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I. EDUCATION

Ph.D. (Biochemistry) Louisiana State University, Baton Rouge. 2005
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II. PROFESSIONAL EXPERIENCE

07/18 – present Associate Professor, Department of Genetics, Rutgers, the State University of New Jersey
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 – 06/18 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. Biswas, L., K. M. Tyc, W. E. Yakoubi, K. Morgan, **J. Xing**, K. Schindler (2021) Meiosis interrupted: the genetics of female infertility via meiotic failure. *Reproduction*

2. Tyc, K. M.*, A. Wong*, R. T. Scott, Jr., X. Tao, K. Schindler, and **J. Xing#** (2021) Analysis of DNA variants in miRNAs and miRNA 3'UTR binding sites in female infertility patients. *Laboratory Investigation*
3. Dymant, D. A.*, A. O'Donnell-Luria*, P. B. Agrawal, Z. Coban Akdemir, K. A. Aleck, D. Antaki, H. Al Sharhan, P. B. Au, H. Aydin, A. H. Beggs, K. Bilguvar, E. Boerwinkle, H. Brand, C. A. Brownstein, S. Buyske, B. Chodirker, J. Choi, A. E. Chudley, C. L. Clericuzio, G. F. Cox, C. Curry, E. de Boer, B. B. A. de Vries, K. Dunn, C. M. Dutmer, E. M. England, J. A. Fahrner, B. B. Geckinli, C. A. Genetti, A. Gezdirici, W. T. Gibson, J. G. Gleeson, C. R. Greenberg, A. Hall, A. Hamosh, T. Hartley, S. N. Jhangiani, E. Karaca, K. Kernohan, J. L. Lauzon, M. E. S. Lewis, R. B. Lowry, F. Lopez-Giraldez, T. C. Matise, J. McEvoy-Venneri, B. McInnes, A. Mhanni, S. Garcia Minaur, J. Moilanen, A. Nguyen, M. J. M. Nowaczyk, J. E. Posey, K. Ounap, D. Pehlivan, S. Pajusalu, L. S. Penney, T. Poterba, P. Prontera, M. J. R. Doriqui, S. L. Sawyer, N. Sobreira, V. Stanley, D. Torun, D. Wargowski, P. D. Witmer, I. Wong, **J. Xing**, M. S. Zaki, Y. Zhang, Care4Rare Consortium, Centers for Mendelian Genomics, K. M. Boycott, M. J. Bamshad, D. A. Nickerson, E. E. Blue#, and A. M. Innes# (2021) Alternative genomic diagnoses for individuals with a clinical diagnosis of Dubowitz syndrome. *American Journal of Medical Genetics Part A* 185:119–133
4. Li, J., Z. Fan, F. Shen, A. L. Pendleton, Y. Song, **J. Xing**, B. Yue, J. M. Kidd#, and J. Li# (2020) Genome-wide CNV study of nine *Macaca* species provides new insights into their genetic divergence, adaptation and biomedical application. *Genome Biology and Evolution* 12:2211–2230 [cover article]
5. Tyc, K. M.*, W. El Yakoubi*, A. Bag, J. Landis, Y. Zhan, N. R. Treff, R. T. Scott, Jr., X. Tao, K. Schindler#, and **J. Xing#** (2020) Exome sequencing links *CEP120* mutation to maternally-derived aneuploid conception risk. *Human Reproduction* 35:2134–2148
6. Yan, C, X. Zhang, L. Zhou, Q. Yang, M. Zhou, L. Zhang, **J. Xing**, Z. Yan, M. Price, J. Li, B. Yue, and Z. Fan (2020) Effects of aging on gene expression in the blood of captive Tibetan Macaques (*Macaca thibetana*) and comparisons with expressions in humans. *Zoological Research* 41:557–563
7. Cao, X.*, Y. Zhang*, L. M. Payer, H. Lords, J. P. Steranka, K. H. Burns, **J. Xing#** (2020) Polymorphic mobile element insertions contribute to gene expression and alternative splicing in human tissues. *Genome Biology* 21:185 (*bioRxiv* <https://doi.org/10.1101/2020.05.23.111310>) (19 pages)
8. Qiu, S., H. Liu, Z. Jian, Z. Fan, S. Liu, **J. Xing**, and J. Li (2020) Characterization of the primate TRIM gene family reveals the recent evolution in primates. *Molecular Genetics and Genomics* 295:1281–1294
9. Abel, H. J., D. E. Larson, A. A. Regier, C. Chiang, I. Das, K. L. Kanchi, R. M. Layer, B. M. Neale, W. J. Salerno, C. Reeves, S. Buyske, NHGRI Centers for Common Disease Genomics (including Y. Zhang and **J. Xing**), T. C. Matise, D. M. Muzny, M. C. Zody, E. S. Lander, S. K. Dutcher, N. O. Stitzel, and I. M. Hall (2020) Mapping and characterization of structural variation in 17,795 human genomes. *Nature* 583:83–89

