z. Ju, S.Y. Wang, 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 (2020) 859-866.

[52] M. Kabir, S. Ahmad, M. Iqbal, M. Hayat, 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 (2020) 276-285.

[53] C. Koyunoğlu, Use Chou's 5-Steps Rule to Reveal Why SARS+ MERS= COVID-19, J Biochem Analyt Stud, 2020, (2020).

[54] W. Lin, X. Xiao, W. Qiu, K.C. Chou, Use Chou's 5-Steps Rule to Predict Remote Homology Proteins by Merging Grey Incidence

Analysis and Domain Similarity Analysis, Natural Science, 12 (2020) 181-198.

[55] D. Nguyen, T. Ho-Quang, L. Nguyen Quoc Khanh, V. Dinh-Phan, Y.Y. Ou, Use Chou's 5-steps rule with different word embedding types to boost performance of electron transport protein prediction model, IEEE/ACM Trans Comput Biol Bioinform, PP (2020).

[56] R.P. Pandey, S. Kumar, S. Ahmad, A. Vibhuti, V.S. Raj, A.K. Verma, P. Sharma, E. Leal, Use Chou's 5-steps rule to evaluate protective efficacy induced by antigenic proteins of Mycobacterium tuberculosis encapsulated in chitosan nanoparticles, Life Sci., 256 (2020) 117961.

[57] T. Roy, P. Bhattacharjee, A LabVIEW-based real-time modeling approach via Chou's 5-steps rule for detection of abnormalities in cancer cells, Gene Reports, (2020) 100788.

[58] H. Vundavilli, A. Datta, C. Sima, J. Hua, R. Lopes, M. Bittner, Using Chou's 5-steps rule to Model Feedback in Lung Cancer IEEE Journal of Biomedical and Health Informatics, 21 (2020) 1-24.

[59] L. Yang, Y. Lv, S. Wang, Q. Zhang, Y. Pan, D. Su, Q. Lu, Y. Zuo, Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule, Genomics, 112 (2020) 1500-1515.

[60] S. Zhang, T. Xue, Use Chou's 5-steps rule to identify DNase I hypersensitive sites via dinucleotide property matrix and extreme gradient boosting, Molecular Genetics and Genomics, 295 (2020).

[61] S. Zhang, T. Xue, Use Chou's 5-steps rule to identify DNase I hypersensitive sites via dinucleotide property matrix and extreme gradient boosting, Molecular genetics and genomics : MGG, (2020).

[62] Z. Zhang, L. Wang, Using Chou's 5-steps rule to identify N(6)-methyladenine sites by ensemble learning combined with multiple feature extraction methods, J. Biomol. Struct. Dyn., (2020) 1-11.

[63] X.F. Zhao, Z. Min, X. Wei, Y. Ju, Using the Chou's 5-steps rule, Transient Overexpression Technique, Subcellular Location, and Bioinformatic Analysis to verify the Function of Vitis vinifera O-methyltranferase 3 (VvOMT3) Protein, Plant Physiology and Biochemistry, 151 (2020) 621-629.

[64] H. Wang, Y. Ding, J. Tang, Q. Zou, F. Guo, Identify RNA-associated subcellular localizations based on multi-label learning using Chou's 5-steps rule, BMC Genomics, 22 (2021) 22-56.

[65] G.P. Zhou, M.H. Deng, An extension of Chou's graphic rules for deriving enzyme kinetic equations to systems involving parallel reaction pathways, Biochem. J., 222 (1984) 169-176.

[66] T.A. Jones, S. Thirup, Using known substructures in protein model building and crystallography, EMBO J., 5 (1986) 819-822.

[67] J.M. Parker, D. Guo, R.S. Hodges, New hydrophilicity scale derived from high-performance liquid chromatography peptide retention data: correlation of predicted surface residues with antigenicity and X-ray-derived accessible sites, Biochemistry, 25 (1986) 5425-5432.

[68] K.C. Chou, Graphic rules in steady and non-steady enzyme kinetics, J. Biol. Chem., 264 (1989) 12074-12079.

