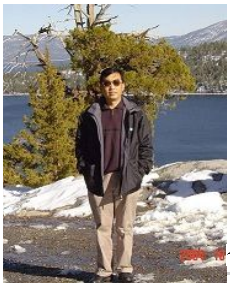
李前忠

2016-07-08 文字： 点击：[2150]



李前忠
教授，博士生导师
内蒙古大学物理科学与技术学院
呼和浩特 010021
电话：0471-4992958
Email：qzli@imu.edu.cn

研究小组网站

个人简历

一、 受教育 情况

1979.09-1983.08. 内蒙古大学物理系，读大学本科；
1983.09-1986.07. 内蒙古大学物理系，读硕士学位；
1991.09-1994.12. 内蒙古大学物理系，读博士学位

二、工作经历

1985.12 –现在 内蒙古大学物理系 讲师(1985),副教授(1995),教授(1997)
2004.3-2005.4 美国加州大学Davis分校（University of California, Davis）做访问学者)

教学

一、曾经主讲的课程

电磁学、量子力学A、大学物理、理论物理、热学、数学物理方法
研究生课程：分子生物物理、生物信息学

二、目前承担的教学任务

量子力学A、物理学与现代科学技术（新生研讨课）
负责自治区级《量子力学》精品课程
负责 自治区级“量子物理系列课程教学团队”建设，

培养研究生情况

截止2016年已指导培养博士毕业生13人，硕士毕业生26人。
现有在读博士研究生6人，硕士生6人。

研究领域

一、研究方向

理论生物物理、生物信息学

二、目前主持和已完成的主要科研项目

2015.01-2018.12,主持国家自然科学基金项目：与肿瘤相关的DNA甲基化和组蛋白修饰数据的分析与研究
2011.1-2013.12, 主持国家自然科学基金项目：“蛋白质亚细胞定位、功能模体和相关问题的理论研究”
2006.1-2008.12, 主持国家自然科学基金项目：“模式生物基因组中非编码序列的信息学特征分析和功能位点研究”
2002.1-2004.12，主持完成国家自然科学基金项目：“热滞蛋白抗冻活性和溶液冰晶生长习性的动力学研究”
1997.1-1999.12，主持完成国家自然科学基金项目：“鱼抗冻蛋白的抗冻机理及相关问题的物理研究”
2011.1-2013.12教育部高等学校博士学科点基金项目，真核基因组调控区启动子和相关问题的理论研究，
2006.10-2008.10, 主持内蒙古优秀学科带头人项目：“真核生物组非编码序列的信息分析和功能位点研究”
2006.7-2009.12, 主持内蒙古自然科学基金(重大项目)：“离子注入对黄芪多倍体诱导及其药用成分含量的影响”
2005.1-2006.12，主持完成教育部高等学校博士点基金项目：“真核生物基因组结构与功能的研究”

奖励、荣誉和学术兼职

一、获奖和荣誉

2012年获国务院特殊津贴，

2011年获内蒙古自治区“中青年科学技术创新奖”，

2009年获首届(2007年度)内蒙古自治区自然科学一等奖；

2007年获宝钢优秀教师奖；

2006年被授予内蒙古自治区突出贡献中青年专家；

1998年，获“第二届内蒙古自治区青年科技奖”，

1998年，被授予“内蒙古自治区青年科技标兵”

