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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

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)

Google Scholar: https://scholar.google.com/citations?user=JE4GTLYAAAAJ&hl
H-index: 54; **total citations:** >38,000

1. Zhou, A., X. Cao, V. Mahaganapathy, M. Azaro, C. Gwin, S. Wilson, S. Buyske, C. W. Bartlett, J. F. Flax, L. M. Brzustowicz, and **J. Xing**# (Under Revision) Common Genetic Risk Factors in ASD and ADHD Co-occurring Families. (*medRxiv*: https://medrxiv.org/cgi/content/short/2022.05.15.22275109v1)
2. Shrestha D.*, A. Bag*, R. Wu, Y. Zhang, X. Tang, Q. Qi, **J. Xing**#, and Y. Cheng# (2022) Genomics and epigenetics guided identification of tissue-specific genomic safe harbors. *Genome Biology* 23:199 (17 pages)
3. Zhang, R.*, C. Zhou*, X. Jin, K. Liu, Z. Fan, **J. Xing**, and J. Li (2022) Chromosome-level genome assembly of Tibetan macaque (*Macaca thibetana*) and species-specific structural variations. *Zoological Research* 43(5): 880-885 (https://doi.org/10.22541/au.164874321.12040091/v1)
4. Paulat, N. S., E. McGuire, K. Subramanian, A. B. Osmanski, D. D. Moreno-Santillán, D. A. Ray#, and **J. Xing**# (2022) Transposable elements in bats show differential accumulation patterns determined by class and functionality. *Life* 12(8):1190
5. Wong A., A. Zhou, X. Cao, V. Mahaganapathy, M. Azaro, C. Gwin, S. Wilson, S. Buyske, C. W. Bartlett, J. F. Flax, L. M. Brzustowicz, and **J. Xing**# (2022) microRNA and microRNA target variants associated with autism spectrum disorder and related disorders. *Genes* 13(8):1329 (16 pages, PMCID: 9329941)
6. Sun, S., M. Miller, Y. Wang, K. M. Tyc, X. Cao, R. T. Scott, Jr., X. Tao, Y. Bromberg, K. Schindler, and **J. Xing**# (2022) Predicting embryonic aneuploidy rate in IVF patients using whole-exome sequencing. *Human Genetics*
7. Baxter, S. M., J. E. Posey, N. J. Lake, N. Sobreira, J. X. Chong, S. Buyske, E. E. Blue, L. H. Chadwick, Z. H. Coban-Akdemir, K. F. Doheny, C. P. Davis, M. Lek, C. Wellington, S. N. Jhangiani, M. Gerstein, R. A. Gibbs, R. P. Lifton, D. G. MacArthur, T. C. Matise, J. R. Lupski, D. Valle, M. J. Bamshad, A. Hamosh, S. Mane, D. A. Nickerson, Centers for Mendelian Genomics Consortium (including X. Cao, Y. Zhang, and **J. Xing**), H. L. Rehm, A. O'Donnell-Luria (2022) Centers for Mendelian Genomics: A decade of facilitating gene discovery. *Genetics in Medicine* 24(4):784-797 (*medRxiv* https://www.medrxiv.org/content/10.1101/2021.08.24.21261656v1) (PMCID: 9119004)
8. Tong, K., O. A. Kothari, K. S. Haro, A. Panda, M. M. Bandari, J. N. Carrick, J. J. Hur, L. Zhang, C. S. Chan, **J. Xing**, M. L. Gatza, S. Ganesan, and M. P. Verzi (2021) SMAD4 is critical in suppression of BRAF-V600E serrated tumorigenesis. *Oncogene* 40(41):6034-6048 (PMCID: 8559887)
9. Cao, X.*, Y. Zhang*, M. Abdulkadir, L. Deng, T. V. Fernandez, B. Garcia-Delgar, J. Hagstrøm, P. J. Hoekstra, R. A. King, J. Koesterich, S. Kuperman, A. Morer, C. Nasello, K. J. Plessen, J. K. Thackray, L. Zhou, Tourette International Collaborative Genetics Study (TIC Genetics), A. Dietrich, J. Tischfield, G. Heiman, and **J. Xing**# (2021) Whole exome sequencing identifies genes associated with Tourette's Disorder in multiplex families. *Molecular Psychiatry* 26(11):6937-6951 (PMCID: 8501157)
10. Cao, X. and **J. Xing**# (2021) PrecisionProDB: improving the proteomics performance for precision medicine. *Bioinformatics* 37(19):3361–3363

