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职位

计算机科学与软件学院副教授

学历

1. **博士学位.** (01/2006 – 09/2011) 阿尔伯塔大学电子和计算机工程,，加拿大。
2. **硕士学位.** (09/2002 – 06/2005) 南开大学数学系，天津。
3. **学士学位.** (09/1998 – 06/2002) 南开大学数学系，天津。

奖励和荣誉（按时间顺序）

1. 2012 年度天津市 131 工程第三层次人选
2. 2008 年度阿尔伯塔大学 Andrew Stewart Memorial 奖章 。
   该奖章每年奖励给阿尔伯塔大学最出色的 25 名研究生。详情请见
   http://www.gradstudies.ualberta.ca/awardsfunding/scholarships/general/generalawardslist.htm
3. 2007 年度国家优秀自费留学生奖学金。详情请见
   http://www.csc.edu.cn
4. 阿尔伯塔省创新奖学金 (Alberta Ingenuity Student Scholarship) 2007-2010。
   该奖学金授予具有创新精神、做出优秀创新成果的学生。详情请见http://www.albertaingenuity.ca/。
5. iCORE 研究奖学金(iCORE Post Graduate Scholarship) 2007-2010。
   该奖学金授予品学兼优、有杰出研究成果的学生。详情请见http://www.albertaingenuity.ca/programs/funding/awards/scholarsihps/ict

科研项目

1. 主持国家自然科学基金《识别蛋白质超家族之间远程同源性的算法研究》 2012
2. 主持天津市自然科学基金《药物的作用靶点预测算法》 2012

研究领域

1. 大数据索引与挖掘算法设计
2. 图像分割、图像识别、视觉智能
3. 无模板基因组拼接技术
4. 蛋白质组数据挖掘与基因调控

发表论文（按时间顺序）

2006 年至今，我已经发表了二十六篇期刊论文（25 篇被 SCI 收录），和五篇国际会议论文（2 篇被 SCI 收录）。这些文章被引用总计超过 450 次，他引超过 350 次。这些论文发表在 *PLOS One*，*Structure, Bioinformatics, Journal of Computational Chemistry* 等本领域的知名期刊上。

1. **Chen K**, Mizianty M, Kurgan LA. NucPred: Prediction of nucleotide-binding residues based on sequence and structure descriptors. *Bioinformatics*, 28:31-341, 2012.
   影响因子：5.5　　引用次数：4
2. **Chen K**, Kurgan Lukasz. Computational prediction of secondary and supersecondary structures. *Methods in Molecular Biology*, 932:63-86, 2013
   SCI 收录
3. **Chen K**, Mizianty M, Gao JZ, Kurgan LA. A critical comparative assessment of predictions of protein binding sites for small organic compound. *Structure*, 19：613-621, 2011.
   影响因子：6.3　　引用次数：6
4. H. Zhang, T. Zhang, **K. Chen,** K. D. Kedarisetti, M. J. Mizianty, Q. Bao, W. Stach, and L. Kurgan. Critical assessment of high-throughput standalone methods for secondary structure prediction. *Briefings in Bioinformatics*, 12:672-688, 2011
   影响因子：5.0　　引用次数：7
5. **Chen K**, Mizianty M, Gao JZ, Kurgan LA. ATPsite: sequence-based prediction of ATP-binding residues. *Proteome Science*, 9:S4, 2011
   影响因子：2.3　　引用次数：2
6. **Chen K**, Stach W, Homaeian L, Kurgan LA, iFC2: An integrated web-server for improved prediction of protein structural class, fold type, and secondary secondary structure content. *Amino Acids*, 40:963-73, 2011
   影响因子：3.3　　引用次数：4
7. Mizianty M, Stach W, **Chen K**, Kedarisetti KD, Miri Disfani F, Kurgan LA. Improved Sequence-based Prediction of Disordered Regions with Multilayer Fusion of Multiple Information Sources. *Bioinformatics*, 26: i489-i496, 2010
   影响因子：5.5　　引用次数：20
8. Zhang T, Zhang H, **Chen K**, Ruan J, Shen S, Kurgan LA, 2010. Analysis and Prediction of RNA-Binding Residues Using Sequence, Evolutionary Conservation, and Predicted Secondary Structure and Solvent Accessibility. *Current Protein and Peptide Science*,special issue on *Protein Folding, Stability and Interactions*, 11:609-628, 2010
   影响因子：3.8　　引用次数：10
9. **Chen K**, Kurgan LA. Atomic investigation of atomic level patterns in protein–small ligand interactions. *PLOS One*. 4:e4473, 2009
   影响因子：4.0　　引用次数：7
10. **Chen K**, Jiang Y, Du L, Kurgan L. Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. *J Comput Chem*. 30:163-72. 2009
    影响因子：4.4　　引用次数：10
11. Zhang H, Zhang T, **Chen K**, Shen S, Ruan J, Kurgan L. On the relation between residue flexibility and local solvent accessibility in proteins. *Proteins*. 76:617-36. 2009
    影响因子：2.8　　引用次数：21
12. **Chen K**, Kurgan LA, Ruan J. Prediction of Protein Structural Class Using Novel Evolutionary Collocation Based Sequence Representation. *Journal of Computational Chemistry*, 29:1596-604. 2008

影响因子：4.1　　引用次数：43

13. **Chen K**, Huzil JT, Freedman H, Ramachandran P, Antoniou A, Tuszynski JA, Kurgan L. Identification of tubulin drug binding sites and prediction of relative differences in binding affinities to tubulin isotypes using digital signal processing. *J Mol Graph Model.* 27:497-505. 2008

