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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. Sun, N., C. Nasello, L. Deng, N. Wang, Y. Zhang, Z. Xu, Z. Song, R. A. King, Z. Pang, **J. Xing**, G. A. Heiman, K. Kwan, and J. A. Tischfield (2017) The *PNKD* gene is associated with Tourette Disorder and Tic disorder in a multiplex family. *Molecular Psychiatry*
2. Wang, N.*, Y. Zhang*, E. Gedvilaite, J. Loh, T. Lin, X. Liu, C. Liu, D. Kumar, R. Donnelly, K. Raymond, E. H. Schuchman, D. Sleat#, P. Lobel#, and **J. Xing**# (2017)

Using whole-exome sequencing to investigate the genetic bases for lysosomal storage diseases of unknown etiology. *Human Mutation*

3. 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 (2017) Identification and characterization of Aurora Kinase B and C variants associated with maternal aneuploidy. *Molecular Human Reproduction* 23:406-416
4. 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
5. 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
6. 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
7. 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 neocorticogenesis. *bioRxiv* doi: https://doi.org/10.1101/106070
8. 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
9. 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
10. 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
11. 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)
12. 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

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14. Fan Z., P. Silva, I. Gronau, S. Wang, A. S. Armero, R. M. Schweizer, O. Ramirez, J. Pollinger, M. Galaverni, D. Ortega Del-Vecchyo, 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)
15. Bruse S.*, M. Moreau*, Y. Bromberg*, J. Jang, N. Wang, H. Ha, M. Picchi, Y. Lin, R. J. Langley, C. Qualls, J. Klensney-Tait, J. Zabner, S. Leng, J. Mao, S. A. Belinsky, **J. Xing**#, and T. Nyunoya# (2016) Whole exome sequencing in severe chronic obstructive pulmonary disease. *Human Genomics* 10:1 (12 pages, PMCID: 4705629)
16. 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)
17. 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)
18. 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)
19. Kwak Y., Y. Kim, **J. Xing**, and K. Han (2015) Evolutionary fate of SVA2 elements in primate genomes. *Genes & Genomics* 37:153–159
20. 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)
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with genes and mobile elements. *BMC Genomics* 15(1):545 (16 pages, PMCID: 4094622)

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29. **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)
30. 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)
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37. Ge R. L., T. S. Simonson, R. C. Cooksey, U. Tanna, G. Qin, C. D. Huff, D. J. Witherspoon, **J. Xing**, B. Zhengzhong, J. T. Prchal, L. B. Jorde, and D. A. McClain (2012) Metabolic insight into mechanisms of high-altitude adaptation in Tibetans. *Molecular Genetics and Metabolism* 106(2):244-247 (PMCID:3437309)
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40. Stewart C.*, D. Kural*, M. P. Stromberg*, J. A. Walker, M. K. Konkel, A. M. Stutz, A. E. Urban, F. Grubert, H. Y. Lam, W.-P. Lee, M. Busby, A. R. Indap, E. Garrison, C. Huff, **J. Xing**, M. P. Snyder, L. B. Jorde, M. A. Batzer, J. O. Korbel, G. T. Marth, and 1000 Genomes Project (2011) A comprehensive map of mobile element insertion polymorphisms in humans. *PLoS Genetics* 7(8): e1002236 (19 pages, PMCID:3158055)
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Jorde, H. Hakonarson, J. R. Lillehaug, L. G. Biesecker, M. Yandell, T. Arnesen, and G. J. Lyon (2011) Using VAAST to identify an X-Linked disorder resulting in lethality in male infants due to N-terminal acetyltransferase deficiency. *American Journal of Human Genetics* 89(1):28-43 (PMCID: 3135802)

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78. **Xing J.**, A.-H. Salem, D. J. Hedges, G. E. Kilroy, W. S. Watkins, J. E. Schienman, C.-B. Stewart, J. Jurka, L. B. Jorde and M. A. Batzer (2003) Comprehensive analysis of two *Alu* Yd subfamilies. *Journal of Molecular Evolution* 57: S76-S89
79. 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
80. 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
81. 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

ACTIVE

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

U01HG007419 09/2013 – 05/2018
NIH/NHGRI
Population Architecture Using Genomics and Epidemiology (PAGE), Phase II – Coordinating Center
Co-Investigator (MPI: Tara Matise, Steve Buyske)

CAUT12APS006 06/2012 – 06/2018
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)

