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### **I. EDUCATION**

Ph.D. (Biochemistry)                      Louisiana State University, Baton Rouge. 2005  
B.S. (Biochemistry)                      Nankai University, Tianjin, P.R. China. 2000

### **II. PROFESSIONAL EXPERIENCE**

11/12 – present Full Member, Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey  
01/12 – present Full Member, Human Genetic Institute of New Jersey, Rutgers, the State University of New Jersey  
01/12 – present Assistant Professor, Department of Genetics, Rutgers, the State University of New Jersey  
08/06 – 12/11 Postdoctoral Fellow, Department of Human Genetics, University of Utah School of Medicine, Salt Lake City.  
05/05 – 08/06 Postdoctoral Fellow, Department of Biological Sciences, Louisiana State University, Baton Rouge.  
01/03 – 05/05 Graduate Research Assistant, Louisiana State University, Baton Rouge. Advisor: Dr. Mark Batzer.  
07/01 – 12/02 Graduate Teaching Assistant, Louisiana State University, Baton Rouge.

### **III. PUBLICATIONS** (\*: equal contribution; †: equal contribution; #: corresponding author; underlined: trainees)

1. Nguyen A. L.\*, D. Marin\*, A. Zhou, A. S. Gentilello, E. M. Smoak, Z. Cao, A. Fedick, Y. Wang, D. Taylor, R. T. Scott Jr., **J. Xing**, N. Treff, and K. Schindler (In Press) Identification and characterization of Aurora Kinase B and C variants associated with maternal aneuploidy. *Molecular Human Reproduction*.
2. Rustagi, N., A. Zhou, W. S. Watkins, E. Gedvilaite, S. Wang, N. Ramesh, D. Muzny, R. A. Gibbs, L. B. Jorde#, F. Yu#, and **J. Xing** # (2017) Extremely low-coverage whole

- genome sequencing in South Asians captures population genomics information. *BMC Genomics* 18:396
3. Willsey, A. J.\*, T. V. Fernandez\*, D. Yu†, R. A. King†, A. Dietrich†, **J. Xing** †, S. J. Sanders, J. D. Mandell, A. Y. Huang, P. Richer, L. Smith, S. Dong, K. E. Samocha, Tourette International Collaborative Genetics (TIC Genetics) (including E. Gedvilaite, S. Wang, Y. Zhang, A. Zhou), Tourette Syndrome Association International Consortium for Genetics (TSAICG), B. M. Neale, G. Coppola, C. A. Mathews, J. A. Tischfield, J. M. Scharf, M. W. State, and G. A. Heiman (2017) *De novo* coding variants are strongly associated with Tourette Disorder *Neuron* 94: 486–499
  4. Ha H., N. Wang, and **J. Xing**# (2017) Library construction for high-throughput mobile element identification and genotyping. *Methods in Molecular Biology* 1589:1-15
  5. Viljetic B \*, L. Diao \*, J. Liu \*, Z. Krsnik \*, S. H. R. Wijeratne, R. Kristopovich, M. L. Kraushar, J. Song, **J. Xing** #, K. C. Chen #, M. R. Rasin # (2017) Multiple roles of PIWIL1 in mouse neocortico-genesis. *bioRxiv* doi: <https://doi.org/10.1101/106070>
  6. Jadot, M., M. Boonen, J. Thirion, N. Wang, **J. Xing**, C. Zhao, M. Qian, H. Zheng, J. Everett, D. Moore, D. Sleat, and P. Lobel (2017) Accounting for protein subcellular localization. *Molecular and Cellular Proteomics* 16: 194-212
  7. Kumar, N., M. Srivillibhuthur, K. D. Walton, A. Zhou, W. J. Faller, A. O. Perekatt, O. J. Sansom, D. L. Gumucio, **J. Xing**, E. M. Bonder, N. Gao, M. P. Verzi (2016) A YY1-dependent increase in aerobic metabolism is indispensable for intestinal organogenesis. *Development* 143: 3711-3722
  8. Sleat, D. #, E. Gedvilaite, Y. Zhang, P. Lobel, and **J. Xing** # (2016) Analysis of large-scale whole exome sequencing data to determine the prevalence of genetically-distinct forms of neuronal ceroid lipofuscinosis. *Gene* 593:284–291
  9. Alexander, J., H. Potamianou, **J. Xing**, L. Deng, I. Karagiannidis, F. Tsetsos, P. Drineas, Z. Tarnok, R. Rizzo, T. Wolanczyk, L. Farkas, P. Nagy, U. Szymanska, C. Androutsos, V. Tsironi, A. Koumoula, C. Barta, TSGeneSEE, P. Sandor, C. L. Barr, J. Tischfield, P. Paschou, G. A. Heiman, and M. Georgitsi (2016) Targeted re-sequencing approach of candidate genes implicates rare potentially functional variants in Tourette Syndrome etiology. *Frontiers in Neuroscience* 10:428 (7 pages)
  10. Ross J.#, E. Gedvilaite, J. A. Badner, C. Erdman, S. Barondes, L. Baird, N. Matsunami, M. Leppert, **J. Xing**#, W. Byerley# (2016) A Rare Variant in *CACNA1D* segregates with 7 Bipolar I cases in a large pedigree. *Molecular Neuropsychiatry* 2:145-150
  11. Ha, H., J. Loh, and **J. Xing**# (2016) Identification of polymorphic full-length SVA retrotransposons using a mobile element scanning method for SVA (ME-Scan-SVA). *Mobile DNA* 7:15 (13 pages, PMID: 4967303)
  12. Fan Z., P. Silva, I. Gronau, S. Wang, A. S. Armero, R. M. Schweizer, O. Ramirez, J. Pollinger, M. Galaverni, D. Ortega Del-Vecchio, L. Du, W. Zhang, Z. Zhang, **J. Xing**, C. Vilá, T. Marques-Bonet, R. Godinho, B. Yue, and R. K. Wayne (2016) Worldwide patterns of genomic variation and admixture in gray wolves. *Genome Research* 26: 163-173 (PMCID: 4728369)

