

Rajiv C. McCoy

Associate Professor, Department of Biology, Johns Hopkins University

Mudd Hall 144 · 3400 N. Charles St.
Baltimore, MD 21218 USA
410-516-0942 · rajiv.mccoy@jhu.edu
mccoy-lab.org

Appointments

- 2025–Present **Associate Professor**, Department of Biology, Johns Hopkins University
- 2018–2025 **Assistant Professor**, Department of Biology, Johns Hopkins University
- 2015–2018 **Postdoctoral Fellow**, Ecology & Evolutionary Biology, Princeton University (2017–2018); Genome Sciences, University of Washington (2015–2017) — advisor Joshua Akey

Education

- 2015 **PhD in Biology**, Stanford University — advisors Dmitri Petrov & Carol Boggs
- 2010 **BS in Biology; Ecosystem Science and Policy**, University of Miami *summa cum laude*

Affiliations

- Secondary Department of Genetic Medicine (2026–); Department of Earth and Planetary Sciences (2024–), Johns Hopkins University
- Graduate Faculty Preceptor, Human Genetics and Genomics (2022–); Training Faculty, Cell, Molecular, Developmental Biology & Biophysics (CMDDB) (2018–)
- Centers & Institutes Member — Data Science and AI Institute (2025–); Institute for Data Intensive Engineering and Science (2024–); Epigenome Sciences Cluster (2023–); Center for Computational Biology (2022–)

Honors & Awards

Since starting faculty position

- 2026 Next Generation Pregnancy Initiative Award, Burroughs Wellcome Fund
- 2025, 2022 Discovery Award, Johns Hopkins University
- 2024 Catalyst Award, Johns Hopkins University
- 2024 Graduate Education Award, CMDDB Graduate Program
- 2021–2023 Technology Fellowship, Center for Educational Resources, Johns Hopkins University

Prior to faculty position

- 2015–2017 Genome Training Grant (NIH/NHGRI T32), University of Washington, Dept. of Genome Sciences
- 2015 Trainee Research Excellence Award — Finalist, American Society of Human Genetics
- 2013, 2012 Excellence in Teaching Award, Stanford University, Department of Biology
- 2012 Rosemary Grant Award, Society for the Study of Evolution
- 2010–2013 Stanford University Graduate Fellowship in Science & Engineering

- 2010 Phi Beta Kappa Society, University of Miami
2010 Abess Center for Ecosystem Science and Policy Award, University of Miami

Research Support

Active

- 2019-2029 **NIH/NIGMS R35GM133747 · Maximizing Investigators' Research Award** PI
"Functional and fitness consequences of human genetic variation"
Total award \$4,186,700 (\$427,965/yr)
- 2026-2030 **Burroughs Wellcome Fund · Next Generation Pregnancy Initiative** PI
"Uncovering genetic mechanisms of pregnancy loss and fetal genomes"
Total award \$499,996
- 2025-2027 **Johns Hopkins University Discovery Award** PI
"Combining statistical and experimental genetics to understand the basis of variation in human fertility"
Co-PIs Yumi Kim, Philip Jordan · Total \$150,000; to lab \$50,000
- 2024-2026 **Johns Hopkins University Catalyst Award** PI
"Genomic sources of variability in human embryonic aneuploidy"
Total award \$75,000
- 2025-2028 **NSF DBI 2504115 · Infrastructure Innovation for Biological Research** CO-I
"Characterizing transposable element contributions to the transcriptome with evidence-based and inferential methods"
PI Liliana Florea · Total \$875,379; to lab \$147,841
- 2025-2029 **NIH/NCI R01CA292812 · Research Project Grant** CO-I
"Cancer genetics of long telomere syndromes"
PI Mary Armanios · Total \$3,872,849; to lab \$55,475
- 2023-2028 **NIH/NICHD R01HD091331 · Research Project Grant** CO-I
"Understanding genetic risk for aneuploid conception"
PI Karen Schindler · Total \$2,474,125; to lab \$55,928

Pending

- 2027-2030 **W. M. Keck Foundation** PI
"Beyond Mendel's Laws: Resolving Genome-Wide Biases in Human Inheritance"
Total award \$1,200,000
- 2026-2028 **NIH R03HG015492 · Small Research Grant** PI
"Extending multi-ancestry genomic datasets with long-read transcriptomics to advance human genome variation research and education on AnVIL"
Total award \$385,745

Completed

- 2023-2025 **NIH OT2OD034190 · Cloud Platform Interoperability Program** CO-I
"AnVIL/Velsera-CGC interoperability project to study the genetic and transcriptomic contributions towards Hispanic colorectal cancer health disparities"
PI Michael Schatz · Dispersed to lab \$54,603

2022-2024 **Johns Hopkins University Discovery Award** PI

“A high-resolution view of human gene expression and splicing diversity with single-molecule long-read sequencing”

Co-PIs Alexis Battle, Winston Timp · Total \$100,000; to lab \$35,069

Publications

[GOOGLE SCHOLAR](#) [ORCID](#)

corresponding author co-author * co-first author † co-corresponding author § lab member / rotation student

Since starting faculty position

Research articles (peer reviewed · 10 corresponding, 21 co-author)

