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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

07/23 – present	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
07/18 – 06/23	Associate Professor, Department of Genetics, 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, Department of Biological Sciences, Louisiana State University, Baton Rouge. Advisor: Dr. Mark Batzer.
07/01 – 12/02	Graduate Teaching Assistant, Department of Biological Sciences, 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: 58; **total citations:** >41,000

1. Sun S., T. Defosse, A. Boyd, J. Sop, F. Verderose, D. Surray, M. Aziz, M. Howland, S. Wu, N. Changela, J. Jang, K. Schindler, **J. Xing**# and K. S. McKim# (2024) Whole Transcriptome and Functional Analyses Identify Novel Genes Involved in Meiosis and Fertility in *Drosophila melanogaster*. *Scientific Reports* 14:3602 (*bioRxiv*: https://www.biorxiv.org/content/10.1101/2023.05.12.540472v1)
2. Cao, X., S. Sun, and **J. Xing**# (2024) A massive proteogenomics screen identifies thousands of novel human coding sequences. *Molecular & Cellular Proteomics* 23(2): 100719 (15 pages)
3. Wang, S., B. Wang, V. Drury, S. Drake, N. Sun, H. Alkhairo, J. Arbelaez, C. Duhn, Tourette International Collaborative Genetics (TIC Genetics, including X. Cao), V. H. Bal, K. Langley, J. Martin, **J. Xing**, G. A. Heiman, J. A. Tischfield, T. V. Fernandez, M. J. Owen, M. C. O'Donovan, A. Thapar, M. W. State, and A. J. Willsey (2023) Rare Maternally Inherited Coding Variants on Chromosome X Carry Predominantly Male Risk in Autism, Tourette Syndrome, and Attention-deficit/Hyperactivity Disorder. *Nature Communication* 14:8077 (PMCID: 10700338, *medRxiv*: https://doi.org/10.1101/2022.09.22.22280248)
4. Sun, S., M. Aboelenain, D. Ariad, M. E. Haywood, C. R. Wageman, M. Duke, A. Bag, M. Viotti, M. Katz-Jaffe, R. C. McCoy, K. Schindler, and **J. Xing**# (2023) Identifying risk genes for embryo aneuploidy using ultra-low coverage whole-genome sequencing. *American Journal of Human Genetics* 110(12):2092-2102 (PMCID: 10716496, *medRxiv*: https://www.medrxiv.org/content/10.1101/2023.07.22.23292618v1).
5. Rybacki, K., M. Xia, M. U. Ahsan, **J. Xing**#, K. Wang# (2023) Assessing the expression of Long INterspersed Elements (LINEs) via long-read sequencing in diverse human tissues and cell lines. *Genes* 14(10):1893 (18 pages, PMCID: 10606529)
6. Alibutud, R.*, S. Hansali*, X. Cao, A. Zhou, V. Mahaganapathy, M. Azaro, C. Gwin, S. Wilson, S. Buyske, C. W. Bartlett, J. F. Flax, L. M. Brzustowicz, and **J. Xing**# (2023) Structural variations contribute to the genetic etiology of autism spectrum disorder and language impairments. *International Journal of Molecular Sciences* 24(17):13248 (20 pages, PMCID: 10487745)
7. Zhang, C., L. Wang, L. Dou, B. Yue, **J. Xing**#, and J. Li# (2023) Transposable Elements Shape the Genome Diversity and the Evolution of Noctuidae Species. *Genes* 14(6):1244 (20 pages, PMCID: 10298559, *Preprints.org*: https://www.preprints.org/manuscript/202305.0213/v1)
8. 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**# (2023) Common Genetic Risk Factors in ASD and ADHD Co-occurring Families. *Human Genetics* 142:217–230 (PMCID: 10177627, *medRxiv*: https://medrxiv.org/cgi/content/short/2022.05.15.22275109v1)
9. Prem S., B. Dev, C. Peng, M. Mehta, R. Alibutud, R. J. Connacher, M. St Thomas, X. Zhou, P. Matteson, **J. Xing**, J. H. Millonig, E. DiCicco-Bloom (2022) Dysregulation of mTOR signaling mediates common neurite and migration defects in both idiopathic and 16p11.2 deletion autism neural precursor cells. (*bioRxiv*: https://doi.org/10.1101/2022.09.17.508382)

10. 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, PMCID: 9490961)
11. 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 (*Authorea*: https://doi.org/10.22541/au.164874321.12040091/v1)
12. 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
13. 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)
14. 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* 141:1615–1627
15. 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)
16. 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)
17. 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)
18. Cao, X. and **J. Xing**# (2021) PrecisionProDB: improving the proteomics performance for precision medicine. *Bioinformatics* 37(19):3361–3363
19. 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)
20. 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)

21. 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)
22. 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)
23. 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)
24. 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)
25. 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)
26. 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)
27. 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)

28. 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
29. 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)
30. 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)
31. 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)
32. 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)
33. 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
34. 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)
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37. 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)

38. 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)
39. 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)
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44. Zhou, A., Y. Zhang, Y. Sun#, and **J. Xing**# (2018) PipelineDog: a simple and flexible pipeline construction and maintenance tool. *Bioinformatics* 34(9):1603–1605
45. 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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Xing, and M. P. Verzi (2017) Degree of tissue differentiation dictates susceptibility to BRAF-driven colorectal cancer. *Cell Reports* 21(13):3833–3845 (PMCID: 5747303)