2011年，获内蒙古自治区高等学校教学名师奖，

2005年，参与完成的项目“新型现代数理科学复合型人才培养模式的探索与实践”获内蒙古自治区教学成果一等奖；

2009年，参与完成的项目“数理科学创新型基础人才培养与数理学基地建设”获内蒙古自治区教学成果二等奖；

2015年被教育部授予 “全国师德标兵”荣誉称号

1998年第一批入选内蒙古自治区“321人才工程”第一层次人选

2002年-2010年连续入选自治区 “321人才工程” 第一层次人选

2011年入选自治区草原英才人选

二、目前主要学术兼职

任中国生物物理学会理事

内蒙古自治区物理学会副理事长

中国细胞学会功能基因组信息学与系统生物学分会理事

中国运筹学会计算系统生物学分会理事

全国高等学校电磁学研究会副理事长

全国高等学校量子力学研究会常务理事

国际学术刊物 “Biophysics Reports”编委

内蒙古自治区离子束生物工程重点实验室主任

学术研究

主要从事理论生物物理和生物信息学研究工作。在鱼抗冻蛋白和抗冻糖蛋白、蛋白质结构与功能预测、基因组功能位点和功能区域预测、基因组信息学和表观遗传等方面的研究，在国内外学术刊物发表学术论文200余篇，其中在“Bioinformatics”，“Genomics”, “Gene”, “J. Theor. Biol.”，“Amino Acids”，“J. Comput. Chem.”和“Biochem. Biophys. Res. Commun.”等SCI学术刊物发表学术论文50余篇，其中在生物信息学的顶级学术刊物“Bioinformatics”发表论文1篇。相关学术论文被SCI他引总次数达1400余次，其中单篇最高被引150余次。

代表性论文

1. 2016, Lu-Qiang Zhang, Qian-Zhong Li∗, Wen-Xia Su, Wen Jin, Predicting gene expression level by the transcription factor bindingsignals in human embryonic stem cells, BioSystems 150: 92–98
2. 2016, Wen-Xia Su , Qian-Zhong Li, Lu-Qiang Zhang , Guo-Liang Fan, Cheng-YanWu,Zhen-He Yan, Yong-Chun Zuo, Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1, Gene 592: 227–234
3. 2016, Cheng-YanWu, Qian-Zhong Li, Zhen-Xing Feng，Non-coding RNA identification based on topology secondary structureand reading frame in organelle genome level, Genomics 107: 9–15
4. 2016, Wen-Xia Su, Qian-Zhong Li , Yong-Chun Zuo, Lu-Qiang Zhang， Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell，Gene 575: 90–100
5. 2014, Zuo, YC; Zhang, PF; Liu, L; Li, T; Peng, Y; Li, GP; Li, QZ，Sequence-specific flexibility organization of splicing flanking sequence and prediction of splice sites in the human genome，CHROMOSOME RESEARCH , 22: 3: 321-334,
6. 2014,Yongchun Zuo, Yu Gao, Guanghua Su1, Chunling Bai1, Zhuying Wei, Kun Liu, Qianzhong Li, Shorgan Bou and Guangpeng Li，Irregular transcriptome reprogramming probably causes thec developmental failure of embryos produced by interspecies somatic cell nuclear transfer between the Przewalski’s gazelle and the bovine，BMC Genomics , 15:1113
7. 2014, Shuai Liu, Xiaochun Cheng , Weina Fu, Yunpeng Zhou, Qianzhong Li，Numeric characteristics of generalized M-set with its asymptote，Applied Mathematics and Computation， 243: 767–774
8. 2013, Tao Li, Qian-Zhong Li,*, Shuai Liu, Guo-Liang Fan, Yong-Chun Zuo and Yong Peng, PreDNA: accurate prediction of DNA-binding sites in proteins by integrating sequence and geometric structure information, Bioinformatics, 29: 678–685
9. 2013, Li Liu, Qian-Zhong Li, Hao Lin, Yong-Chun Zuo,The effect of regions flanking target site on siRNA potency, Genomics, 102: 215–222
10. 2013,Yong-Chun Zuo • Wei Chen • Guo-Liang Fan, Qian-Zhong Li, A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. Amino Acids, 44:573–580
11. 2013, Guo-Liang Fan, Qian-Zhong Li, 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
12. 2013, Guo-Liang Fan, Qian-Zhong Li, Yong-Chun Zuo, 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