- 2026 Das, A., [§]Biddanda, A., **McCoy, R. C.**, Schatz, M. C. Assembling unmapped reads reveals hidden variation in South Asian genomes. *Nature Communications*, 17: 5095.
- 2026 *[§]Carioscia, S. A., *[§]Biddanda, A., [§]Starostik, M. R., Tang, X., Hoffmann, E. R., Demko, Z. P., **McCoy, R. C.** Common variation in meiosis genes shapes human recombination and aneuploidy risk. *Nature*, 651: 146–153.
| See editorial: [§]Carioscia, S. A., [§]Biddanda, A. Common genetic variants affect risk of a major cause of pregnancy loss. *Nature*.
- 2025 [§]Yang, Q., [§]Carioscia, S. A., [§]Isada, M., **McCoy, R. C.** Approximate Bayesian computation supports a high incidence of chromosomal mosaicism in blastocyst-stage human embryos. *Genetics*, 231(2): iyaf149.
- 2025 McDaniel, J. H., Patel, V., Olson, N. D., ... **McCoy, R. C.**, ... Liss, A. S., Zook, J. M. Development and extensive sequencing of a broadly-consented Genome in a Bottle matched tumor-normal pair for somatic benchmarks. *Scientific Data*, 12: 1195.
- 2025 Wang, D., Cearlock, A., Lane, K., Jan, I., **McCoy, R. C.**, Yang, M. Chromosomal instability in human trophoblast stem cells and placentas. *Nature Communications*, 16: 3918.
- 2025 Yoo, D., Rhie, A., Hebbar, P., ... **McCoy, R. C.**, ... Phillippy, A. M., Eichler, E. E. Complete sequencing of ape genomes. *Nature*, 641: 401–418.
- 2025 Liang, S., Ren, T., Zhang, J., ... **McCoy, R. C.**, ... Mao, Y., Chen, L. A refined analysis of Neanderthal-introgressed sequences in modern humans with a complete reference genome. *Genome Biology*, 26: 32.
- 2024 [§]Taylor, D. J., Chhetri, S. B., [§]Tassia, M. G., [§]Biddanda, A., [§]Yan, S. M., Wojcik, G. L., Battle, A., **McCoy, R. C.** Sources of gene expression variation in a globally diverse human cohort. *Nature*, 632: 122–130.
| See editorial: [§]Taylor, D. J., [§]Yan, S. M. A broader view of the diversity of human gene expression. *Nature*.
- 2024 Xiang, G., He, X., Giardine, B. M., ... [§]Taylor, D. J., **McCoy, R. C.**, ... Li, Q., Mahony, S., Hardison, R. C. Interspecies regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. *Genome Research*, 34: 1089–1105.
- 2024 Makova, K. D., Pickett, B. D., Harris, R. S., ... [§]Biddanda, A., ... **McCoy, R. C.**, ... Eichler, E. E., Phillippy, A. M. The complete sequence and comparative analysis of ape sex chromosomes. *Nature*, 630: 401–411.
- 2024 Hadyniak, S. E., Eldred, K. C., Brennerman, B., Hussey, K. A., **McCoy, R. C.**, Sauria, M. E. G., Kuchenbeker, J. A., Neitz, M., Neitz, J., Taylor, J., Johnston, R. J. Retinoic acid signaling regulates spatiotemporal specification of human green and red cones. *PLoS Biology*, 22(1): e3002464.
- 2024 [§]Ariad, D., Madjunkova, S., Madjunkov, M., Chen, S., Abramov, R., Librach, C., **McCoy, R. C.** Aberrant landscapes of maternal meiotic crossovers contribute to aneuploidies in human embryos. *Genome Research*, 34: 70–84.