[69] K.C. Chou, Review: Applications of graph theory to enzyme kinetics and protein folding kinetics. Steady and non-steady state systems, Biophysical Chemistry, 35 (1990) 1-24.

[70] K.C. Chou, Graphic rule for non-steady-state enzyme kinetics and protein folding kinetics, Journal of Mathematical Chemistry, 12 (1993) 97-108.

[71] C.T. Zhang, K.C. Chou, Graphic analysis of codon usage strategy in 1490 human proteins, J. Protein Chem., 12 (1993) 329-335.

[72] P.J. Artymiuk, A.R. Poirrette, H.M. Grindley, D.W. Rice, P. Willett, A graph-theoretic approach to the identification of three-dimensional patterns of amino acid side-chains in protein structures, J. Mol. Biol., 243 (1994) 327-344.

[73] D. Fischer, H. Wolfson, S.L. Lin, R. Nussinov, Three-dimensional, sequence order-independent structural comparison of a serine protease against the crystallographic database reveals active site similarities: potential implications to evolution and to protein folding, Protein Science, 3 (1994) 769-778.

[74] J.P. Hays, S.H. Myint, PCR sequencing of the spike genes of geographically and chronologically distinct human coronaviruses 229E, Journal of Virology Methods, 75 (1998) 179-193.

[75] N.R. Taylor, A. Cleasby, O. Singh, T. Skarzynski, A.J. Wonacott, P.W. Smith, S.L. Sollis, P.D. Howes, P.C. Cherry, R. Bethell, P. Colman, J. Varghese, Dihydropyrancarboxamides related to zanamivir: a new series of inhibitors of influenza virus sialidases. 2. Crystallographic and molecular modeling study of complexes of 4-amino-4H-pyran-6-carboxamides and sialidase from influenza virus types A and B, J. Med. Chem., 41 (1998) 798-807.

[76] Editorial, Whither crystallography, Nature Structural Biology, 8 (2001) 909.

[77] A. Schmidt, C. Jelsch, P. Ostergaard, W. Rypniewski, V.S. Lamzin, Trypsin revisited: crystallography AT (SUB) atomic resolution and quantum chemistry revealing details of catalysis, J. Biol. Chem., 278 (2003) 43357-43362.

[78] X.Q. Qi, J. Wen, Z.H. Qi, New 3D graphical representation of DNA sequence based on dual nucleotides, Journal of Thereoretical Biology, 249 (2007) 681–690.

[79] J. Andraos, Kinetic plasticity and the determination of product ratios for kinetic schemes leading to multiple products without rate laws: new methods based on directed graphs, Can. J. Chem., 86 (2008) 342-357.

[80] H. Gonzalez-Diaz, L.G. Perez-Montoto, A. Duardo-Sanchez, E. Paniagua, S. Vazquez-Prieto, R. Vilas, M.A. Dea-Ayuela, F. Bolas-Fernandez, C.R. Munteanu, J. Dorado, J. Costas, F.M. Ubeira, Generalized lattice graphs for 2D-visualization of biological information, J. Theor. Biol., 261 (2009) 136-147.

[81] C.R. Munteanu, A.L. Magalhaes, E. Uriarte, H. Gonzalez-Diaz, Multi-target QPDR classification model for human breast and colon cancer-related proteins using star graph topological indices, J. Theor. Biol., 257 (2009) 303-311.

[82] A. Perez-Bello, C.R. Munteanu, F.M. Ubeira, A.L. De Magalhaes, E. Uriarte, H. Gonzalez-Diaz, Alignment-free prediction of mycobacterial DNA promoters based on pseudo-folding lattice network or star-graph topological indices, J. Theor. Biol., 256 (2009) 458-466.

[83] L.G. Perez-Montoto, L. Santana, H. Gonzalez-Diaz, Scoring function for DNA-drug docking of anticancer and antiparasitic compounds based on spectral moments of 2D lattice graphs for molecular dynamics trajectories, Eur. J. Med. Chem., 44 (2009) 4461-4469.

