

BIOGRAPHICAL SKETCH

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NAME Xing, Yi		POSITION TITLE Associate Professor	
eRA COMMONS USER NAME (credential, e.g., agency login) XINGYI			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	MM/YY	FIELD OF STUDY
University of Science and Technology of China	B.S.	09/1996- 07/2001	Molecular and Cell Biology
University of Science and Technology of China	B.E.	09/1996- 07/2001	Computer Science and Technology
University of California, Los Angeles	Ph.D.	09/2001- 06/2006	Molecular Biology (Bioinformatics)
Stanford University	Postdoc	04/2006- 09/2007	Dept. of Statistics and Dept. of Developmental Biology

A. Personal Statement

I have the suitable expertise and research experience to carry out the proposed project. I am a tenured Associate Professor in the UCLA Department of Microbiology, Immunology, and Molecular Genetics. I have an outstanding track record in genomic and bioinformatic studies of transcriptome regulation and post-transcriptional RNA processing. During my doctoral and postdoctoral training, I developed widely-used algorithms for computational analysis of alternative splicing incorporating mRNA, EST and splicing sensitive microarray data. My research provided fundamental and novel insights into how alternative splicing affects protein domain interactions, protein localization, tissue-specific gene regulation, and mammalian genome evolution. Since I became an independent investigator in 2007, I have built a multidisciplinary research team consisting of computational biologists and wet lab scientists. My group studies pre-mRNA alternative splicing and transcriptome regulation by combining genomic, bioinformatic, and molecular approaches. We have published a series of high impact studies on alternative splicing regulation and evolution in normal and diseased tissues across mammalian species. We have also developed powerful bioinformatic approaches for exon-level and nucleotide-level analysis of mammalian transcriptomes using high-throughput sequencing technologies (RNA-Seq, PAS-Seq, etc), and have combined computational and experimental approaches to elucidate transcriptome changes and alternative splicing regulation in a variety of developmental and disease contexts. In summary, I have over 10 years of highly productive research in genomic and bioinformatic studies of mammalian gene regulation and RNA processing. My lab is very well equipped and trained for the work to be carried out in this proposal.

B. Positions and Honors

Positions and Employment

- 2000-01 School of Life Sciences, University of Science and Technology of China, undergraduate research assistant with Dr. Jing Liu.
- 2001-06 Molecular Biology Institute, University of California, Los Angeles, graduate research assistant with Dr. Christopher Lee.
- 2006-07 Department of Statistics and Department of Developmental Biology, Stanford University, postdoc with Dr. Wing Hung Wong (statistics) and Dr. Matthew Scott (developmental biology).
- 2007-12 University of Iowa, Assistant Professor, Dept. of Internal Medicine, College of Medicine; Dept. of Biomedical Engineering, College of Engineering; Dept. of Biostatistics, College of Public Health.
- 2012 University of Iowa, Associate Professor (with tenure), Dept. of Internal Medicine, College of Medicine; Dept. of Biomedical Engineering, College of Engineering; Dept. of Biostatistics, College of Public Health.

2013- University of California, Los Angeles, Associate Professor (with tenure), Department of Microbiology, Immunology, and Molecular Genetics.

Honors and Awards

1997-2000 Outstanding Student Award, University of Science and Technology of China.
2005 RNA Society Student Fellow Award.
2005-06 Dissertation Year Fellowship, University of California, Los Angeles.
2005 Amgen Dissertation Award, Molecular Biology Institute, University of California, Los Angeles.
2006 Finalist, Walter M. Fitch Prize, Society for Molecular Biology and Evolution.
2009 Translational Research Award, Department of Internal Medicine, University of Iowa
2009 Junior Faculty Grant, Edward Mallinckrodt Jr. Foundation
2010-12 Basil O'Connor Starter Scholar Research Award, March of Dimes Foundation
2011 Senior Visiting Fellow, UCLA Institute for Pure and Applied Mathematics
2013-15 Alfred P. Sloan Research Fellowship