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14. 1000 Genomes Project Consortium, A. Auton, L. D. Brooks, R. M. Durbin, E. P. Garrison, H. M. Kang, J. O. Korbel, J. L. Marchini, S. McCarthy, G. A. McVean, and G. R. Abecasis (2015) A global reference for human genetic variation. *Nature* 526:68-74 (PMCID: 4750478)
15. Parrish N. F., K. Fujino, Y. Shiromoto, Y. W. Iwasaki, H. Ha, **J. Xing**, A. Makino, S. Kuramochi-Miyagawa, T. Nakano, H. Siomi, T. Honda, and K. Tomonaga (2015) piRNA derived from ancient viral processed pseudogenes suggests transgenerational sequence-specific immunity in mammals. *RNA* 21:1691-1703 (PMCID: 4574747)
16. Platt II R. N., Y. Zhang, D. J. Witherspoon, **J. Xing**, A. Suh, M. S. Keith, L. B. Jorde, R. D. Stevens, and D. A. Ray (2015) Targeted capture of phylogenetically-informative Ves SINE insertions in genus *Myotis*. *Genome Biology and Evolution* 7:1664-1675 (PMCID: 4494050)
17. Kwak Y., Y. Kim, **J. Xing**, and K. Han (2015) Evolutionary fate of SVA2 elements in primate genomes. *Genes & Genomics* 37:153-159
18. Song J., J. Liu, S. L. Schnakenberg, H. Ha, **J. Xing**, and K. C. Chen (2014) Variation in piRNA and transposable element content in strains of *Drosophila melanogaster*. *Genome Biology and Evolution* 6(10):2786-2798 (PMCID: PMC4224344)
19. Lorenzo F. R., C. Huff, M. Myllymäki, B. Olenchock, S. Swierczek, T. Tashi, V. Gordeuk, T. Wuren, R. L. Ge, D. A. McClain, T. M. Khan, P. A. Koul, P. Guchhait, M. E. Salama, **J. Xing**, G. L. Semenza, E. Liberzon, A. Wilson, T. S. Simonson, L. B. Jorde, W. G. Kaelin Jr., P. Koivunen, and J. T. Prchal (2014) A genetic mechanism for Tibetan high-altitude adaptation. *Nature Genetics* 46(9):951-956
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- (*Macaca thibetana*) provides new insight into the macaque evolutionary history. *Molecular Biology and Evolution* 31(6):1475–1489 (PMCID: 4032132)
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  26. Wang S., J. Lachance, S. Tishkoff, J. Hey, and **J. Xing**<sup>#</sup> (2013) Apparent variation in Neanderthal admixture among African populations is consistent with gene flow from non-African populations. *Genome Biology and Evolution* 5(11): 2075-2081 (PMCID: 3845641)
  27. **Xing J.\***, T. Wuren\*, T. S. Simonson\*, W. S. Watkins, D. J. Witherspoon, W. Wu, G. Qin, C. D. Huff, L. B. Jorde, and R. L. Ge (2013) Genomic analysis of nature selection and phenotypic variation in high-altitude Mongolians. *PLOS Genetics* 9(7): e1003634 (12 pages, PMCID: 3715426)
