JINCHUAN XING, Ph.D.

Department of Genetics
Human Genetic Institute of New Jersey
Center for Human Evolutionary Studies
Rutgers, the State University of New Jersey
145 Bevier Road, Piscataway, NJ, 08854
Phone: 848-445-9663
Email: Xing@biology.rutgers.edu

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: 59; **total citations:** >46,000

1. Tanimura K., M. C. Aldrich, J. Jaworski, **J. Xing**, S. Okawa, D. Chandra, S. M. Nouraie, and T. Nyunoya (2025) Identifying a genetic link between lung function and psoriasis. *Annals of Human Genetics* (*Research Square*: https://doi.org/10.21203/rs.3.rs-4474529/v1)
2. Biswas L.*, K. M. Tyc*, M. Aboelenain, S. Sun, I. Dundović, K. Vukušić, J. Liu, V. Guo, M. Xu, R. T. Scott, Jr., X. Tao, I. M. Tolić, **J. Xing**#, and K. Schindler# (2024) Maternal genetic variants in kinesin motor domains prematurely increase egg aneuploidy Aneuploidy. *Proceedings of the National Academy of Sciences, USA* 121(45):e2414963121 (*medRxiv*: https://www.medrxiv.org/content/10.1101/2024.07.04.24309950v1) (12 pages)
3. Fan, Z., R. Zhang, A. Zhou, J. Hey, Y. Song, N. Osada, Y. Hamada, B. Yue, **J. Xing**, and J. Li (2024) Genomic evidence for the complex evolutionary history of macaques (genus *Macaca*). *Journal of Molecular Evolution* 92(3):286–299
4. 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, and E. DiCicco-Bloom (2024) Dysregulation of mTOR signaling mediates common neurite and migration defects in both idiopathic and 16p11.2 deletion autism neural precursor cells. *eLife* 13:e82809 (*bioRxiv*: https://doi.org/10.1101/2022.09.17.508382) (36 pages, PMCID: 11003747)
5. 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) (15 pages, PMCID: 10864285)
6. 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, PMCID: 10867589)
7. 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 (18 pages, PMCID: 10700338, *medRxiv*: https://doi.org/10.1101/2022.09.22.22280248)
8. 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).
9. 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)

10. 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)
11. 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)
12. 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)
13. 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)
14. 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)
15. 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
16. 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)
17. 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
18. 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)
19. 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)

20. 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)
21. Cao, X. and **J. Xing**# (2021) PrecisionProDB: improving the proteomics performance for precision medicine. *Bioinformatics* 37(19):3361–3363
22. 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)
23. 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)
24. 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)
25. 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)
26. 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)
27. 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)

28. 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)
29. 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)
30. 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)
31. 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
32. 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)
33. 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)
34. 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)
35. 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)
36. 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
37. 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)

38. 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)
39. 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)
40. 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)
41. 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)
42. 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)
43. 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)
44. 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)
45. Perekatt, A. O., P. P. Shah, S. Cheung, N. Jariwala, A. Wu, V. Gandhi, N. Kumar, Q. Feng, N. Patel, L. Chen, S. Joshi, A. Zhou, M. M. Taketo, **J. Xing**, E. White, N. Gao, M. L. Gatza, and M. P. Verzi (2018) SMAD4 suppresses WNT-driven de-

differentiation and oncogenesis in the differentiated gut epithelium. *Cancer Research* 78(17):4878-4890 (PMCID: 6125228)

46. 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
47. 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
48. 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
49. Tong K.*, O. Pellón-Cárdenas*, V. R. Sirihorachai, B. N. Warder, O. A. Kothari, A. O. Perekatt, E. E. Fokas, R. L. Fullem, A. Zhou, J. K. Thackray, H. Tran, L. Zhang, **J. 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)
50. 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* 38(11):1491-1499
51. 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
52. 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)
53. 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)
54. 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
55. 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

56. 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)
57. 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)
58. 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)
59. 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, PMCID: 5030307)
60. 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(3):145-150 (PMCID: 5109989)
61. Ha, H., J. Loh, and **J. Xing**# (2016) Identification of polymorphic full-length SVA retrotransposons using a mobile element scanning method for SVA (ME-Scan-SVA). *Mobile DNA* 7:15 (13 pages, PMCID: 4967303)
62. 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(2):163-173 (PMCID: 4728369)
63. 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)
64. 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(7571):68-74 (PMCID: 4750478)
65. 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(10):1691-1703 (PMCID: 4574747)