Other Experience and Professional Activities

2010- NIH Study Sections:
Genomics, Computational Biology and Technology (GCAT) (*Ad Hoc* member: 2010, 2011, 2012)
ZMH1 ERB-S(05) (*Ad Hoc* member: 2012)
Genomics, Computational Biology and Technology (GCAT) (regular member: 2013-2019)

C. Publications (selected from 59 peer-reviewed publications)

Most relevant to the current application

1. **Xing, Y.**, Resch, A., Lee, C. (2004) The multiassembly problem: reconstructing multiple transcript isoforms from EST fragment mixtures, *Genome Research*. 14(3):426-41. PMID: PMC353230
2. Warzecha, CC., Jiang, P., Amirikian, K., Dittmar, KA., Lu, H., Shen, S., Guo, W., **Xing, Y.**, Carstens, RP. (2010) An extensive ESRP-regulated epithelial-specific splicing program is abrogated during the Epithelial Mesenchymal Transition. *EMBO J*, 29(19):3286-300. PMID: PMC2957203
3. Shen, S., Park, JW., Huang, J., Dittmar, KA., Lu, ZX., Zhou, Q., Carstens, RP. and **Xing, Y.** (2012) MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. *Nucleic Acids Res*. 40(8): e61. PMID: PMC3333886
4. Dittmar, KA.* , Jiang, P.* , Park, JW.* , Amirikian, K., Wan, J., Shen, S., **Xing, Y.**⁺, Carstens, RP.⁺. (2012) Genome-wide determination of a broad ESRP-regulated epithelial splicing network by RNA-Seq and SELEX-Seq. *Molecular and Cellular Biology*. 32(8):1468-1482. (⁺ joint corresponding authors; * joint first authors). PMID: PMC3318588
5. Zhao, K., Lu, ZX., Park, JW., Zhou, Q., **Xing, Y.** (2013) GLiMMPs: Robust statistical model for regulatory variation of alternative splicing using RNA-seq data. *Genome Biology*, 14:R74. PMID: In progress

Additional recent publications of importance in the field (in chronological order)

1. **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. PMID: PMC1224612
2. **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. PMID: PMC1201369
3. **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 Res*. 34:3150-3160 (⁺ joint corresponding authors; * joint first authors). PMID: PMC1475746
4. **Xing, Y.**, Lee, C. (2006) Alternative splicing and RNA selection pressure: evolutionary consequences for eukaryotic genomes. *Nature Reviews Genetics*. 7:499-509.

5. Lee, JA., **Xing, Y.**, Nguyen, D., Xie, J., Lee, C., Black, DL. (2007) Depolarization and CaM Kinase IV Modulate NMDA Receptor Splicing through Two Essential RNA Elements. *PLoS Biology*. 5(2):e40. PMID: PMC1790950
6. Calarco, JA.* , **Xing, Y.***, Caceres, M.* , Calarco, JP., Xiao, X., Pan, Q., Lee, C., Preuss, T. and Blencowe, B. (2007) Global analysis of alternative splicing differences between humans and chimpanzees. *Genes and Development*. 21: 2963-2975. (* joint first authors). PMID: PMC2049197
7. **Xing, Y.**⁺, Stoilov, P., Kapur, K., Han, A., Jiang, H., Shen, S., Black, DL, Wong, WH.⁺ (2008) MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. *RNA*,14(8): 1470-1479. (⁺ joint corresponding authors). PMID: PMC2491471
8. Lin, L., Shen, S., Tye, A., Cai, JJ., Jiang, P., Davidson, BL., **Xing, Y.** (2008) Diverse splicing patterns of exonized Alu elements in human tissues. *PLoS Genetics*. 4(10): e1000225. PMID: PMC2562518
9. Shen, S.* , Lin, L.* , Cai, JJ., Jiang, P., Kenkel, EJ., Stroik, MR., Sato, S., Davidson, BL., **Xing, Y.** (2011) Widespread establishment and regulatory impact of Alu exons in human genes. *Proc. Natl. Acad. Sci. U.S.A.*, 108(7):2837-2842 (* joint first authors). PMID: PMC3041063
10. Boudreau, RL., Jiang, P., Gilmore, BL., Spengler, RM., Tirabassi, R., Nelson, JA., Ross, CA., **Xing, Y.**⁺, **Davidson BL.**⁺ (2014) Transcriptome-wide discovery of microRNA binding sites in human brain, *Neuron*, in press. (⁺ joint corresponding authors)