  28. Wu W., E. A. Clark, G. J. Stoddard, W. S. Watkins, M. S. Esplin, T. A. Manuck, **J. Xing**, M. W. Varner, and L. B. Jorde (2013) Effect of interleukin-6 polymorphism on risk of preterm birth within population strata: a meta-analysis. *BMC Genetics* 14:30 (9 pages, PMCID: 3639799)
  29. Witherspoon D. J., Y. Zhang, **J. Xing**, W. S. Watkins, H. Ha, M. A. Batzer, and L. B. Jorde (2013) Mobile Element Scanning (ME-Scan) identifies thousands of novel Alu insertions in diverse human populations. *Genome Research* 23(7):1170-1181 (PMCID: 3698510)
  30. Ge R. L., Q. Cai, Y. Y. Shen, A. San, L. Ma, Y. Zhang, X. Yi, Y. Chen, L. Yang, Y. Huang, R. He, Y. Hui, M. Hao, Y. Li, B. Wang, X. Ou, J. Xu, Y. Zhang, K. Wu, C. Geng, W. Zhou, T. Zhou, D. M. Irwin, Y. Yang, L. Ying, H. Bao, J. Kim, D. M. Larkin, J. Ma, H. A. Lewin, **J. Xing**, R. N. Platt II, D. A. Ray, L. Auvil, B. Capitanu, X. Zhang, G. Zhang, R. W. Murphy, J. Wang, Y. P. Zhang, and J. Wang (2013) Draft genome sequence of the Tibetan antelope. *Nature Communications* 4:1858 (7 pages, PMCID: 3674232)
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- selection in Bolivian and Totonac populations of the New World. *BMC Genetics* 13(1):39 (14 pages, PMID:3432609)
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  39. Lyon G. J. , T. Jiang, R. Van Wijk, W. Wang, P. M. Bodily, **J. Xing**, L. Tian, R. J. Robison, M. Clement, Y. Lin, P. Zhang, Y. Liu, B. Moore, J. T. Glessner, J. Elia, F. Reimherr, W. W. van Solinge, M. Yandell, H. Hakonarson, J. Wang, W. E. Johnson, Z. Wei, and K. Wang (2011) Exome sequencing and unrelated findings in the context of complex disease research: ethical and clinical implications. *Discovery Medicine* 12(62):41-55 (PMCID: 3544941)
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77. Callinan P. A., D. J. Hedges, A.-H. Salem, **J. Xing**, J. A. Walker, R. K. Garber, W. S. Watkins, M. J. Bamshad, L. B. Jorde and M. A. Batzer (2003) Comprehensive analysis of *Alu* associated diversity on the human sex chromosomes. *Gene* 317: 103-110
78. Walker J. A., G. E. Kilroy, **J. Xing**, J. Shewale, S. Sinha, and M. A. Batzer (2003) Human DNA quantitation using *Alu* element based PCR. *Analytical Biochemistry* 315: 122-128
79. Gao Y, **J. Xing**, M. Streuli, T.L. Leto and Y. Zheng (2001) Trp(56) of Rac1 specifies interaction with a subset of guanine nucleotide exchange factors. *Journal of Biological Chemistry* 276: 47530-4754