[84] J.H. Wong, T.B. Ng, Studies on an Antifungal Protein and a Chromatographically and Structurally Related Protein Isolated from the Culture Broth of Bacillus amyloliquefaciens, Protein & Peptide Letters, 16 (2009) 1399-1406.

[85] J.F. Yu, X. Sun, J.H. Wang, TN curve: a novel 3D graphical representation of DNA sequence based on trinucleotides and its applications, J. Theor. Biol., 261 (2009) 459-468.

[86] K.C. Chou, Graphic rule for drug metabolism systems, Current Drug Metabolism, 11 (2010) 369-378.

[87] Z.C. Wu, X. Xiao, K.C. Chou, 2D-MH: A web-server for generating graphic representation of protein sequences based on the physicochemical properties of their constituent amino acids, J. Theor. Biol., 267 (2010) 29-34.

[88] T. Huang, L. Chen, Y.D. Cai, K.C. Chou, Classification and analysis of regulatory pathways using graph property, biochemical and physicochemical property, and functional property, PLoS ONE, 6 (2011) e25297.

[89] Z.H. Qi, L. Li, Z.M. Zhang, X.Q. Qi, Self-similarity analysis of eubacteria genome based on weighted graph, J. Theor. Biol., 280 (2011) 10-18.

[90] G. Xie, Z. Mo, Three 3D graphical representations of DNA primary sequences based on the classifications of DNA bases and their applications, J. Theor. Biol., 269 (2011) 123-130.

[91] V. Aguiar-Pulido, C.R. Munteanu, J.A. Seoane, E. Fernandez-Blanco, L.G. Perez-Montoto, H. Gonzalez-Diaz, J. Dorado, Naive Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer, Mol Biosyst, 8 (2012) 1716-1722.

[92] P. Tripathi, P.N. Pandey, A novel alignment-free method to classify protein folding types by combining spectral graph clustering with Chou's pseudo amino acid composition, J. Theor. Biol., 424 (2017) 49-54.

[93] K.C. Chou, A Stimulating Recollection of Chou's Graph Theory in Enzyme Kinetics, Voice of Publication (VP), 2020 (2020) 161-163.

[94] K.C. Chou, Applications of graph theory to enzyme kinetics and protein folding kinetics: steady and non-steady state systems (Short Communication), Journal of Sensor Networks and Data Communications, 1 (2020) 06-07.

[95] K.C. Chou, Revisiting the paper on "Applications of graph theory to enzyme kinetics and protein folding kinetics: steady and non-steady state systems" (Short Communication), J, Biotechnology and Bioprocessing, 1 (2020) 1-2.

[96] K.C. Chou, N.Y. Chen, The biological functions of low-frequency phonons, Scientia Sinica, 20 (1977) 447-457.

[97] P.C. Painter, L.E. Mosher, C. Rhoads, Low-frequency modes in the Raman spectrum of DNA, Biopolymers, 20 (1981) 243-247.

[98] P.C. Painter, L.E. Mosher, C. Rhoads, Low-frequency modes in the Raman spectra of proteins, Biopolymers, 21 (1982) 1469-1472.

[99] H. Urabe, Y. Tominaga, Low-frequency collective modes of DNA double helix by Raman spectroscopy, Biopolymers, 21 (1982) 2477-2481.

[100] K.C. Chou, Low-frequency vibrations of helical structures in protein molecules, Biochem. J., 209 (1983) 573-580.

[101] K.C. Chou, Identification of low-frequency modes in protein molecules, Biochem. J., 215 (1983) 465-469.

[102] K.C. Chou, Biological functions of low-frequency vibrations (phonons). 3. Helical structures and microenvironment, Biophys. J., 45 (1984) 881-889.

[103] K.C. Chou, The biological functions of low-frequency phonons. 4. Resonance effects and allosteric transition, Biophysical Chemistry, 20 (1984) 61-71.

[104] K.C. Chou, Low-frequency vibrations of DNA molecules, Biochem. J., 221 (1984) 27-31.

[105] K.C. Chou, Low-frequency motions in protein molecules: beta-sheet and beta-barrel, Biophys. J., 48 (1985) 289-297.