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# Yi Xing, Ph.D.

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## Professional Experiences

- 7/2006-present Assistant Professor  
Department of Internal Medicine  
Roy J. and Lucille A. Carver College of Medicine, University of Iowa
- 4/2006-present Visiting Scholar  
Department of Statistics, Stanford University, Prof. Wing Wong.  
Department of Developmental Biology, Stanford University, Prof. Matthew Scott.
- 9/2001-4/2006 Graduate Research Assistant  
Molecular Biology Institute, University of California Los Angeles, Prof. Christopher Lee.
- 1/2000-7/2001 Undergraduate Research Assistant  
School of Life Sciences, University of Science and Technology of China, Prof. Jing Liu.

## Education

- 2001-2006- Ph.D. Molecular Biology, University of California Los Angeles  
1996-2001- B.S. Molecular and Cell Biology; B.E. Computer Science and Technology  
University of Science and Technology of China

## Awards

- 2006 Finalist, Walter M. Fitch Prize, Society for Molecular Biology and Evolution  
2005 UCLA MBI Amgen Dissertation Award  
2005 UCLA Dissertation Year Fellowship (2005-2006)  
2005 RNA Society Student Fellow Award (Travel Fellowship to ISMB2005)  
2003 Outstanding Poster Award, 25<sup>th</sup> UCLA MBI Arrowhead Research Conference

## Research Interests

- Pre-mRNA Splicing and Alternative Splicing
- Comparative and Evolutionary Genomics
- Microarray Data Analysis

## Publications

19. Xing, Y., Kapur, K., Wong, WH. *In preparation.*
18. Lee, JA., Xing, Y., Nguyen, D., Xie, J., Lee, C., Black, DL. *In preparation.*
17. Parker, DS., Hsiao, RL., Xing, Y., Resch, A., Lee, C. (2006) Solving the problem of trans-genomic query with alignment tables. *Revised.*
16. Xing, Y., Wang, Q., Lee, C. (2006) Evolutionary divergence of exon flanks: A dissection of mutability and selection. *Genetics*, 173(3):1787-91.
15. Xing, Y., Lee, C. (2006) Alternative splicing and RNA selection pressure: evolutionary consequences for eukaryotic genomes. *Nature Reviews Genetics*, 7:499-509.

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14. Xing, Y. \*, Yu, T. \*, Wu, Y., Roy, M., Kim, J., Lee, C. # (2006) An expectation-maximization algorithm for probabilistic reconstruction of full-length isoforms from splice graphs. *Nucleic Acids Research*, 34:3150-3160 (# joint corresponding authors; \* joint first authors)
  13. Xing, Y., Lee, C. (2005) Can RNA selection pressure distort the measurement of Ka/Ks? *Gene*, 370:1-5
  12. Xing, Y., Lee, C. (2005) Assessing the application of Ka/Ks ratio test to alternatively spliced exons. *Bioinformatics*, 21: 3701-3703.
  11. Xing, Y., Lee, C. (2005) Evidence of functional selection pressure for alternative splicing events that accelerate evolution of protein subsequences. *Proc. Natl. Acad. Sci. U.S.A.*, 102:13526-13531.
  10. Xing, Y., Lee, C. (2005) Protein modularity of alternatively spliced exons is associated with tissue-specific regulation of alternative splicing. *PLoS Genetics*, 1(3):e34
  9. Xing, Y., Lee, C. (2004) Negative selection pressure against premature protein truncation is reduced by alternative splicing and diploidy. *Trends in Genetics*. 20:472-5
  8. Resch, A., Xing, Y., Alekseyenko, A., Modrek, B., Lee, C. (2004) Evidence for a subpopulation of conserved alternative splicing events under selection pressure for protein reading frame preservation. *Nucleic Acids Res.* 32:1261-9
  7. Xing, Y., Resch, A., Lee, C. (2004) The multiassembly problem: reconstructing multiple transcript isoforms from EST fragment mixtures, *Genome Research*. 14(3):426-41
  6. Resch, A., Xing, Y., Modrek, B., Gorlick, M., Riley, R., Lee, C. (2004) Assessing the impact of alternative splicing on domain interactions in the human proteome, *Journal of Proteome Research*. 3:76-83
  5. Grasso, C., Modrek, B., Xing, Y., Lee, C. (2004) Genome-wide detection of alternative splicing in expressed sequences using partial order multiple sequence alignment graphs. *Pac. Symp. Biocomputing*. World Scientific: Singapore 29-41
  4. Xing, Y., Xu, Q., Lee, C. (2003) Widespread production of novel soluble protein isoforms by alternative splicing removal of transmembrane anchoring domains, *FEBS Letters* 555(3):572-8
  3. Zewail, A. \*, Xie, M. W. \*, Xing, Y., Lin, L., Zhang, P. F., Zou, W., Saxe, J. P., and Huang, J. (2003) Novel functions of the phosphatidylinositol metabolic pathway discovered by a chemical genomics screen with wortmannin. *Proc. Natl. Acad. Sci. U.S.A.* 100: 3345-3350.
  2. Lee C, Atanelov L, Modrek B, Xing Y. (2003) ASAP: the Alternative Splicing Annotation Project. *Nucleic Acids Res.* 31(1):101-5.
  1. Cheng, L. S., Xing, Y., Liu J. (2002) Antibody humanization design by computer modeling. *Journal of University of Science and Technology of China* 32(5):591-601.

## Conferences and Professional Presentations

- 2006.1 - Evidence of functional selection pressure for tissue-specific alternative splicing events, *Poster*, UCLA-IPAM Workshop on Sequence Analysis toward Systems Biology
- 2006.1 - A genomic view of alternative splicing: How alternative splicing helped build the genomes and proteomes. *Invited Talk*, Stanford University, Palo Alto, CA
- 2005.9 - Alternative splicing and genome evolution. *Invited Talk*, Fudan University, Shanghai, China
- 2005.8 - RNA alternative splicing as an evolutionary strategy. *Invited Talk*, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China
- 2005.6 - Solving the isoform problem: a key connection between raw alternative splicing data and protein functions. *Invited Talk*, Alternative Splicing SIG, ISMB2005, Detroit, MI

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- 2005.4 - From genome-wide discoveries of alternative splicing to understanding its impact on the entire proteome. *Invited Talk*, Experimental Biology 2005, San Diego, CA
- 2004.10 - Alternative splicing opens neutral paths for evolution, *Poster*, 2004 NAS Sackler Colloquia on Bioinformatics, Irvine, CA
- 2004.5 - Alternative splicing and human proteome diversity, *Invited Talk*, 2004, IPAM Proteomics Symposium, Los Angeles, CA
- 2004.2 - Inferring full-length transcript and protein isoforms from fragmentary sequence data, *Poster*, 2004 Gordon Research Conference on Structural, Functional and Evolutionary Genomics, Ventura, CA
- 2004.1 - Widespread production of novel soluble protein isoforms by alternative splicing removal of transmembrane anchoring domains, *Poster*, 2004 Pacific Symposium of Biocomputing, Big Island, HI
- 2003.10 - Reconstructing human transcriptome by multi-assembly of human expressed sequences, *Poster*, 25<sup>th</sup> UCLA MBI Arrowhead Research Conference, Lake Arrowhead, CA

## **Societies**

- Member of the International Society for Computational Biology  
Member of the RNA Society  
Member of the Sigma Xi Society  
Member of the Society for Molecular Biology and Evolution

## **Academic Service**

- Reviewer for: Nucleic Acids Research, Molecular Biology and Evolution, BMC Genomics, Genome Biology, PNAS, Bioinformatics, PLoS Computational Biology, PLoS Biology