#### IV. RESEARCH SUPPORT

##### COMPLETED

K99HG005846

09/26/2010 – 03/31/2012

NIH Pathway to Independence Award (K99/R00)

NIH/NHGRI

*High-throughput Mobile Element Genotyping Using Next-generation Sequencing*

Principal Investigator



Busch Biomedical Grant 07/01/2012 – 05/01/2014  
Busch Biomedical Grant Program  
*Correlating piRNA and mobile element expression in human individuals*  
Principal Investigator

R00HG005846 04/01/2012 – 02/28/2016  
NIH Pathway to Independence Award (K99/R00)  
NIH/NHGRI  
*High-throughput Mobile Element Genotyping Using Next-generation Sequencing*  
Principal Investigator

## ACTIVE

CAUT12APS006 06/15/2012-06/15/2017  
New Jersey Governor's Council for Medical Research and Treatment of Autism  
*Elucidating Genetic Components of Autism and Related Disorders*  
Co-Investigator (PI: Linda Brzustowicz)

U01HG007419 09/01/2013 – 05/31/2017  
NIH/NHGRI  
*Population Architecture Using Genomics and Epidemiology (PAGE), Phase II – Coordinating Center*  
Co-Investigator (PI Tara Matisse)

U24HG008956 01/14/2016–11/30/2019  
NIH/NHGRI  
*NHGRI Genome Sequencing Program Coordinating Center*  
Co-Investigator (MPI: Tara Matisse, Steve Buyske)

## V. PRESENTATIONS

### Platform and Invited Talks

Understanding human genomic variation via high-throughput sequencing Genomic Instability & Cancer Genetics Research Program Meeting, Rutgers Cancer Institute of New Jersey, Dec 2016. *Invited talk*

Disease gene identification in the genomics era ChemBio specialization program (CK2), Dankook University, Cheonan, Korea, Oct 2016. *Invited talk*

Understanding mobile element biology using high-throughput sequencing International Conference of the Korean Society for Molecular and Cellular Biology, Seoul, Korea, Oct 2016. *Invited talk*

Understanding human genomic variation via high throughput sequencing The Human Genetics Association of New Jersey Conference, Sep 2016. *Invited talk*

- Novel Candidate Genes that Modify Chronic Obstructive Pulmonary Disease Susceptibility Human Genetics in New York City Second Symposium, Jun 2016. *Invited talk*
- Disease gene identification in the genomics era Institute of Development and Regenerative Biology, Hangzhou Normal University, Hangzhou, Zhejiang, China, May 2016. *Invited talk*
- Understanding genomic variation via high throughput sequencing Center for primate translational medicine research, Kunming University of Science and Technology, Kunming, Yunnan, China, Apr 2015. *Invited talk*
- Understanding genomic variation via high throughput sequencing College of Life Sciences, Sichuan University, Apr 2015. *Invited talk*
- Pedigree-based disease-gene identification using high-throughput sequencing Columbia University Seminars in Genetic Epidemiology, Columbia University, Dec 2014. *Invited talk*
- VAAST projects at Rutgers VAAST developer annual meeting, University of Utah, Jun 2014. *Invited talk*
- Understanding human genomic variation via high throughput sequencing School of Molecular Biosciences, Washington State University, Feb 2014. *Invited talk*
- Disease gene identification using high throughput sequencing data Department of Nuclear Medicine, Tianjin Medical University General Hospital, Tianjin, China, Jan 2014. *Invited talk*
- Understanding human genomic variation via high throughput sequencing Department of Biological Sciences, Texas Tech University, Dec 2013. *Invited talk*
- Disease gene identification in the genomics era – a case study of Tourette syndrome The Interactive Group in Human Genetics, Rutgers, the State University of New Jersey, Jul 2013. *Invited talk*
- Characterization of piRNA genomic distribution and expression variation in human individuals FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Big Sky, MT., Jun 2013. *Platform Presentation*
- Understanding human evolutionary history in the genomics era Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, Nov 2012. *Invited talk*
- Population dynamics of human mobile elements 63rd Fujihara Seminar, a new horizon of retroposon research, Kyoto, Japan, Aug 2012. *Invited talk*
- Mobile elements demonstrate that *Australopithecus* effective population size was twice that of *Homo* FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Snowmass, CO., Aug 2011. *Platform Presentation*
- Toward a more uniform sampling of human genetic diversity The American Society of Human Genetics 59<sup>th</sup> annual meeting, Honolulu, HI, Oct 2009. *Platform Presentation*
- Genetic variation associated with mobile elements in an individual human genome The genome instability satellite meeting of the American Society of Human Genetics 58<sup>th</sup> annual meeting, Philadelphia, PA, Nov 2008. *Platform Presentation*