66. 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(6):1664-1675 (PMCID: 4494050)
67. Kwak Y., Y. Kim, **J. Xing**, and K. Han (2015) Evolutionary fate of SVA2 elements in primate genomes. *Genes & Genomics* 37:153–159
68. 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: 4224344)
69. Lorenzo F. R., C. Huff, M. Myllymäki, B. Olenchock, S. Swierczek, T. Tashi, V. Gordeuk, T. Wuren, R. L. Ge, D. A. McClain, T. M. Khan, P. A. Koul, P. Guchhait, M. E. Salama, **J. Xing**, G. L. Semenza, E. Liberzon, A. Wilson, T. S. Simonson, L. B. Jorde, W. G. Kaelin Jr., P. Koivunen, and J. T. Prchal (2014) A genetic mechanism for Tibetan high-altitude adaptation. *Nature Genetics* 46(9):951-956 (PMCID: 4473257)
70. The Marmoset Genome Sequencing and Analysis Consortium (2014) The common marmoset genome provides insight into primate biology and evolution. *Nature Genetics* 46(8):850-857 (PMCID: 4138798)
71. Ha H.*, J. Song*, S. Wang, A. Kapusta, C. Feschotte, K. C. Chen, and **J. Xing**# (2014) A comprehensive analysis of piRNAs from adult human testis and their relationship with genes and mobile elements. *BMC Genomics* 15(1):545 (16 pages, PMCID: 4094622)
72. Hu H., J. C. Roach, H. Coon, S. L. Guthery, K. V. Volkerding, R. L. Margraf, J. D. Durtschi, S. V. Tavtigian, Shankaracharya, W. Wu, P. Scheet, S. Wang, **J. Xing**, G. Glusman, R. Hubley, H. Li, V. Garg, B. Moore, L. Hood, D. J. Galas, D. Srivastava, M. G. Reese, L. B. Jorde, M. Yandell, C. D. Huff (2014) A unified test of linkage analysis and rare-variant association. *Nature Biotechnology* 32(7):663-669 (PMCID: 4157619)
73. Fan Z., G. Zhao, P. Li, N. Osada, **J. Xing**, Y. Yi, L. Du, P. Silva, H. Wang, R. Sakate, X. Zhang, H. Xu, B. Yue, J. Li (2014) Whole genome sequencing of Tibetan macaque (*Macaca thibetana*) provides new insight into the macaque evolutionary history. *Molecular Biology and Evolution* 31(6):1475–1489 (PMCID: 4032132)
74. Wuren T., T. S. Simonson, G. Qin, **J. Xing**, C. D. Huff, D. J. Witherspoon, L. B. Jorde, and R. L. Ge (2014) Shared and unique signals of high-altitude adaptation in geographically distinct Tibetan populations. *PLoS One* 9(3):e88252 (7 pages, PMCID: 3958363)
75. Wang S., and **J. Xing**# (2013) A primer for disease gene prioritization using next generation sequencing data. *Genomics & Informatics* 11(4):191-199 (PMCID: 3897846)
76. Wang S., J. Lachance, S. Tishkoff, J. Hey, and **J. Xing**# (2013) Apparent variation in Neanderthal admixture among African populations is consistent with gene flow from non-African populations. *Genome Biology and Evolution* 5(11):2075-2081 (PMCID: 3845641)
77. **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)
78. 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)
79. Witherspoon D. J., Y. Zhang, **J. Xing**, W. S. Watkins, H. Ha, M. A. Batzer, and L. B. Jorde (2013) Mobile Element Scanning (ME-Scan) identifies thousands of novel Alu insertions in diverse human populations. *Genome Research* 23(7):1170-1181 (PMCID: 3698510)
80. Ge R. L., Q. Cai, Y. Y. Shen, A. San, L. Ma, Y. Zhang, X. Yi, Y. Chen, L. Yang, Y. Huang, R. He, Y. Hui, M. Hao, Y. Li, B. Wang, X. Ou, J. Xu, Y. Zhang, K. Wu, C. Geng, W. Zhou, T. Zhou, D. M. Irwin, Y. Yang, L. Ying, H. Bao, J. Kim, D. M. Larkin, J. Ma, H. A. Lewin, **J. Xing**, R. N. Platt II, D. A. Ray, L. Auvil, B. Capitanu, X. Zhang, G. Zhang, R. W. Murphy, J. Wang, Y. P. Zhang, and J. Wang (2013) Draft genome sequence of the Tibetan antelope. *Nature Communications* 4:1858 (7 pages, PMCID: 3674232)
81. **Xing J.**, D. J. Witherspoon, and L. B. Jorde (2013) Mobile element biology – new possibilities with high-throughput sequencing. *Trends in Genetics* 29(5):280–289 (PMCID: 3938198)
82. Kim W., D. Londono, L. Zhou, **J. Xing**, A. Nato, A. Musolf, T. C. Matise, S. J. Finch, and D. Gordon (2012) Single variant and multi-variant trend tests for genetic association with next generation sequencing that are robust to sequencing error. *Human Heredity* 74(3-4):172-183 (PMCID: 3863939)
83. The 1000 Genomes Project Consortium (2012) An integrated map of genetic variation from 1,092 human genomes. *Nature* 491(7422):56–65 (PMCID: 3498066)
84. Watkins W. S., **J. Xing,** C. Huff, D. J. Witherspoon, Y. Zhang, U. A. Perego, S. R. Woodward, and L. B. Jorde (2012) Genetic analysis of ancestry, admixture and selection in Bolivian and Totonac populations of the New World. *BMC Genetics* 13(1):39 (14 pages, PMCID: 3432609)
85. 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)
86. Stringham S. A., E. E., Mulroy, **J. Xing**, D. Record, M. W. Guernsey, J. T. Aldenhoven, E. J. Osborne, and M. D. Shapiro (2012) Divergence, convergence, and the origins of feral populations in Darwin's pigeons. *Current Biology* 22(4):302-308 (PMCID: 3288640)
87. Huff C. D., D. J. Witherspoon, Y. Zhang, C. Gatenbee, S. Kugathasan, H. Hakonarson, A. Whiting, C. Davis, W. Wu, **J. Xing**, W. S. Watkins, M. Bamshad, K. Bulayeva, T. S. Simonson, L. B. Jorde, and S. L. Guthery (2012) Crohn's disease and genetic hitchhiking at IBD5. *Molecular Biology and Evolution* 29(1):101–111 (PMCID: 3245542)