- 2023 ○ Sun, S., Aboelenain, M., §Ariad, D., Haywood, M. E., Wageman, C. R., Duke, M., Bag, A., Viotti, M., Katz-Jaffe, M., **McCoy, R. C.**, Schindler, K., Xing, J. Identifying risk variants for embryo aneuploidy using ultra-low coverage whole-genome sequencing from preimplantation genetic testing. *American Journal of Human Genetics*, 110(12): 2092-2102.
- 2023 ● **McCoy, R. C.**, Summers, M. C., McCollin, A., Ottolini, C. S., Ahuja, K., Handyside, A. H. Meiotic and mitotic aneuploidies drive arrest of in vitro fertilized human preimplantation embryos. *Genome Medicine*, 15: 77.
- 2023 ○ *Rhie, A., *Nurk, S., *Cechova, M., *Hoyt, S., *§Taylor, Da., ... **McCoy, R. C.** (44/81), ... Miga, K. H., Makova, K. D., Phillippy, A. M. The complete sequence of a human Y chromosome. *Nature*, 621(7978): 344-354.
- 2023 ○ Yang, X., Wang, X., Zou, Y., ... §Taylor, D. J., **McCoy, R. C.**, Schatz, M. C., ... Lu, Q., Mao, Y. Characterization of large-scale genomic differences in the first complete human genome. *Genome Biology*, 24(1): 157.
- 2023 ○ Giraldo, D., Rankin-Turner, S., Corver, A., ... **McCoy, R. C.**, ... Simulundu, E., McMeniman, C. J. Human scent guides mosquito thermotaxis and host selection under naturalistic conditions. *Current Biology*, 33(12): 2367-2382.e7.
- 2023 ○ *DeBoy, E. A., *§Tassia, M. G., Schratz, K. E., §Yan, S. M., ... **McCoy, R. C.**, Armanios, M. Familial clonal hematopoiesis in a long telomere syndrome. *New England Journal of Medicine*, 388(26): 2422-2433.
 | See editorial: Vassiliou, G. Telomere length and clonal hematopoiesis. *New England Journal of Medicine*, 388(26): 2481-2484.
- 2022 ● *§Carioscia, S. A., *§Weaver, K. J., §Bortvin, A. N., §Pan, H., §Ariad, D., Bell, A. D., **McCoy, R. C.** A method for low-coverage single-gamete sequence analysis demonstrates adherence to Mendel's first law across a large sample of human sperm. *eLife*, 11: e76383.
- 2022 ○ Griffin, D. K., Brezina, P. R., Tobler, K., Silvestri, G., **McCoy, R. C.**, Anchan, R., Benner, A., Cutting, G. R., Kearns, W. G. The human embryonic genome is karyotypically complex, with chromosomally abnormal cells preferentially located away from the developing fetus. *Human Reproduction*, 38(1): 180-188.
- 2022 ● *Aganezov, S., *§Yan, S. M., *Soto, D. C., *Kirsche, M., *Zarate, S., ... §Taylor, D. J., ... †**McCoy, R. C.**, †Dennis, M. Y., †Zook, J. M., †Schatz, M. C. A complete reference genome improves analysis of human genetic variation. *Science*, 376(6588): eabl3533.
- 2022 ○ Nurk, S., Koren, S., Rhie, A., ... §Yan, S. M., ... **McCoy, R. C.** (89/99), ... Eichler, E. E., Miga, K. H., Phillippy, A. M. The complete sequence of a human genome. *Science*, 376(6588): eabj6987.
- 2021 ● §Ariad, D., §Yan, S. M., Victor, A. R., Barnes, F. L., Zouves, C. G., Viotti, M., **McCoy, R. C.** Haplotype-aware inference of human chromosome abnormalities. *Proceedings of the National Academy of Sciences USA*, 118(46): e2109307118.
- 2021 ● §Yan, S. M., Sherman, R. M., §Taylor, D. J., §Nair, D. R., §Bortvin, A. N., Schatz, M. C., **McCoy, R. C.** Local adaptation and archaic introgression shape global diversity at human structural variant loci. *eLife*, 10: e67615.
- 2021 ○ Ranallo-Benavidez, T. R., Lemmon, Z. H., Soyk, S., Aganezov, S., Salerno, W. J., **McCoy, R. C.**, Lippman, Z. B., Schatz, M. C., Sedlazeck, F. J. SVCollector: Optimized sample selection for cost-efficient long-read population sequencing. *Genome Research*, 31(5): 910-918.
- 2020 ● §Starostik, M. R., Sosina, O. A., **McCoy, R. C.** Single-cell analysis of human embryos reveals diverse patterns of aneuploidy and mosaicism. *Genome Research*, 30(6): 814-825.
- 2020 ○ Tyc, K. M., **McCoy, R. C.**, Schindler, K., Xing, J. Mathematical modeling of human oocyte aneuploidy. *Proceedings of the National Academy of Sciences USA*, 117(19): 10455-10464.
- 2020 ○ Sharma, R., Singh, P., **McCoy, R. C.**, ... Truman, R. W., Adams, L. B. Isolation of *Mycobacterium lepromatosis* and development of molecular diagnostic assays to distinguish *M. leprae* and *M. lepromatosis*. *Clinical Infectious Diseases*, 71(8): e262-e269.
- 2019 ○ Gruhn, J. R., Zielinska, A., Shukla, V., ... **McCoy, R. C.** (23/28), ... Hoffmann, E. R. Chromosome errors in human eggs shape natural fertility over reproductive lifespan. *Science*, 365(6460): 1466-1469.

- 2019 ○ Victor, A. R., Tyndall, J. C., Brake, A. J., Lepkowski, L. T., Murphy, A., Griffin, D. K., **McCoy, R. C.**, Barnes, F. L., Zouves, C. G., Viotti, M. One hundred mosaic embryos transferred prospectively in a single clinic: exploring when and why they result in normal pregnancies. *Fertility & Sterility*, 111(2): 280-293.
- 2019 ○ Victor, A. R., Griffin, D. K., Brake, A. J., Tyndall, J. C., Murphy, A., Lepkowski, L. T., Lal, A., Zouves, C. G., Barnes, F. L., **McCoy, R. C.**, Viotti, M. Assessment of aneuploidy concordance between clinical trophectoderm biopsy and blastocyst. *Human Reproduction*, 34(1): 181-192.