Under the genomic radar: the stealth model of *Alu* amplification FASEB Summer Research Conferences on Mobile Elements in Mammalian Genomes 2005, Tucson, AZ, Jun 2005. *Platform Presentation*

Under the genomic radar: the stealth model of *Alu* amplification CBMM Seminar Series, Louisiana State University, Baton Rouge, LA, May 2005. *Platform Presentation*

## VI. TEACHING

Fall 2013-2015,2017 Effective Communication Skills in Genetics (01:447:430), Rutgers, the State University of New Jersey

Spring 2013 Honors Seminar (01:447:404), Rutgers, the State University of New Jersey

## VII. PROFESSIONAL SERVICE

### Editorial Activities

**Associate Editor:** *Gene* (2013-2016)

**Editorial Board:** *Analytical Biochemistry* (2012-), *Gene* (2011-), *Mobile DNA* (2014-)

**Guest Editor:** *Comparative and Functional Genomics*, for the special issue "Genomic Impact of Transposable Elements in Mammals" (2012)

### Ad-hoc Review Activities

**Study sections:** 2017: Member, NIH Genetic Variation and Evolution; 2013: Member, NIEHS Special Emphasis Panel

**Grant proposals:** National Science Foundation (NSF), Netherlands Organisation for Health Research and Development (ZonMw)

**Book Chapter:** *Human Evolutionary Genetics, Scientific Writing and Communication*

**Journal articles (24 journals, >100 articles):** *American Journal of Human Genetics*, *Analytical Biochemistry*, *Annals of Human Genetics*, *Bioinformatics*, *Biotechniques*, *BMC Bioinformatics*, *BMC Genetics*, *Gene*, *Genetica*, *Genome Biology and Evolution*, *Genome Research*, *Genomics*, *European Journal of Human Genetics*, *Human Immunology*, *Human Molecular Genetics*, *Human Mutation*, *Mobile DNA*, *Molecular Biology and Evolution*, *Nucleic Acids Research*, *PLoS Computational Biology*, *PLoS Genetics*, *PLoS One*, *Zoological Science*.

### Professional Societies

Member, American Heart Association 2014 - 2015

Member, American Association for the Advancement of Science 2010 - 2012

Member, American Society of Human Genetics 2007 - present

Full Member, Sigma Xi 2007

Member, American Society for Microbiology 2006

### **VIII. HONORS & AWARDS**

- 2011            Nominee for the Searle Scholars Program
- 2010            Science Program for Excellence in Science - The American Association for  
the Advancement of Science
- 2009            ASHG Trainee Research Award finalist - The American Society of Human  
Genetics
- 2005            The Robert Scott and Louise Pierce Allen Award for the outstanding  
graduate student in biochemistry - Louisiana State University, Baton  
Rouge, LA