88. 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)
89. Lyon G. J., T. Jiang, R. Van Wijk, W. Wang, P. M. Bodily, **J. Xing**, L. Tian, R. J. Robison, M. Clement, Y. Lin, P. Zhang, Y. Liu, B. Moore, J. T. Glessner, J. Elia, F. Reimherr, W. W. van Solinge, M. Yandell, H. Hakonarson, J. Wang, W. E. Johnson, Z. Wei, and K. Wang (2011) Exome sequencing and unrelated findings in the context of complex disease research: ethical and clinical implications. *Discovery Medicine* 12(62):41-55 (PMCID: 3544941)
90. Yandell M., C. D. Huff, H. Hu, M. Singleton, B. Moore, **J. Xing**, L. B. Jorde, and M. G. Reese (2011) A probabilistic disease-gene finder for personal genomes. *Genome Research* 21(9):1529-1542 (PMCID: 3166837)
91. Rope A. F., K. Wang, R. Evjenth, **J. Xing**, J. J. Johnston, J. J. Swensen, W. E. Johnson, B. Moore, C. D. Huff, L. M. Bird, J. C. Carey, J. M. Opitz, C. A. Stevens, T. Jiang, C. Schank, H. D. Fain, R. Robison, B. Dalley, S. Chin, S. T. South, T. J. Pysher, L. B. 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)
92. Roos C., D. Zinner, L. S. Kubatko, C. Schwarz, M. Yang, D. Meyer, S. D. Nash, **J. Xing**, M. A. Batzer, M. Brameier, F. H. Leendertz, T. Ziegler, D. Perwitasari-Farajallah, T. Nadler, L. Walter and M. Osterholz (2011) Nuclear versus mitochondrial DNA: Evidence for hybridization in colobine monkeys. *BMC Evolutionary Biology* 11:77 (13 pages, PMCID: 3068967)
93. Huff C. D.*, Witherspoon, D. J.*, Simonson, T. S., **J. Xing**, W. S. Watkins, Y. Zhang, T. M. Tuohy, D. W. Neklason, R. W. Burt, S. L. Guthery, S. R. Woodward, and L. B. Jorde (2011) Maximum-likelihood estimation of recent shared ancestry (ERSA) using shared genome segments. *Genome Research* 21(5):768-774 (PMCID: 3083094)
94. Simonson T. S., **J. Xing**, R. Barrett, E. Jerah, P. Loa, Y. Zhang, W. S. Watkins, D. J. Witherspoon, C. D. Huff, S. Woodward, B. Mowry, and L. B. Jorde (2011) Ancestry of the Iban is predominantly Southeast Asian: genetic evidence from autosomal, mitochondrial, and Y Chromosomes. *PLoS One* 6(1):e16338 (8 pages, PMCID: 3031551)
95. **Xing J.**, W. S. Watkins, Y. Hu, C. D. Huff, A. Sabo, D. M. Muzny, M. J. Bamshad, R. A. Gibbs, L. B. Jorde, and F. Yu (2010) Inference of human expansion in Eurasia and genetic diversity in India. *Genome Biology* 11:R113 (13 pages, PMCID: 3156952)
96. The 1000 Genomes Project Consortium (2010) A map of human genome variation from population scale sequencing. *Nature* 467(7319):1061-1073 (PMCID: 3042601)
97. **Xing J.**, W. S. Watkins, A. Shlien, E. Walker, C. D. Huff, D. J. Witherspoon, Y. Zhang, T. S. Simonson, R. B. Weiss, J. D. Schiffman, D. Malkin, S. R. Woodward and L. B. Jorde (2010) Toward a more uniform sampling of human genetic diversity: a survey