Review articles (peer reviewed · 3 corresponding, 5 co-author)

- 2025 ● *Moya, N., *§Yan, S. M., †**McCoy, R. C.**, †Andersen, E. C. The long and short of hyperdivergent regions. *Trends in Genetics*, 41(4): 303-314.
- 2024 ● §Taylor, D. J., Eizenga, J. M., Li, Q., Das, A., Jenike, K. M., Kenny, E. E., Miga, K. H., †Monlong, J., †**McCoy, R. C.**, †Paten, B., †Schatz, M. C. Beyond the Human Genome Project: the age of complete human genome sequences and pangenome references. *Annual Review of Genomics and Human Genetics*, 25: 77-104.
- 2023 ○ Muter, J., Lynch, V. J., **McCoy, R. C.**, Brosens, J. J. Human embryo implantation. *Development*, 150(10): dev201507.
- 2022 ○ Brosens, J. J., Bennett, P. R., Abrahams, V., Ramhorst, R., Coomarasamy, A., Quenby, S., Lucas, E. S., **McCoy, R. C.** Maternal selection of human embryos in early gestation: insights from recurrent miscarriage. *Seminars in Cell and Developmental Biology*, 131: 14-24.
- 2021 ○ Quenby, S., Gallos, I. D., Dhillon-Smith, R. K., ... **McCoy, R. C.**, ... Petrou, S., Coomarasamy, A. Miscarriage matters: the epidemiological, physical, psychological, and economic costs of early pregnancy loss. *The Lancet*, 397(10285): 1658-1667.
- 2021 ○ Levy, B., Hoffmann, E. R., **McCoy, R. C.**, Grati, F. R. Chromosomal mosaicism: origins and clinical implications in preimplantation and prenatal diagnosis. *Prenatal Diagnosis*, 41(5): 631-641.
- 2021 ○ Wartosch, L., Schindler, K., Schuh, M., Gruhn, J. R., Hoffmann, E. R., **McCoy, R. C.**, Xing, J. Origins and mechanisms leading to aneuploidy in human eggs. *Prenatal Diagnosis*, 41(5): 620-630.
- 2020 ● §Yan, S. M., **McCoy, R. C.** Archaic hominin genomics provides a window into gene expression evolution. *Current Opinion in Genetics & Development*, 62: 44-49.

Editorials & commentaries (2 corresponding, 2 co-author)

- 2024 ● §Carioscia, S., **McCoy, R. C.** A rare genetic variant biases maternal meiotic recombination toward risk of pregnancy loss. *Nature Structural & Molecular Biology*, 31: 584-585.
- 2021 ○ Viotti, M., **McCoy, R. C.**, Griffin, D. K., Spinella, F., Greco, E., Madjunkov, M., Madjunkova, S., Librach, C. L., Victor, A. R., Barnes, F. L., Zouves, C. G. Let the data do the talking: the need to consider mosaicism during embryo selection. *Fertility & Sterility*, 116(5): 1212-1219.
- 2019 ● §Yan, S. M., **McCoy, R. C.** Functional divergence among hominins. *Nature Ecology & Evolution*, 3(11): 1507-1508.
- 2019 ○ **McCoy, R. C.**, Kort, J. D. Quantifying the transcriptional impacts of aneuploidy in human blastocysts. *Fertility & Sterility*, 111(5): 888-889.

Under review & preprints (3 corresponding, 3 co-author)

- ● §Biddanda, A., §Carioscia, S. A., Hoffmann, E. R., **McCoy, R. C.**† The spectrum of de novo lethal mutations in human prenatal development. *Nature Reviews Genetics*: under review.
- ● *Aqil, A., *§Huang, B. Y. H., Pavlidis, P., **McCoy, R. C.**†, Gokcumen, O.† Mismapping of sequencing reads from polymorphic duplications generates spurious trans-eQTLs. *American Journal of Human Genetics*: under review.

- ● Lalli, J. L., §Bortvin, A. N., †McCoy, R. C., †Werling, D. M. A T2T-CHM13 recombination map and globally diverse haplotype reference panel improves phasing and imputation. *Nature Genetics*: under review. [bioRxiv](#): 2025.02.24.639687.
- ○ Riahi, P., Raghupathy, S., Le, B., Taylor-Brill, S., §Taylor, D., McCoy, R. C., Ramdas, S., Zaidi, A. A. Beyond copy number: the regulatory architecture of mitochondrial DNA gene expression. *Cell Genomics*: under review.
- ○ Cechova, M., Potapova, T. A., Rechtsteiner, A., ... §Yan, S. M., ... McCoy, R. C., ... Greider, C. W., Miga, K. H. Complete genomes of a multi-generational pedigree to expand studies of genetic and epigenetic inheritance. *Cell*: under review. [bioRxiv](#): 2025.12.14.693655.
- ○ DeGorter, M. K., Goddard, P. C., Karakoc, E., ... §Yan, S. M., ... McCoy, R. C., ... Gurdasani, D., Montgomery, S. B. Transcriptomics and chromatin accessibility in multiple African population samples. [bioRxiv](#): 2023.11.04.564839.