11. Wartosch, L., K. Schindler, M. Schuh, J. R. Gruhn, E. R. Hoffmann, R. C. McCoy, and **J. Xing** (2021) Origins and Mechanisms Leading to Aneuploidy in Human Eggs. *Prenatal Diagnosis* 41(5):620–630 (PMCID: 8237340)
12. Collantes J. C., V. M. Tan, H. Xu, M. Ruiz-Urigüen, A. Alasadi, J. Guo, H. Tao, C. Su, K. M. Tyc, T. Selmi, J. J. Lambourne, J. A. Harbottle, J. Stombaugh, **J. Xing**, C. M. Wiggins, and S. Jin (2021) Development and characterization of a modular CRISPR and RNA aptamer mediated base editing system. *The CRISPR Journal* 4(1):58–68 (PMCID: 7898459)
13. 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* 161(2):R13-R35 (PMCID: 7855740)
14. 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* 101(4):503-512 (PMCID: 7987713)
15. Dyment, 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(1):119–133 (PMCID: 8197629)
16. 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(12):2211-2230 [cover article] (PMCID: 846157)
17. 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(9):2134–2148 (PMCID: 7828473)
18. 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(5):557-563 (PMCID: 7475009)

19. 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(1):185 (*bioRxiv* https://doi.org/10.1101/2020.05.23.111310) (19 pages, PMCID: 7385971)
20. 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(5):1281–1294
21. 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. Stitziel, and I. M. Hall (2020) Mapping and characterization of structural variation in 17,795 human genomes. *Nature* 583(7814):83–89 (PMCID: 7547914)
22. 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, PMCID: 7198316)
23. 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* 117(19):10455-10464 (PMCID: 7229693)
24. 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, PMCID: 7035633)
25. Liu, S.*, M. Tian*, F. He*, J. Li*, H. Xie*, W. Liu, Y. Zhang, R. Zhang, M. Yi, F. Che, X. Ma, Y. Zheng, H. Deng, G. Wang, L. Chen, X. Sun, Y. Xu, J. Wang, Y. Zang, M. Han, X. Wang, H. Guan, Y. Ge, C. Wu, H. Wang, H. Liang, H. Li, N. Ran, Z. Yang, H. Huang, Y. Wei, X. Zheng, X. Sun, X. Feng, L. Zheng, T. Zhu, W. Luo, Q. Chen, Y. Yan, Z. Huang, Z. Jing, Y. Guo, X. Zhang, C. P. Schaaf, **J. Xing**, C. Wang#, F. Yu#, and J. Guan# (2020) Mutations in *ASH1L* confer susceptibility to Tourette Syndrome. *Molecular Psychiatry* 25(2):476–490
26. 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(1):3677–3683 (*bioRxiv* https://doi.org/10.1101/840207) (PMCID: 6953811)
27. Zhou, A., T. Lin, and **J. Xing**# (2019) Evaluating nanopore sequencing data processing pipelines for structural variation identification. *Genome Biology* 20(1):237 (13 pages, PMCID: 6857234)
28. 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(10):1567–1577 (*bioRxiv* https://doi.org/10.1101/506691) [cover article] (PMCID: 6771411)