of worldwide populations by high-density genotyping. *Genomics* 96(4):199–210 (PMCID: 2945611)

98. Witherspoon D. J., **J. Xing**, Y. Zhang, W. S. Watkins, M. A. Batzer and L. B. Jorde (2010) Mobile element scanning (ME-Scan) by targeted high-throughput sequencing. *BMC Genomics* 11(1):410 (15 pages, PMCID: 2996938)
99. Simonson T. S., Y. Yang, C. D. Huff, H. Yun, G. Qin, D. J. Witherspoon, Z. Bai, F. R. Lorenzo, **J. Xing**, L. B. Jorde, J. T. Prchal, and R. Ge (2010) Genetic evidence for high-altitude adaptation in Tibet. *Science* 329(5987):72-75
100. Simonson T. S., Y. Zhang, C. D. Huff, **J. Xing**, W. S. Watkins, D. J. Witherspoon, S. R. Woodward and L. B. Jorde (2010) Limited distribution of a cardiomyopathy-associated variant in India. *Annals of Human Genetics* 74(2):184-188 (PMCID: 2901538)
101. Huff C. D., **J. Xing**, A. R. Rogers, D. J. Witherspoon, and L. B. Jorde (2010) Mobile elements reveal small population size in the ancient ancestors of *Homo sapiens*. *Proceedings of the National Academy of Sciences, USA* 107:2147-2152 (PMCID: 2836654)
102. Witherspoon D. J., W. S. Watkins, Y. Zhang, **J. Xing**, W. L. Tolpinrud, D. J. Hedges, M. A. Batzer and L. B. Jorde (2009) *Alu* repeats increase local recombination rates. *BMC Genomics* 10:530 (11 pages, PMCID: 2785838)
103. Damert A., J. Raiz, A. V. Horn, J. Löwer, H. Wang, **J. Xing**, M. A. Batzer, R. Löwer and G. G. Schumann (2009) 5'-transducing SVA retrotransposon groups spread efficiently throughout the human genome. *Genome Research* 19(11):1992-2008 (PMCID: 2775593)
104. Li J., K. Han, **J. Xing**, H.-S. Kim, J. Rogers, O. A. Ryder, T. Disotell, B. Yue and M. A. Batzer (2009) Phylogeny of the macaques (Cercopithecidae: Macaca) based on Alu elements. *Gene* 448(2):242-249 (PMCID: 2783879)
105. **Xing J.**, Y. Zhang, K. Han, A. H. Salem, S. K. Sen, C. D. Huff, Q. Zhou, E. F. Kirkness, S. Levy, M.A. Batzer, and L. B. Jorde (2009) Mobile elements create structural variation: analysis of a complete human genome**.** *Genome Research* 19(9):1516-1526 (PMCID: 2752133)
106. Marchani E. E., **J. Xing**, D. J. Witherspoon, L. B. Jorde, and A. R. Rogers (2009) Estimating the age of retrotransposon subfamilies using maximum likelihood. *Genomics* 94(1):78-82 (PMCID: 2703446)
107. **Xing J.**, W. S. Watkins, D. J. Witherspoon, Y. Zhang, S. L. Guthery, R. Thara, B. J. Mowry, K. Bulayeva, R. B. Weiss, and L. B. Jorde (2009) Fine-scaled human genetic structure revealed by SNP microarrays. *Genome Research* 19(5):815-825 (PMCID: 2675970)
108. **Xing J.**, W. S. Watkins, Y. Zhang, D. J. Witherspoon, and L. B. Jorde (2008) High fidelity of whole-genome amplified DNA on high-density single nucleotide polymorphism arrays. *Genomics* 92(6):452-456 (PMCID: 2659594)
109. **Xing J.**, D. J. Witherspoon, W. S. Watkins, Y. Zhang, W. Tolpinrud and L. B. Jorde. (2008) HapMap tagSNP transferability in multiple populations: general guidelines. *Genomics* 92(1):41-51 (PMCID: 2471876)