13. 2012, Guo-Liang Fan, Qian-Zhong Li, 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
14. 2012, Tao Li, Qian-Zhong Li, Annotating the protein-RNA interaction sites in proteins using evolutionary information and protein backbone structure, Journal of Theoretical Biology , 312 (2012) 55–64
15. 2012, Guo-Liang Fan, Qian-Zhong Li,, Predicting protein sub mitochondria locations by combining different descriptors into the general form of Chou’s pseudo amino acid composition, Amino Acids, 43:545–555
16. 2012. Ying-Li Chen Qian-Zhong Li and Liqing Zhang, Using increment of diversity to predict mitochondrial proteins of malaria parasite: integrating pseudo amino acid composition and structural alphabet. Amino Acids (2012) 42:1309–1316,
17. 2011, Yongchun Zuo, Qianzhong Li, The DNA geometric flexibility of promoter in model organism genomes, Energy Procedia 11 2732-2737
18. 2011. Zuoyongchun and Qian-Zhong Li, Identification of TATA and TATA-less promoters in plant genomes by integrating diversity measure, GC-Skew and DNA geometric flexibility. Genomics 97 (2011) 112–120, doi:10.1016/j.ygeno.2010.11.002.
19. 2011. Hao Lin and Qian-Zhong Li. Eukaryotic and prokaryotic promoter prediction using hybrid approach, Theory in Biosciences 130(6):91-100
20. 2010. Zuoyongchun and Qian-Zhong Li, Using K-minimum increment of diversity to predict secretory proteins of malaria parasite based on groupings of amino acids. Amino Acids 2010(3) 38:859–867.
21. 2010. Xiuzhen Hu and Qian-Zhong Li and Chun-Lian Wang, Recognition of β-hairpin motifs in proteins by using the composite vector, Amino Acids 2010(3) 38:915–921.
22. 2010. Zuoyongchun and Qian-Zhong Li, The hidden physical codes for modulating the prokaryotic transcription initiation. Physica A 2010 389(19) 4217–4223
23. 2010. Lifen Li, Xixia Liang and Qian-Zhong Li, statistical thermodynamic properties of linear protein solution, chinese J Chem. Phys. 2010 23(2) 180-184 .
24. 2009. Zuoyongchun and Qian-Zhong Li, Using reduced amino acid composition to predict defensin family and subfamily: Integrating similarity measure and structural alphabet. Peptides 30 (10) 1788–1793.
25. 2009. Lei Yong and Qian-Zhong Li, Prediction of presynaptic and postsynaptic neurotoxins by the increment of diversity. Toxicology in vitro 29, 346-348.
26. 2009. Lifen Li, Xixia Liang and Qian-Zhong Li, The thermal hysteresis activity of the type I antifreeze protein: A statistical mechanics model. Chem. Phys. Letts., 472:124-127.
27. 2009. Huaiguang Zhang,Xiuzhen Hu and Qian-Zhong Li The Recognition of 27-Class Protein Folds: Approached by Increment of Diversity Based on Multi-Characteristic Parameters. Protein & Peptide Lett (2009. 16(9)1112-1119
28. 2009. Hao Lin, Hao Wang, Hui Ding, Yingli Chen and Qian-Zhong Li, Qianzhong Li, Prediction of subcellular localization of apoptosis protein using chou’s pseudo amino acid composition. Acta Biotheoretica. 57(3):321-330.
29. 2009. 左永春，李前忠, 基于序列和结构特征分析植物TATA和TATA-less启动子. 生物化学与生物物理进展. 36(7): 863-871.
30. 2008. Xiuzhen Hu and Qian-Zhong Li, Using Support Vector Machine to Predict β- and γ-Turns in Proteins, Journal of Computational Chemistry 29:1867-1875.
31. 2008. Wuritu Yang and Qian-Zhong Li, One parameter to describe the mechanism of splice sites competition. Biochemical and Biophysical Research Communications 368: 379-381.
32. 2008. Feng-Min Li and Qian-Zhong Li. Using pseudo amino acid composition to predict protein subnuclear location with improved hybrid approach, Amino Acids 34: 119–125.
33. 2008. Feng-Min Li, Qian-Zhong Li Predicting Protein Subcellular Location Using Chou’s Pseudo Amino Acid Composition and Improved Hybrid Approach. Protein & Peptide Lett (2008) 15: 612-616.
34. 2008. Xiu Zhen Hu and Qian-Zhong Li, Prediction of the β-Hairpins in Proteins Using Support Vector Machine，Protein J 27:115–122.
35. 2007. Hao Lin and Qian-Zhong Li. Using Pseudo Amino Acid Composition to predict Protein Structural Class: Approached by Incorporating 400 Dipeptide, Journal of Computational Chemistry 28: 1463-1466.
36. 2007. Hao Lin and Qian-Zhong Li. Predicting conotoxin superfamily and family by using pseudo amino acid composition and modified Mahalanobis discriminant, Biochemical and Biophysical Research Communications 354: 548-551.
37. 2007. Ying-Li Chen and Qian-Zhong Li. Prediction of the subcellular location of apoptosis proteins, Journal of Theoretical Biology 245: 775-783.
38. 2007. Ying-Li Chen and Qian-Zhong Li. Prediction of apoptosis protein subcellular location using improved hybrid approach and pseudo amino acid composition, Journal of Theoretical Biology 248:377–381
39. 2006. Q.Z. Li, Y. Yeh, J.J. Liu, R.E. Feeney, V.V. Krishnan. A two-dimensional adsorption kinetic model for thermal hyteresis activity in antifreeze proteins, Journal of chemical physics 124: 204702-1.
40. 2006. Qian-Zhong Li and Hao Lin. The recognition and prediction of sigma70 promoters in Escherichia coli K-12, Journal of Theoretical Biology 242:135-141.
41. 2006. Junjie Liu and Qianzhong Li. Theoretical model of antifreeze protein–ice adsorption: Binding of large ligands to a two-dimensional homogeneous lattice, Chemical Physics Letters 422: 67–71.
42. 2003. Jun-Jie Liu and Qianzhong Li. A theoretical model on thermal hysteresis activity of the winter flounder protein “HPLC-6”, Chemical Physics Letters 378: 238-243.