29. 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(15):7870-7885 (PMCID: 6735864)
30. Kumar, N.*, Y. Tsai*, L. Chen*, A. Zhou, K. K. Banerjee, M. Saxena, S. Huang, N. H. Toke, **J. Xing**, R. A. Shivdasani, J. R. Spence, and M. P. Verzi (2019) The lineage-specific transcription factor CDX2 navigates dynamic chromatin to control distinct stages of intestine development. *Development* 146(5):dev172189 (*bioRxiv* https://doi.org/10.1101/425827) (13 pages, PMCID: 6432663)
31. Peng, C., L. Niu, J. Deng, J. Yu, X. Zhang, C. Zhou, **J. Xing**#, and J. Li# (2018) Can-SINE dynamics in the giant panda and three other Caniformia genomes. *Mobile DNA* 9:32 (14 pages, PMCID: 6230240)
32. Regier, A. A., Y. Farjoun, D. E. Larson, O. Krasheninina, H. M. Kang, D. P. Howrigan, B. Chen, M. Kher, E. Banks, D. C. Ames, A. C. English, H. Li, **J. Xing**, Y. Zhang, T. Matise, G. R. Abecasis, W. Salerno, M. C. Zody, B. M. Neale, and I. M. Hall (2018) Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. *Nature Communication* 9(1):4038 (*bioRxiv* https://doi.org/10.1101/269316) (8 pages, PMCID: 6168605)
33. Wang S., J. D. Mandell, Y. Kumar, N. Sun, M. T. Morris, J. Arbelaez, C. Nasello, S. Dong, C. Duhn, X. Zhao, Z. Yang, S. S. Padmanabhuni, D. Yu, R. A. King, A. Dietrich, N. Khalifa, N. Dahl, A. Y. Huang, B. M. Neale, G. Coppola, C. A. Mathews, J. M. Scharf, Tourette International Collaborative Genetics Study (TIC Genetics) (including H. Poisner and Y. Zhang), Tourette Syndrome Genetics Southern and Eastern Europe Initiative (TSGENESEE), Tourette Association of America International Consortium for Genetics (TAAICG), T. V. Fernandez, J. D. Buxbaum, S. De Rubeis, D. E. Grice, **J. Xing**, G. A. Heiman, J. A. Tischfield, P. Paschou, A. J. Willsey, M. W. State (2018) *de novo* sequence and copy number variants are strongly associated with Tourette Disorder and implicate cell polarity in pathogenesis. *Cell Reports* 24(13):3441–3454 (PMCID: 6475626)
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35. 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
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37. 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 (2018) The *PNKD* gene is

associated with Tourette Disorder and Tic disorder in a multiplex family. *Molecular Psychiatry* 23(6):1487-1495

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40. 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
41. 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(1):396 (12 pages, PMCID: 5440948)
42. 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(3):486–499.e9 [cover article] (PMCID: 5769876)
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45. 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(2):194-212 (PMCID: 5294208)
46. 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(20):3711-3722 (PMCID: 5087649)
47. 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(2):284–291 (PMCID: 5505770)

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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 (PMCID: 4473257)

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IV. RESEARCH SUPPORT

ACTIVE

2128307 10/2021 - 09/2023
NSF/IIS
Integration and analysis of high-dimensional datasets
Co-Investigator (PI: Lanjing Zhang, total cost: $199,999)

R01MH092293 06/2018 - 03/2023
NIH/NIMH
1/7 Collaborative Genomic Studies of Tourette Disorder
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)

COMPLETED

U24HG008956 01/2016 – 07/2022
NIH/NHGRI
NHGRI Genome Sequencing Program Coordinating Center
Co-Investigator (MPI: Tara Matise, Steve Buyske)

CAUT19APL028 06/2019 - 05/2022
New Jersey Governor's Council for Medical Research and Treatment of Autism
Elucidating Genetics of Autism and Co-occurring Conditions using Whole Genome Sequence

Principal Investigator (MPI: Jinchuan Xing, Linda Brzustowicz)

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 Matise, 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

Genetic factors contributing to meiosis errors and female infertility in human
Department of Hematology, St. Jude Children's Research Hospital, Memphis, TN, Mar 2023. *Invited talk*

Functional impact and implication of mobile DNA elements in the human genome Department of Biostatistics, Virginia Commonwealth University, Richmond, VA, Jan 2023. *Invited talk*

Understanding genetic factors contributing to meiosis errors and female infertility in human School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX, Nov 2022. *Invited talk*

Genetic factors contributing to meiosis errors and female infertility in human Department of Pharmaceutical Sciences, South Dakota State University, Brookings, SD, Oct 2022. *Invited talk*

Genetic factors contributing to meiosis errors and female infertility in human Department of Biological Sciences, Brock University, St. Catharines, Canada, Sep 2022. *Invited talk*

Predicting embryonic aneuploidy rate in IVF patients using whole-exome sequencing Science Society on Clubhouse, Virtual, Aug 2022. *Invited talk*

microRNA and microRNA target variants associated with autism spectrum disorder and related disorders International Conference on Intelligent Biology and Medicine (ICIBM 2022), Philadelphia, PA, Aug 2022. *Platform Presentation*