110. **Xing J.**, D. J. Witherspoon, D. A. Ray, M. A. Batzer and L. B. Jorde (2007) Mobile elements and primate evolution. *American journal of physical anthropology* Suppl 45:2-19
111. Han K.*, M. K. Konkel*, **J. Xing***, H. Wang*, J. Lee, T. J. Meyer, C. T. Huang, E. Sandifer, K. Hebert, E. W. Barnes, R. Hubley, W. Miller, A. F. A. Smit, B. Ullmer and M. A. Batzer (2007) Mobile DNA in Old World monkeys: a glimpse through the rhesus macaque genome. *Science* 316(5822):238-240
112. Rhesus Macaque Genome Sequencing and Analysis Consortium (2007) Evolutionary and biomedical insights from the rhesus macaque genome. *Science* 316(5822):222-234 [cover article]
113. **Xing J.**, H. Wang, Y. Zhang, D. A. Ray, A. J. Tosi, T. R. Disotell and M. A. Batzer (2007) A mobile element based evolutionary history of guenons (Tribe Cercopithecini). *BMC Biology* 5:5 (10 pages, PMCID: 1797000)
114. Herke S. W., **J. Xing**, D. A. Ray, J. W. Zimmerman, R. Cordaux and M. A. Batzer (2007) A SINE-based dichotomous key for primate identification. *Gene* 390(1-2):39-51
115. Ray D. A., **J. Xing**, A.-H. Salem and M. A. Batzer (2006) SINEs of a nearly perfect character. *Systematic Biology* 55(6):928-935
116. **Xing J.***, H. Wang*, V. P. Belancio, R. Cordaux, P. L. Deininger and M. A. Batzer (2006) Emergence of new primate genes by retrotransposon-mediated sequence transduction. *Proceedings of the National Academy of Sciences, USA* 103(47):17608-17613 [cover article] (PMCID: 1693794)
117. Wang H.*, **J. Xing***, D. Grover*, D. J. Hedges, K. Han, J. A. Walker and M. A. Batzer (2005) SVA elements: a hominid specific retroposon family. *Journal of Molecular Biology* 354(4):994-1007 [cover article]
118. **Xing J.**, H. Wang, K. Han, D. A. Ray, C. H. Huang, L. G. Chemnick, C.-B. Stewart, T. Disotell, O. A. Ryder and M. A. Batzer (2005) A mobile element based phylogeny of Old World monkeys. *Molecular Phylogenetics and Evolution* 37(3):872-880
119. Hedges D. J., R. Cordaux, **J. Xing**, D. J. Witherspoon, A. R. Rogers, L. B. Jorde and M. A. Batzer (2005) Modeling the amplification dynamics of human *Alu* retrotransposons. *PLOS Computational Biology* 1(4):e44 (8 pages, PMCID: 1239904)
120. Han K.*, **J. Xing***, H. Wang, D. J. Hedges, R. K. Garber, R. Cordaux and M. A. Batzer (2005) Under the genomic radar: the stealth model of *Alu* amplification. *Genome Research* 15(5):655-664 [cover article] (PMCID: 1088293)
121. Ray D. A., **J. Xing**, D. J. Hedges, M. Hall, M. E. Laborde, B. A. Anders, B. R. White, J. D. Fowlkes, L. Chemnick, O. A. Ryder, and M. A. Batzer (2005) *Alu* insertion loci and platyrrhine primate phylogeny. *Molecular Phylogenetics and Evolution* 35(1):117-126
122. **Xing J.**, D. J. Hedges, K.D. Han, H. Wang, R. Cordaux and M.A. Batzer (2004) *Alu* elements mutation spectra: Molecular clocks and the effect of DNA methylation. *Journal of Molecular Biology* 344(3):657-682
123. Hedges D. J., P. A. Callinan, R. Cordaux, **J. Xing**, E. Barnes and M. A. Batzer (2004) Differential *Alu* mobilization and polymorphism among the human and chimpanzee lineages. *Genome Research* 14(6):1068-1075 (8 pages, PMCID: 419785)