10. Du, L.*, T. Guo*, Q. Liu, J. Li, X. Zhang, **J. Xing**, B. Yue, J. Li#, and Z. Fan# (2020) MACSNVdb: a high-quality SNV database for interspecies genetic divergence investigation among macaques. *Database (Oxford)* 2020:baaa027 (8 pages)
11. Tyc, K. M., R. C. McCoy, K. Schindler, and **J. Xing**# (2020) Mathematical modeling of human oocyte aneuploidy. *Proceedings of the National Academy of Sciences, USA* 19:10455-10464
12. Loh, J.*, H. Ha*, T. Lin, N. Sun, K. H. Burns, and **J. Xing**# (2020) Integrated Mobile Element Scanning (ME-Scan) method for identifying multiple types of polymorphic mobile element insertions. *Mobile DNA* 11:12 (13 pages)
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14. Oppenheim, S.* , X. Cao*, O. Rueppel, S. Krongdang, P. Phokasem, R. DeSalle, S. Goodwin, **J. Xing**, P. Chantawannakul, and J. Rosenfeld (2020) Whole genome sequencing and assembly of the Asian honey bee *Apis dorsata*. *Genome Biology and Evolution* 12:3677–3683 (*bioRxiv* <https://doi.org/10.1101/840207>)
15. Zhou, A., T. Lin, and **J. Xing**# (2019) Evaluating nanopore sequencing data processing pipelines for structural variation identification. *Genome Biology* 20:237 (13 pages)
16. Feusier, J., W. S. Watkins, J. Thomas, A. Farrell, D. J. Witherspoon, L. Baird, H. Ha, **J. Xing**, and L. B. Jorde (2019) Pedigree-based estimation of mobile element retrotransposition rates in humans. *Genome Research* 29:1567–1577 (*bioRxiv* <https://doi.org/10.1101/506691>) [cover article]
17. Vazquez, B. N.* , J. K. Thackray*, N. G. Simonet, S. Chahar, N. Kane-Goldsmith, S. J. Newkirk, S. Lee, **J. Xing**, M. P. Verzi, W. An, A. Vaquero, J. A. Tischfield, and L. Serrano (2019) SIRT7 mediates L1 elements transcriptional repression and their association with the nuclear lamina. *Nucleic Acids Research* 47:7870-7885
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- harmonized variant calling across human genetics projects. *Nature Communication* 9:4038 (*bioRxiv* <https://doi.org/10.1101/269316>) (8 pages)
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 23. Fan Z., A. Zhou, N. Osada, J. Yu, J. Jiang, P. Li, L. Du, L. Niu, J. Deng, H. Xu, **J. Xing**, B. Yue, and J. Li (2018) Ancient hybridization and admixture in macaques (genus *Macaca*) inferred from whole genome sequences. *Molecular Phylogenetics and Evolution* 127:376-386
 24. Zhou, A., Y. Zhang, Y. Sun[#], and **J. Xing**[#] (2018) PipelineDog: a simple and flexible pipeline construction and maintenance tool. *Bioinformatics* 34:1603-1605
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 28. 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
 29. 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
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 33. 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
 34. 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
 35. 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
 36. 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)
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IV. RESEARCH SUPPORT

ACTIVE

CAUT19APL028

06/2019 - 05/2021

New Jersey Governor's Council for Medical Research and Treatment of Autism
Elucidating Genetics of Autism and Co-occurring Conditions using Whole Genome
Sequence

Role: Principal Investigator (MPI: Jinchuan Xing, Linda Brzustowicz)

R01MH092293 06/2018 - 03/2023
NIH/NIMH
1/7 Collaborative Genomic Studies of Tourette Disorder
Role: Co-Investigator (MPI: Gary Heiman, Jay Tischfield)