Prior to faculty position

- 2018 Tucci, S., Vohr, S. H., McCoy, R. C., Vernot, B., ... Visscher, P. M., Akey, J. M., Green, R. E. Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. *Science*, 361(6401): 511-516.
- 2018 Press, M. O., McCoy, R. C., Hall, A. N., Akey, J. M., Queitsch, C. Short tandem repeats with massive variation and functional consequences across strains of *Arabidopsis thaliana*. *Genome Research*, 28(8): 1169-1178.
- 2018 *McCoy, R. C., *Newnham, L. J., Ottolini, C. S., ... Sigurjonsson, S., Handyside, A. H. Tripolar chromosome segregation drives the association between maternal genotype at variants spanning *PLK4* and aneuploidy in human preimplantation embryos. *Human Molecular Genetics*, 27(14): 2573-2585.
- 2018 Kort, J. D., McCoy, R. C., Demko, Z. P., Lathi, R. B. Are blastocyst aneuploidy rates different between fertile and infertile populations? *Journal of Assisted Reproduction and Genetics*, 35(3): 403-408.
- 2017 McCoy, R. C. Mosaicism in preimplantation human embryos: when chromosomal abnormalities are the norm. *Trends in Genetics*, 33(7): 448-463.
- 2017 McCoy, R. C., Akey, J. M. Selection plays the hand it was dealt: evidence that human adaptation commonly targets standing genetic variation. *Genome Biology*, 18(1): 139.
- 2017 Adashi, E. Y., McCoy, R. C. Technology versus biology: the limits of pre-implantation genetic screening. *EMBO Reports*, 18(5): 670-672.
- 2017 McCoy, R. C., Wakefield, J., Akey, J. M. Impacts of Neanderthal-introgressed sequences on the landscape of human gene expression. *Cell*, 168(5): 916-927.e12.
- 2016 Vernot, B., Tucci, S., Kelso, J., ... McCoy, R. C., ... Pääbo, S., Akey, J. M. Excavating Neanderthal and Denisovan DNA from the genomes of Melanesian individuals. *Science*, 352(6282): 235-239.
- 2016 McCoy, R. C., Akey, J. M. Patterns of deleterious variation between human populations reveal an unbalanced load. *Proceedings of the National Academy of Sciences USA*, 113(4): 809-811.
- 2016 Demko, Z. P., Simon, A. L., McCoy, R. C., Petrov, D. A., Rabinowitz, M. Effects of maternal age on euploidy in a large cohort of embryos analyzed with 24-chromosome SNP-based preimplantation genetic screening. *Fertility & Sterility*, 105(5): 1307-1313.
- 2015 McCoy, R. C., Demko, Z., Ryan, A., ... Rabinowitz, M., Petrov, D. A. Evidence of selection against complex mitotic-origin aneuploidy during preimplantation development. *PLoS Genetics*, 11(10): e1005601.
- 2015 McCoy, R. C., Demko, Z., Ryan, A., ... Fraser, H. B., Petrov, D. A. Common variants spanning *PLK4* are associated with mitotic-origin aneuploidy in human embryos. *Science*, 348(6231): 235-238.
- See editorial: Vohr, S. H., Green, R. E. Aneuploidy and mother's genes. *Science*, 348(6231): 180-181.
- 2014 Ahola, V., Lehtonen, R., Somervuo, P., ... McCoy, R. C. (18/45), ... Hanski, I. The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. *Nature Communications*, 5: 4737.

- 2014 **McCoy, R. C.**, Taylor, R., Blauwkamp, T. A., Kelley, J. L., Kertesz, M., Pushkarev, D., Petrov, D. A., Fiston-Lavier, A. S. Illumina TruSeq synthetic long reads empower *de novo* assembly and resolve complex, highly repetitive transposable elements. *PLoS ONE*, 9(9): e106689.
- 2014 **McCoy, R. C.**, Garud, N. R., Kelley, J. L., Boggs, C. L., Petrov, D. A. Genomic inference accurately predicts the timing and severity of a recent bottleneck in a non-model insect population. *Molecular Ecology*, 23(1): 136–150.

Patents

- 2025 Ariad, D., **McCoy, R. C.**, Viotti, M. Methods and related aspects for analyzing chromosome number status. US Patent #12,322,509.

Oral Presentations

plenary / keynote * postponed or cancelled (COVID-19 / personal)

Invited (58 · since faculty position)

- Spring 2027* Molecular & Cell Biology, University of California, Berkeley, CA
- Spring 2027* Biological Sciences, University of Buffalo, Buffalo, NY
- Fall 2026* Biological Sciences, George Washington University, Washington, DC
- 2026 Genetics, University of Alabama at Birmingham, Birmingham, AL
- 2026 Interurban Clinical Club, Baltimore, MD
- 2026 Center for Human Reproduction / Foundation for Reproductive Medicine Grand Rounds, New York, NY
- 2026 Center for Computational Molecular Biology, Brown University, Providence, RI
- 2026 Human Genetics, University of Utah, Salt Lake City, UT
- 2025 Key Aspects of Reproductive Medicine, Interdisciplinary Clinical Assoc. for Reproductive Medicine, Moscow, Russia
- 2025 Human Genetics, University of Michigan, Ann Arbor, MI
- 2025 Artificial Intelligence and the Study of Life Symposium, Johns Hopkins University, Baltimore, MD
- 2025 #Annual International Conference on Preimplantation Genetics (PGDIS), Leuven, Belgium
- 2025 Biological Anthropology Colloquium, Anthropology, Yale University, New Haven, CT
- 2024 Center for Theoretical & Evolutionary Genetics, University of California, Berkeley, CA
- 2024 Lieber Institute for Brain Development, Maltz Research Laboratories, Baltimore, MD
- 2024 Consequences of Aneuploidy Meeting, FASEB, Melbourne, FL
- 2024 Center for Genetic Epidemiology, University of Southern California, CA
- 2024 Genome Sciences, University of Washington, Seattle, WA
- 2024 Biology of Genomes, Cold Spring Harbor Laboratory, NY
- 2024 Genetics, University of Pennsylvania, Philadelphia, PA
- 2024 Molecular Biology & Genetics, Johns Hopkins University, Baltimore, MD
- 2024 Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX
- 2023 World Congress on Controversies in Preconception, Preimplantation and Prenatal Genetic Diagnosis, Online
- 2023 International IVF Initiative (i3) Webinar, Online
- 2023 *Origins of Human Aneuploidy Meeting, Florence, Italy
- 2023 #National Association of Biology Teachers Conference, Baltimore, MD
- 2023 JHU CMDDB Graduate Program Retreat, Hershey, PA
- 2023 Statistical Genetics Working Group, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD
- 2023 Genetics, Cell Biology & Development, University of Minnesota, Minneapolis, MN
- 2023 Cellular & Molecular Medicine, University of Copenhagen & ReproUnion, Copenhagen, Denmark