Functional impact and implication of mobile DNA elements in the human genome The Northwest Institute of Plateau Biology (NWIPB), Xining, China, Virtual, Aug 2022. *Invited talk*

The combination of multiple types of evidence to prioritize candidate genes for Tourette's Disorder International Mouse Phenotyping Consortium (IMPC) 10th Anniversary Conference, Virtual, Sep 2021. *Invited talk*

Machine learning to predict aneuploid conception risk Origins of Aneuploidy Research Consortium Annual Meeting, Virtual, Sep 2021. *Invited talk*

Current Computational challenges in genomics RCAF Forum: Challenges and Opportunities in Computational Biology, Rutgers, the State University of New Jersey, New Brunswick, NJ, Aug 2020. *Invited talk*

Understanding human genomic variation via high-throughput sequencing RCAF webinar series, Rutgers, the State University of New Jersey, New Brunswick, NJ, Jul 2020. *Invited talk*

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*

Media interviews

Machine learning and human health Podcast, Discovery Matters (https://anchor.fm/discovery-matters), Aug 2022.

VI. TEACHING

Rutgers, the State University of New Jersey

Fall 2018-2019, 2021-2022 Genomes (01:447:451)
Fall 2013-2015, 2017 Effective Communication Skills in Genetics (01:447:430)
Spring 2013 Honors Seminar (01:447:404)

VII. PROFESSIONAL SERVICE

Editorial Activities
Associate Editor:

Gene (2013–2016)

Editorial Board:
Mobile DNA (2014–present)
Analytical Biochemistry (2012–present)
Gene (2011–2014)

Guest Editor:
Genes, for the special issue "Selected Papers from the International Conference on Intelligent Biology and Medicine (ICIBM 2022)" (2022)
Cancers, for the special issue "Advance in Computational Methods in Cancer Research" (2022)
Comparative and Functional Genomics, for the special issue "Genomic Impact of Transposable Elements in Mammals" (2012)

Review Activities
Study sections:
Member, CIDR Access Committee (2021-present)
Member, NIH Fellowships: Genes, Genomes and Genetics (2021)
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:
Marsden Fund, Royal Society of New Zealand
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 (44 journals, >140 articles):
American Journal of Human Genetics; American Journal of Medical Genetics Part B: Neuropsychiatric Genetics; Analytical Biochemistry; Annals of Human Genetics; Bioinformatics; Biotechniques; BMC Bioinformatics; BMC Genetics; BMC Supplements; Briefings in Bioinformatics; Communications Biology; Computational and Structural Biotechnology Journal; European Journal of Human Genetics; Fertility and Sterility;

Frontiers in Genetics; Gene; Genetica; Genetics in Medicine; Genome Biology; Genome Biology and Evolution; Genome Research; Genomics; Genomics, Proteomics & Bioinformatics; 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; Nature Biotechnology; Nucleic Acids Research; PLoS Computational Biology; PLoS Genetics; PLoS One; Prenatal Diagnosis; Quantitative Biology; Recent Patents on Food, Nutrition & Agriculture; Science Advances; Systematic Biology; Zoological Science.

Professional Societies

Member, Origins of Aneuploidy Research Consortium 2021-present
Member, International Association for Intelligent Biology and Medicine 2021-present
Member, American Society of Human Genetics 2007–present
Member, International Genetic Epidemiology Society 2015
Member, American Heart Association 2014–2015
Member, Sigma Xi 2007
Member, American Society for Microbiology 2006

Public Service

Chair, Program Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2022)
Advisory Board, Montgomery Data Science Club (2021-present)
Chair, Award Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2020-2021)
Member, Program Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2021)
Session Chair, International Conference on Intelligent Biology and Medicine (ICIBM 2020)
Mentor, HEROES Academy for the Gifted Summer Program (Summer 2014)

VIII. HONORS & AWARDS

2021	Provost's Award for Excellence in Cross-Disciplinary Research – Rutgers, The State University of New Jersey
2020	Board of Trustees Award for Excellence in Research – Rutgers, The State University of New Jersey
2011	Nominee for the Searle Scholars Program
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