R01HD082242 12/2017 - 11/2022
NIH/NICHD
Association of the Maternal Exome with Risk of an Aneuploid Conception
Principal Investigator (MPI: Karen Schindler, Jinchuan Xing)

U24HG008956 01/2016 - 11/2021
NIH/NHGRI
NHGRI Genome Sequencing Program Coordinating Center
Co-Investigator (MPI: Tara Matisse, Steve Buyske)

COMPLETED

Agrmt 5.15.19 06/2019 - 05/2020
Shannon Genomics
Bioinformatics technical documents review and revision service
Role: Principal Investigator

U01HG007419 09/2013 - 05/2019
NIH/NHGRI
Population Architecture Using Genomics and Epidemiology (PAGE), Phase II -
Coordinating Center
Co-Investigator (MPI: Tara Matisse, Steve Buyske)

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)

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)

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

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

Invited Talks and Platform Presentations

Identifying genetic factors that contribute to female infertility in humans 4th Annual Mid-Atlantic Bioinformatics Conference, Philadelphia, PA, Oct 2019. *Lightning talk*

Can-SINE dynamics in the giant panda and three other Caniformia genomes FASEB Summer Research Conferences: The Mobile DNA Conference: 25 Years of Discussion and Research, Palm Springs, CA, Jun 2019. *Platform Presentation*

From primate to human: What we can learn from genomic data Department of Biology, Temple University, Philadelphia, PA, Nov 2018. *Invited talk*

From primate to human: What we can learn from genomic data Featured CHES Research Evening, Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, New Brunswick, NJ, Oct 2018. *Invited talk*

Population genetics and disease gene identification in the genomics era College of Life Sciences, Sichuan University, Chengdu, Sichuan, China, May 2018. *Invited talk*

Investigate lysosomal disease etiology by exome sequencing International Symposium on Molecular Evolution and Medicine, Philadelphia, PA, Sep 2017. *Platform Presentation*

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, New Brunswick, NJ, 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, New Brunswick, NJ, Sep 2016. *Invited talk*

- Novel Candidate Genes that Modify Chronic Obstructive Pulmonary Disease Susceptibility Human Genetics in New York City Second Symposium, New York, NY, 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, Chengdu, China, Apr 2015. *Invited talk*
- Pedigree-based disease-gene identification using high-throughput sequencing Columbia University Seminars in Genetic Epidemiology, Columbia University, New York, NY, Dec 2014. *Invited talk*
- VAAST projects at Rutgers VAAST developer annual meeting, University of Utah, Salt Lake City, UT, Jun 2014. *Invited talk*
- Understanding human genomic variation via high throughput sequencing School of Molecular Biosciences, Washington State University, Pullman, WA, 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, Lubbock, TX, 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, Piscataway, NJ, 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, New Brunswick, NJ, 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*

VI. TEACHING

Fall 2018-2019 Genomes (01:447:451), Rutgers, the State University of New Jersey

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* (2011-2014), *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 Genomics, Computational Biology and Technology (2020)

Member, NIH Genetic Variation and Evolution (2017)

Member, Busch Biomedical Research Award (2013, 2014, 2016)

Member, NIH NIEHS Special Emphasis Panel (2013)

Grant proposals:

Busch Biomedical Research Award

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

Writing in the Biological Sciences

Journal articles (36 journals, >100 articles):

American Journal of Human Genetics, Analytical Biochemistry, Annals of Human Genetics, Bioinformatics, Biotechniques, BMC Bioinformatics, BMC Genetics, Briefings in Bioinformatics, Communications Biology, Computational and Structural Biotechnology Journal, Gene, Genetica, Genetics in Medicine, Genome Biology, Genome Biology and Evolution, Genome Research, Genomics, European Journal of Human Genetics, Human Genetics and Genomics Advances, Human Immunology, Human Molecular Genetics, Human Mutation, International Journal of Molecular Sciences, JoVE, Mobile DNA, Molecular Biology and Evolution, Molecular Immunology, Nature Communications, Nucleic Acids Research, PLoS Computational Biology, PLoS Genetics, PLoS One, Prenatal Diagnosis, Recent Patents on Food, Nutrition & Agriculture, Systematic Biology, 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

Member, Sigma Xi 2007

Member, American Society for Microbiology 2006

VIII. HONORS & AWARDS

- | | |
|------|--|
| 2020 | Board of Trustees Award for Excellence in Research – Rutgers, The State University of New Jersey |
| 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 |