2023 Globe Institute, University of Copenhagen, Denmark

2023 Max Planck Institute for Evolutionary Biology, Plön, Germany

2023 Annual International Conference on Preimplantation Genetics (PGDIS), Paris, France

2023 Department Colloquium, Biology, Johns Hopkins University, Baltimore, MD

2022 Origins of Human Aneuploidy Meeting, Paris, France

2022 Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD

2022 Joint Didactic Session, Reproductive Endocrinology & Infertility / Medical Genetics Fellowship, JHSOM, Baltimore, MD

2022 Maimon M. Cohen Genetics Colloquium, Greater Baltimore Medical Center, Towson, MD

2021 Cell Bio Virtual, American Society of Cell Biology / EMBO, Online

2021 Howard & Georgeanna Jones Endowed Symposium on ART, Annual Meeting of the ASRM, Baltimore, MD

2021 Origins of Human Aneuploidy Meeting, Online

2021 Biomedical Sciences, Warwick Medical School, Coventry, UK

2021 Center for Reproductive Medicine, Weill Cornell Medicine, New York, NY

2020 Zouves Foundation for Reproductive Medicine, Foster City, CA

2020 World Congress on Controversies in Obstetrics, Gynecology & Infertility, Online

2020 *Molecular & Cellular Biology, Harvard University, Cambridge, MA

2020 Origins of Human Aneuploidy Meeting, Online

2020 Embryology, Carnegie Institution, Baltimore, MD

2020 Computational Biology, Carnegie Mellon University, Pittsburgh, PA

2020 CReATe Fertility Centre, Toronto, Canada

2019 Annual Conference of the Foundation for Reproductive Medicine, New York, NY

2019 Origins of Human Aneuploidy Meeting, Paris, France

2019 Genetics, Rutgers University, Piscataway, NJ

2019 Biology, Catholic University, Washington, DC

2018 Annual Conference of the Foundation for Reproductive Medicine, New York, NY

2018 Genomics & Bioinformatics Symposium, Johns Hopkins University, Baltimore, MD

2018 JHU CMDB Graduate Program Retreat, Rocky Gap State Park, MD

2018 Origins of Human Aneuploidy Meeting, Toronto, Canada

Contributed (5)

2024 #Annual Meeting of the American Society of Human Genetics, Denver, CO

2022 Annual Meeting of the American Society of Human Genetics, Los Angeles, CA

2022 #Annual Meeting of the American Society for Reproductive Medicine, Anaheim, CA

2021 Chromatin, Chromosomes & Epigenomes Workshop, Johns Hopkins University, Baltimore, MD

2019 Annual Meeting of the American Society of Human Genetics, Houston, TX

Prior to faculty position

2017 Marabou Symposium on Nutrition and Human Development, Stockholm, Sweden

2017 Origins of Human Aneuploidy Meeting, Barcelona, Spain

2017 Annual International Conference on Preimplantation Genetics (PGDIS), Valencia, Spain

2017 Genome Sciences / Computational Molecular Biology Combi Seminar, University of Washington, Seattle, WA

2016 Genotype-Tissue Expression (GTEx) Project Community Meeting, Stanford, CA

2015 Annual Meeting of the American Society of Human Genetics, Baltimore, MD

2014 Illumina Long-Reads Applications Symposium, University of California, Davis, CA

2014 Presentation to Management Team at Natera, Inc., San Carlos, CA

2014 Bay Area Population Genomics Meeting, University of California, Davis, CA

Senior author on 27 trainee oral presentations at national and international meetings (2019–2026), including Biology of Genomes (CSHL), ASHG, SMBE, and RECOMB-Genetics.

Poster Presentations

As presenting author (5)

- 2025 Annual Meeting of the American Society of Human Genetics (Reviewers' Choice Abstract Award), Boston, MA
- 2023 Annual Meeting of the American Society of Human Genetics, Washington, DC
- 2020 *Society for Molecular Biology & Evolution, Québec City, Canada
- 2020 *The Allied Genetics Conference, Genetics Society of America
- 2019 Society for Molecular Biology & Evolution, Manchester, England

Senior author on 40 trainee poster presentations at national and international meetings (2018–2026), including Biology of Genomes (CSHL), ASHG, SMBE, RECOMB, and The Allied Genetics Conference.