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variants in Tourette Syndrome etiology. *Frontiers in Neuroscience* 10:428 (7 pages, PMCID: 5030307)
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IV. RESEARCH SUPPORT

ACTIVE

U01DK062431 09/2022 - 06/2027
NIH/NIDDK
IBD Gene Mapping by Clinical and Population Subset
Co-Investigator (PI: Steven Brant)

2128307 10/2021 - 09/2024
NSF/IIS
Integration and analysis of high-dimensional datasets
Co-Investigator (PI: Lanjing Zhang)

R01MH092293 06/2018 - 03/2024
NIH/NIMH
1/7 Collaborative Genomic Studies of Tourette Disorder
Co-Investigator (MPI: Gary Heiman, Jay Tischfield)

R01HD091331 12/2017 - 06/2028
NIH/NICHD
Understanding genetic risk for 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)

K99/R00HG005846 09/2010 – 02/2016
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

Functional impact and implication of mobile DNA elements in the human genome The 2023 International Conference, Korean Society for Molecular and Cellular Biology (ICKSMCB 2023), Jeju, Korea, Nov 2023. *Invited talk*

Understanding genetic factors contributing to meiosis errors and female infertility in human International Conference of Genetics Society of Korea 2023 (ICGSK 2023), Busan, Korea, Oct 2023. *Invited talk*

Genetic factors contributing to meiosis errors and female infertility in human Genes, Genomes and Pediatric Disease (GGPD) Research Affinity Group Series, Children's Hospital of Philadelphia, Philadelphia, PA, Sep 2023. *Invited talk*

A massive proteogenomic screen identifies thousands of novel peptides from the human "dark" proteome 2nd Rutgers Chinese Faculty Research Symposium, Rutgers, the State University of New Jersey, New Brunswick, NJ, Jul 2023. *Invited Talk*

A massive proteogenomic screen identifies thousands of novel peptides from the human "dark" proteome International Conference on Intelligent Biology and Medicine (ICIBM 2023), Saint Petersburg, FL, Jul 2023. *Flash Talk*

Protegenomics approach for novel protein identification Department of Genetics Retreat, Rutgers, the State University of New Jersey, New Brunswick, NJ, May 2023. *Platform Presentation*

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*

Functional impact and implication of mobile DNA elements in the human genome Joint epigenetic group meeting, Rutgers, the State University of New Jersey, New Brunswick, NJ, Nov 2022. *Invited talk*

Identification of genetic loci associated with the risk of aneuploidy using PGT-A Origins of Aneuploidy Research Consortium Annual Meeting, Paris, France, 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/episodes/61--Genetic-and-genomic-databases-e1piunm), Oct 2022.

VI. TEACHING

Rutgers, the State University of New Jersey

Genomes (01:447:451)
- Fall 2018-2019, 2021-2022

Effective Communication Skills in Genetics (01:447:430)
- Fall 2013-2015, 2017, Spring 2023

Honors Seminar (01:447:404)
- Spring 2013

VII. PROFESSIONAL SERVICE

Editorial Activities

Associate Editor:

Gene (2013–2016)

Editorial Board:

Mobile DNA (2014–present)
Analytical Biochemistry (2012–present)
Gene (2011–2016)

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:
Arabian Gulf University Research Committee
Busch Biomedical Research Award
Natural Sciences and Engineering Research Council of Canada
National Science Foundation (NSF)
Marsden Fund, Royal Society of New Zealand
Netherlands Organisation for Health Research and Development (ZonMw)
Louisiana Board of Regents' Research Competitiveness Subprogram

Book Chapter:
Human Evolutionary Genetics
Scientific Writing and Communication
Writing in the Biological Sciences

Journal articles (51 journals, >160 articles):
Ageing Research Reviews; American Journal of Human Genetics; American Journal of Medical Genetics Part B: Neuropsychiatric Genetics; Analytical Biochemistry; Annals of Human Genetics; Bioinformatics; Biology; 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; Genes; Genetica; Genetics in Medicine; Genome Biology; Genome Biology and Evolution; Genome Research; Genomics; Genomics, Proteomics & Bioinformatics; Human Genetics and Genomics Advances; Human Genomics; Human Immunology; Human Molecular Genetics; Human Mutation; International Journal of Molecular Sciences; JoVE; Life; Mobile DNA; Molecular Biology and Evolution; Molecular Genetics & Genomic Medicine; Molecular Immunology; Nature Biotechnology; Nature Communications; Nature Genetics; 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, Society for the Study of Reproduction 2024-present
Member, American Society for Biochemistry and Molecular Biology 2024-present
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

Advisory Board, Montgomery Data Science Club (2021-2023)
Co-Chair, Program Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2022)
Member, Program Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2021, 2023)
Co-Chair, Award Committee, International Conference on Intelligent Biology and Medicine (ICIBM) (2020-2021)
Session Chair, International Conference on Intelligent Biology and Medicine (ICIBM) (2020, 2021, 2023)
Mentor, HEROES Academy for the Gifted Summer Program (Summer 2014)

VIII. HONORS & AWARDS

2023	Distinguished Service Award – International Association for Intelligent Biology and Medicine (IAIBM)
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