COMPLETED

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

Busch Biomedical Grant 07/2012 – 05/2014
Busch Biomedical Grant Program
Correlating piRNA and mobile element expression in human individuals
Principal Investigator (Co-PI Kevin Chen)

K99HG005846 09/2010 – 03/2012
NIH Pathway to Independence Award (K99/R00)
NIH/NHGRI
High-throughput Mobile Element Genotyping Using Next-generation Sequencing
Principal Investigator

V. PRESENTATIONS

Platform and Invited Talks

Lighthouses for safe harbors: using mobile element insertions to identify genomic regions for gene therapy FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Big Sky, MT, Jun 2017. *Platform Presentation*

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 59th 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 58th 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*

Poster Presentations

Analysis of large-scale whole exome sequencing data to determine the prevalence of genetically-distinct forms of neuronal ceroid lipofuscinosis American Society of Human Genetics 66th annual meeting, Vancouver, BC, Canada, Oct 2016.

Exome sequencing to identify the genetic bases for lysosomal storage diseases of unknown etiology The 24th Annual International Genetic Epidemiology Society Meeting, Baltimore, MD, Oct 2015.

Exome sequencing to identify the genetic bases for lysosomal storage diseases of unknown etiology American Society of Human Genetics 65th annual meeting, Baltimore, MD, Oct 2015.

High-throughput mobile element genotyping in human populations FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Palm Beach, FL, Jun 2015.

Whole exome sequencing in severe chronic obstructive pulmonary disease The American Society of Human Genetics 64th annual meeting, San Diego, CA, Oct 2014.

Studying Indian genetic diversity using extremely low-coverage whole-genome sequencing Biology of Genomes, Cold Spring Harbor, NY, May 2014.

Characterization of piRNA genomic distribution and expression variation in human individuals The American Society of Human Genetics 63nd annual meeting, Boston, MA, Oct 2013.

piRNA cluster identification and expression variation in human individuals Biology of Genomes, Cold Spring Harbor, NY, May 2013.

Genomic analysis of natural selection and phenotypic variation in high-altitude Mongolians The American Society of Human Genetics 62nd annual meeting, San Francisco, CA, Nov 2012.

Mobile elements demonstrate that *Australopithecus* effective population size was twice that of *Homo* Biology of Genomes, Cold Spring Harbor, NY, May 2012.

Whole genome sequencing and rare variant analyses of a multiplex bipolar pedigree 12th International Congress of Human Genetics/American Society of Human Genetics 61st annual meeting, Montreal, QC, Canada, Oct 2011.

Ancestry, admixture and natural selection: a genetic analysis of New World populations Biology of Genomes, Cold Spring Harbor, NY, May 2011.

Genetic diversity in India and the inference of Eurasian population expansion The American Society of Human Genetics 60th annual meeting, Washington D.C., Nov 2010.

Mobile elements reveal small population sizes in the ancient ancestors of *Homo sapiens* FASEB Summer Research Conferences on Mobile Elements in Mammalian Genomes 2009, Snowmass, CO, Jul 2009.

Mobile elements create structure variation in an individual human genome The American Society of Human Genetics 58th annual meeting, Philadelphia, PA, Nov 2008.

Analyses of human genetic structure using SNP microarrays Biology of Genomes, Cold Spring Harbor, NY, May 2008.

Linkage disequilibrium patterns and tagSNP transferability in multiple populations The American Society of Human Genetics 57th annual meeting, San Diego, CA, Oct 2007.

Alu subfamilies and human recombination hotspots FASEB Summer Research Conferences on Mobile Elements in Mammalian Genomes 2007, Tucson, AZ, Jun 2007.

SVA elements are novel sources for genomic variation ASM Conference on Mobile DNA, Banff, AB, Canada, Feb 2006.

Molecular phylogeny of Cercopithecidae (Old World Monkeys) as inferred by *Alu* insertions Genomes and Evolution (Joint annual meeting of the International Society for Molecular Biology and Evolution and the American Genetic Association) 2004, State College, PA, Jun 2004.

Comprehensive analysis of two *Alu* Yd subfamilies 13th International Symposium on Human Identification, Phoenix, AZ, Oct 2002.

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:
Member, NIH Genetic Variation and Evolution (2017)
Member, Busch Biomedical Research Award (2013, 2014, 2016)
Member, NIH NIEHS Special Emphasis Panel (2013)
Grant proposals:
National Science Foundation (NSF)
Louisiana Board of Regents' Research Competitiveness Subprogram
Netherlands Organisation for Health Research and Development (ZonMw)
Arabian Gulf University Research Committee
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