Prior to faculty position

- 2017 Annual Meeting of the American Society of Human Genetics (Reviewers' Choice Abstract Award), Orlando, FL
- 2017 NHGRI Annual Training and Career Development Meeting, St. Louis, MO
- 2016 Annual Meeting of the American Society of Human Genetics, Vancouver, Canada
- 2016 NHGRI Annual Training and Career Development Meeting, Bethesda, MD
- 2014 Bay Area Population Genomics Meeting, University of California, Davis, CA
- 2014 Stanford Biosciences Student Association Poster Session, Stanford, CA
- 2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [1/2]
- 2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [2/2]
- 2014 Center for Computational, Evolutionary, and Human Genomics Symposium, Palo Alto, CA
- 2013 Bay Area Population Genomics Meeting, Stanford, CA
- 2013 Annual Meeting of the Society for Integrative & Comparative Biology, San Francisco, CA
- 2012 Arthropod Genomics Symposium, Kansas City, MO
- 2012 Joint Congress on Evolutionary Biology, Ottawa, Canada

Research Mentoring

Postdoctoral (3 current, 1 graduated)

- 2024–Present **Margaret Starostik**, Postdoctoral Fellow
- 2023–Present **Arjun Biddanda**, Postdoctoral Fellow
Lalor Foundation Fellowship (2024–2026), \$110,000
- 2022–Present **Michael Tassia**, Postdoctoral Fellow
NIH Training Program in Hematology (T32); American Society of Hematology Fellowship (2024–2026), \$100,000
- 2020–2022 **Daniel Ariad**, Postdoctoral Fellow — now Senior Data Scientist, PrognomiQ, Inc.

Graduate thesis (3 current, 7 graduated)

- 2026–Present **Graydon Moorhead**, PhD in CMDB
- 2025–Present **Joshua Bauman**, PhD in CMDB

2024-Present	Betty Huang , PhD in CMDB
2025-2026	Sukriti Gupta , MS in Data Science
2021-2026	Andrew Bortvin , PhD in CMDB JHU Dissertation Prize Fellowship (2025-2026); JHU Dean's Teaching Fellowship (2024-2025), \$21,212
2020-2025	Sara Carioscia , PhD in CMDB — now Data Scientist, Valo Health Oppenheimer Thesis Award & Weintraub Award Nominee (2025); NSF Graduate Research Fellowship (2021-2026), \$138,000; JHU Teaching Excellence Technology Fellowship (2021-2022), \$5,500 (\$2,000 to student)
2020-2024	Dylan Taylor , PhD in CMDB — now Bioinformatics Scientist, Zephyr AI Oppenheimer Thesis Award (2025) & Weintraub Award Nominee (2024); NIH/NHGRI F31 Predoctoral Fellowship (2023-2024), \$95,388; JHU Teaching Excellence Technology Fellowship (2021-2022), \$5,500 (\$2,000 to student)
2019-2024	Stephanie Yan , PhD in CMDB — now Scientist, Genomics Plc Oppenheimer Thesis Award (2024); NIH/NHGRI F31 Predoctoral Fellowship (2022-2024), \$94,446; JHU Teaching Excellence Technology Fellowship (2021-2023), \$5,500 (\$2,000 to student)
2020-2023	Kathryn Isaac (Weaver) , PhD in CMDB — now Postdoc, Fred Hutchinson Cancer Center Oppenheimer Thesis Award (2023); JHU Dean's Teaching Fellowship (2022-2023), \$19,664; JHU Teaching Excellence Technology Fellowship (2021-2023), \$5,500 (\$2,000 to student)
2018-2020	Arta Seyedian , MS in Bioinformatics — now Bioinformatician, Children's Hospital of Philadelphia

Graduate qualifying project (2)

2024-2025	Arun Das , PhD in Computer Science
2021	Taher Mun , PhD in Computer Science — now Senior Bioinformatics Scientist, Illumina, Inc.

Undergraduate & high school (13 undergraduate, 3 high school)

Undergraduate	Lana Cheng (2026-), Angela Yang (2023-, Provost's Undergraduate Research Award), Sukriti Gupta (2024-25), Ameena Beg (2024), Hao Pan (2022-24), Anika Misra (2022-23), Emma Smith (REU, 2023), Divya Nair (2020-23), Katherine Gilbert (REU, 2022), Joel Espinoza (2018-20), Peter Huang (2019-20), Nicholas Parente (2019-20), Vincent Huang (2018)
High school	Cosima Billotte Bermudez (2022-23), Miles Fancher (2020-21), Aram Zaproshyan (2020-21) — Ingenuity Project, Baltimore Polytechnic Institute
Rotation	37 graduate rotation students in CMDB and Human Genetics, Johns Hopkins University (2018-present)
2014-2015	Jack McGregor, Undergraduate Senior Honors Thesis (co-advised), Stanford University

Teaching

Instructor of record (~40 hours/year, Johns Hopkins University)

2020-Present	Quantitative Biology Lab (AS.020.617, graduate; co-instructors F. Tan, M. Sauria)
2020-Present	Quantitative Biology Bootcamp (AS.020.607, graduate; co-instructors F. Tan, M. Sauria)
2020-Present	Human Genome Variation Computational Lab (AS.020.321, undergraduate)
2020-Present	Human Genome Variation (AS.020.319, undergraduate; co-instructor K. Cunningham)

Guest lectures (~7 hours/year)