D. Research Support

Ongoing

R01GM088342 (PI: Xing)

04/05/10 – 03/31/15

NIH/NIGMS

Evolution of pre-mRNA splicing in primates

Role: PI.

The goal of this project is to survey the evolution of pre-mRNA splicing in primates and elucidate the molecular mechanisms that created species-specific splicing patterns.

Preterm Birth Initiative Full Grant (PI: Murray)

04/01/11 – 03/31/15

Burroughs Wellcome Fund

Genomic signatures of gene expression and alternative splicing in preterm birth

Role: Co-Principal Investigator.

This project will identify the transcriptome signature of preterm birth in the human placenta.

R21NS075825 (PI: Xing/Margolis)

06/01/12 – 05/31/14

NIH/NINDS

Transcriptome in Huntington's disease and Huntington's disease-like 2

Role: Principal Investigator of Multi-PI grant.

This project will identify convergent pathogenic pathways, via parallel transcriptome characterization of mouse models and human patient samples of HD and HDL2.

CHDI Research Contract (PI: Davidson)

04/01/13 – 03/31/14

CHDI

Transcription Profiling of HD and HDL2 Postmortem Brain Tissues

Role: Co-PI.

This CHDI grant supports RNA-seq profiling and AGO2 HITS-CLIP (for mapping microRNA target sites) of HD, HDL2, and control human brain samples (BA4 region).

R01GM105431 (PI: Zhou)

04/01/13 – 03/31/17

NIH/NIGMS

Integrative Analysis of Public RNA-seq Repositories

Role: Subcontract PI.

The goal of this project is to develop computational tools to infer alternative splicing network and transcription-splicing coupling from large amount of public RNA-seq data.

Alfred P. Sloan Research Fellowship (PI: Xing)

09/15/13 – 09/15/15

Alfred P. Sloan Foundation

Role: PI.

This Alfred P. Sloan Research Fellowship will support the overall research of Dr. Xing.

R01NS076631 (PI: Davidson/Ross/Xing)

09/30/13 – 08/31/18

NIH/NINDS

Genomic and functional analysis of transcriptome changes in Huntington's disease

Role: Principal Investigator of Multi-PI grant.

The goal of this project is to perform RNA-Seq and functional analysis of transcriptome changes in Huntington's disease.

Completed

Junior Faculty Award (PI: Xing)

10/01/09 – 09/30/12

Edward Mallinckrodt Jr. Foundation

Decipher the splicing code of mammalian cells using ultra-deep RNA sequencing

Role: PI.

FSHS-08200902 (PI: Xing)

12/01/09 – 06/30/11

FSH Society

Aubrie Lee Family Research Grant for Infantile FSHD & Fire Island Fellowship

Role: PI.

R01HG004634 (PI: Wong)

09/18/08 – 06/30/12

NIH/NHGRI (subcontract)

Statistical analysis of exon arrays

Role: Sub-PI.

MOD-#5-FY10-60 (PI: Xing)

02/01/10 – 06/30/13

March of Dimes Foundation

Basil O'Connor Starter Scholar Research Award

Role: PI.

R21DK089417 (PI: Xing/Kwitek)

07/01/10 – 06/30/13

NIH/NIDDK

Identification of a metabolic syndrome transcriptome signature in the LH rat

Role: Principal Investigator of Multi-PI grant.

R21HL104337 (PI: McCray/Xing)

07/01/10 – 06/30/13

NIH/NHLBI

Altered MicroRNA function in Cystic Fibrosis airway epithelia

Role: Principal Investigator of Multi-PI grant.