影响因子：2.0　　引用次数：6

14. Ruan J, Chen H, Kurgan L, **Chen K**, Kang C, Pu P. HuMiTar: A sequence-based method for prediction of human microRNA targets. *Algorithms Mol Biol*. 3:16. 2008

影响因子：2.8　　引用次数：11

15. Zhang H, Zhang T, **Chen K**, Shen S, Ruan J, Kurgan L. Sequence based residue depth prediction using evolutionary information and predicted secondary structure. *BMC Bioinformatics*. 9:388. 2008

影响因子：3.0　　引用次数：14

16. Zhang T, Zhang H, **Chen K**, Shen S, Ruan J, Kurgan L. Accurate sequence-based prediction of catalytic residues. *Bioinformatics*. 24:2329-38. 2008

影响因子：5.5　　引用次数：29

17. **Chen K**, Kurgan M, Kurgan LA. Sequence Based Prediction of Relative Solvent Accessibility Using Two-stage Support Vector Regression with Confidence Values. *Journal of Biomedical Science and Engineering*, 1:1-9. 2008

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18. Kurgan L, Cios K, Zhang H, Zhang T, **Chen K**, Shen S, Ruan J. Sequence-Based Methods for Real Value Predictions of Protein Structure. *Current Bioinformatics*. 3:183-196. 2008

影响因子：1.2　　引用次数：5

19. Mou SS, Gao HJ, Qiang WY, **Chen K**. New delay-dependent exponential stability for neural networks with time delay. *IEEE TRANSACTIONS ON SYSTEMS MAN AND CYBERNETICS PART B-CYBERNETICS*. 38: 571-576. 2008

影响因子：2.7　　引用次数：63

20. Kurgan L, Cios K, **Chen K**. SCPRED: accurate prediction of protein structural class for sequences of twilight-zone similarity with predicting sequences. *BMC Bioinformatics*. 9:226. 2008

影响因子：3.0　　引用次数：26

21. **Chen K**, Kurgan LA, Ruan J. Prediction of flexible/rigid regions from protein sequences using k-spaced amino acid pairs. *BMC Struct Biol.* 7:25. 207

影响因子：2.3　　引用次数：26

22. **Chen K**, Kurgan L, Rahbari M. Prediction of protein crystallization using collocation of amino acid pairs. *Biochem Biophys Res Commun*. 355:764-9. 2007

影响因子：2.6　　引用次数：29

23. **Chen K**, Kurgan L. PFRES: Protein Fold Classification by Using Evolutionary Information and Predicted Secondary Structure. *Bioinformatics*. 23:2843-50. 2007

影响因子：5.5　　引用次数：47

24. Homaeian L, Kurgan LA, Ruan J, Cios KJ, **Chen K**. Prediction of protein secondary structure content for the twilight zone sequences. *Proteins*. 69:486-98. 2007

影响因子：2.8　　引用次数：17

25. Kurgan L, **Chen K**. Prediction of protein structural class for the twilight zone sequences. *Biochem Biophys Res Commun*. 357:453-60, 2007

影响因子：2.6　　引用次数：43

26. Huzil T, **Chen K**, Kurgan LA, Tuszynski JA. The Roles of β-Tubulin Mutations and Isotype Expression in Acquired Drug Resistance. *Cancer Informatics*, 3: 159–181, 2007

影响因子：1.6　　引用次数：13

27. Ruan J, **Chen K**, Tuszynski JA, Kurgan LA. Quantitative analysis of the conservation of the tertiary structure of protein segments. *Protein J*. 25:301-15. 2006

影响因子：1.1　　引用次数：5

28. **Chen K**, Ruan J, Kurgan LA. Prediction of three dimensional structure of calmodulin. *Protein J*.; 25:57-70. 2006

影响因子：1.1　　引用次数：5

国际会议文章

29. **Chen K**, Mizianty M, Kurgan LA. Accurate Prediction of ATP-binding Residues Using Sequence and Sequence-derived Structural Descriptors. 2010. IEEE International Conference on Bioinformatics and Biomedical Engineering.

30. **Chen K,** Kurgan LA, Ruan JS. Prediction of Protein Structural Class Using PSI-BLAST Profile Based Collocation of Amino Acid Pairs. *Bioinformatics and Biomedical Engineering, 2007. ICBBE 2007. The 1st International Conference on***,** 17-20.

31. **Chen K**, Kurgan M, Kurgan LA. Improved Prediction of Relative Solvent Accessibility Using Two-stage Support Vector Regression. *Bioinformatics and Biomedical Engineering, 2007. ICBBE 2007. The 1st International Conference on***,** 37-40

32. **Chen K**, Kurgan LA, Ruan JS. Optimization of the Sliding Window Size for Protein Structure Prediction. *Computational Intelligence and Bioinformatics and Computational Biology, 2006. CIBCB '06*. 2006 IEEE Symposium on. 366-372. （该会议被SCI检索）

33. Kedarisetti K, **Chen K**, Kapoor A, Kurgan LA. Prediction of the Number of Helices for the Twilight Zone Proteins. *Computational Intelligence and Bioinformatics and Computational Biology, 2006. CIBCB '06*. 2006 IEEE Symposium on. 459-465 （该会议被SCI检索）

丛书章节

1. **Chen K**, Kurgan LA. Neural Networks in Bioinformatics. In: Rozenberg, Grzegorz; Bäck, Thomas H.W.; Kok, Joost N. (Eds.), Handbook of Natural Computing. In Press（已接收，正在出版中）

为以下期刊承担审稿工作

- *Bioinformatics*
- *BMC Bioinformatics*
- *BMC Structural Biology*
- *Journal of Computational Chemistry*
- *Journal of Theoretical Biology*
- *Protein & Peptide Letters*