43. 2002. Qian-Zhong Li, Liao-Fu Luo and Li-Rong Zhang. Study on the model for regulation of the allosteric enzyme activity, Chinese Journal of Chemistry 20: 1506-1513.
44. 2002. Wei-Sheng Guo, Liao-Fu Luo and Qian-Zhong Li. A chemical kinetic theory on muscle contraction and spontaneous oscillation, Chemical Physics Letters 363: 471-478.
45. 2001. Qianzhong Li and Zhiqing Lu.The Prediction of the Structural Class of Proein: Application of the Measure of Diversity，Journal of Theoretical Biology 213: 493-502.
46. 2000. Qianzhong Li and Liaofu Luo. Adsorption kinetics in the solution of a thermal hysteresis protein, Chemical Physics Letters 320: 335-338.
47. 1996. Qianzhong Li and Liaofu Luo. A study of the growth and growth habit of ice crystals in a solution of antifreeze (glyco)proteins, Chemical Physics Letters 263: 651-654.
48. 1994. Qianzhong Li and Liaofu Luo. Further Discussion on the thermal Hysteresis of the ice growth inhibitor, Chemical Physics Letters 223: 181-184.
49. 1993. Qianzhong Li and Liaofu Luo. The kinetic theory of thermal hysteresis of a macromolecle solution, Chemical Physics Letters 216: 453-457.
50. 1986. Liaofu Luo and Qianzhong Li. Why are Terminator UAA UAG and UGA? Origins of Life, p263.
51. 1985. 罗辽复, 李前忠. 突变率的S4对称破缺和终止密码子,科学通报, 30: 1056.

上一篇：李宏 下一篇：刘建
【关闭】