124. Walker J. A., R. K. Garber, D. J. Hedges, G. E. Kilroy, **J. Xing**, and M. A. Batzer (2004) Resolution of mixed human DNA samples using mtDNA sequence variants. *Analytical Biochemistry* 325(1):171-173
125. Salem A.-H., D. A. Ray, **J. Xing**, P. A. Callinan, J. S. Myers, D. J. Hedges, R. K. Garber, D. J. Witherspoon, L. B. Jorde and M. A. Batzer(2003) *Alu* elements and Hominid phylogenetics. *Proceedings of the National Academy of Sciences, USA*. 100(22):12787-12791 (PMCID: 240696)
126. **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 Suppl 1:S76-S89
127. 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(1-2):103-110
128. 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(1):122-128
129. 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(50):47530-47541

IV. RESEARCH SUPPORT

ACTIVE

R01GM157610 09/2024 - 08/2027
NIH/NIGMS
DMS/NIGMS 1: Disease gene discovery by Markovian gene network
Principal Investigator (Co-PI: Min Xu, Jinchuan Xing, Minge Xu, Sijian Wang)

Life Sciences Alliance Pilot Seed Funding 06/2024 - 06/2026
Rutgers–New Brunswick Office for the Vice Provost for Research
Disease Gene Discovery on Gene Interaction Networks with Hidden Nodes
Principal Investigator (Co-PI: Min Xu, Jinchuan Xing)

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

R01MH092293 06/2018 - 03/2025
NIH/NIMH

1/7 Collaborative Genomic Studies of Tourette Disorder
Co-Investigator (MPI: Gary Heiman, Jay Tischfield)

R01HD091331 12/2017 - 04/2028
NIH/NICHD
Understanding genetic risk for aneuploid conception
Principal Investigator (MPI: Karen Schindler, Jinchuan Xing)

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

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

Understanding genetic factors contributing to meiosis errors and female infertility in human College of Life Sciences, Sichuan University, Chengdu, China, Aug 2024. *Invited talk*

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

Human Genetics (16:681:535)

- Fall 2024

Genomes (01:447:451)

- Fall 2018-2019, 2021-2022, Spring 2025

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

Executive Editor:

Analytical Biochemistry (2024–present)

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
Israel Science Foundation (ISF)
Louisiana Board of Regents' Research Competitiveness Subprogram
Marsden Fund, Royal Society of New Zealand

Netherlands Organisation for Health Research and Development (ZonMw)
National Science Foundation (NSF)
Natural Sciences and Engineering Research Council of Canada (NSERC)

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

Journal articles (52 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; Journal of Bone and Mineral Research; 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, Origins of Aneuploidy Research Consortium 2021-present
Member, American Association for the Advancement of Science (2010–2012, 2024-present)
Member, American Society of Human Genetics 2007–present
Member, American Society for Biochemistry and Molecular Biology 2024
Member, International Association for Intelligent Biology and Medicine 2021-2023
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