2025-2026	Advanced Topics in Human Genetics (ME.710.700, graduate)
2021-2025	Genetics (AS.020.303, undergraduate, 300-400 students)
2021-2025	Biology of Disease (AS.020.314, undergraduate)

- 2019, 2022 Human Genome Variation (AS.020.319, undergraduate)
- 2018-2019 Quantitative Biology Bootcamp (AS.020.607, graduate)

Workshops

- 2019 Participant, Best Practices in University Teaching Workshop, Johns Hopkins University

Prior to faculty position

- 2017-2018 Science Teaching Experience for Postdocs (STEP) Program, University of Washington
- 2017 Participant, Undergraduate Faculty Genetics Education Workshop, American Society of Human Genetics
- 2014 Teaching Assistant Mentor, Department of Biology, Stanford University
- 2013, 2011 Teaching Assistant, Ecology, Evolution & Plant Biology, Stanford University
- 2013, 2012 Biocore Explorations Course Instructor, Department of Biology, Stanford University
- 2012 Teaching Assistant, Conservation Biology, Stanford University
- 2010 Undergraduate Workshop Leader, Evolution & Biodiversity, University of Miami
- 2009-2010 Peer Tutor, Camner Academic Resource Center, University of Miami

Service

Trainee examination & thesis committees

- Thesis **20 doctoral thesis committees** (2020–present) — CMDB (17), plus Earth & Planetary Sciences, Pathobiology, and Biomedical Engineering, Johns Hopkins University
- GBO **22 graduate board oral examination committees** (2021-2026) — Computer Science (8), CMDB (7), Human Genetics & Genomics (3), Biomedical Engineering (3), Cross-Disciplinary Biology (1), Johns Hopkins University
- Qualifying **1 department qualifying examination committee** (2026) — Earth & Planetary Sciences, Johns Hopkins University

University & departmental

- 2026–Present Member, Program Executive Committee, Human Genetics & Genomics Graduate Program, Johns Hopkins School of Medicine
- 2026–Present Chair, Committee for Department Chair Selection, Department of Biology
- 2025–Present Undergraduate Mentoring Committee, Department of Biology
- 2023–Present Organizer, Ruh Chih Huang Colloquium Series, Department of Biology
- 2022–Present CMDB Admissions Committee
- 2022–Present Graduate Curriculum Committee, Department of Biology
- 2020–Present Undergraduate Curriculum Committee, Department of Biology
- 2019–Present CMDB Awards Committee
- 2023–2024 Search Committee for Open Rank and Open Research Topic Position, Department of Biology
- 2021–2023 Diversity Advocate & Member, Search Committee for Computational Genomics, Department of Biology
- 2022 Faculty Focus Group Panelist, External Review of Research Compliance Program, Johns Hopkins University

Professional organizations & conferences

- 2024-Present Awards Committee, American Society of Human Genetics
- 2021-Present Co-Chair (2021–2024) & Organizing Committee, Origins of Human Aneuploidy Research Consortium & Meeting
- 2024 Session Co-Chair, Complex Traits & Genomic Medicine, Biology of Genomes (CSHL)
- 2019 Pre-Conference Workshop Chair, Annual Conference of the Foundation for Reproductive Medicine, New York, NY
- 2019 Session Moderator, Reproductive Fitness — The Genetics of Infertility, Annual Meeting of the American Society of Human Genetics, Houston, TX

Peer & grant review

- 2024-Present Editorial Board Member, *Journal of Assisted Reproduction & Genetics*
- 2013-Present Ad hoc journal reviewer: *American Journal of Human Genetics, American Journal of Obstetrics & Gynecology, BioData Mining, Bioinformatics, BMC Biology, Cell Genomics, Cell Proliferation, Current Urology, Development, eLife, G3, Genes, Genetics, Genome Biology, Genome Biology and Evolution, Genome Research, Human Reproduction, Journal of Assisted Reproduction & Genetics, Journal of Biogeography, Journal of Heredity, Journal of Ovarian Research, Molecular Biology and Evolution, Molecular Ecology, Nature, Nature Communications, Nature Ecology & Evolution, Nature Medicine, Nature Structural & Molecular Biology, PLoS Biology, PLoS Genetics, PLoS One, Prenatal Diagnosis, Proceedings of the National Academy of Sciences U.S.A., Proceedings of the Royal Society B, Reproduction, Science, Science Advances*

Grant & fellowship review

- 2026 Ad Hoc Panelist & Co-Chair, Maximizing Investigators' Research Award Special Emphasis Panel, Center for Scientific Review, National Institutes of Health
- 2024, 2026 Ad Hoc Panelist, Maximizing Investigators' Research Award A Study Section (MRAA), Center for Scientific Review, National Institutes of Health
- 2022–2024, 2026 Ad Hoc Reviewer, Annual Meeting of the European Society of Human Reproduction and Embryology
- 2025–2026 Ad Hoc Reviewer, Office of Undergraduate Research, Scholarly, and Creative Activity, Johns Hopkins University
- 2025–2026 Ad Hoc Reviewer, Research Foundation Flanders (FWO)
- 2023, 2026 Ad Hoc Reviewer, Discovery and Catalyst Awards, Johns Hopkins University
- 2023–2026 Ad Hoc Reviewer, Provost's Undergraduate Research Award, Johns Hopkins University
- 2022, 2024 Outside Reviewer, Israel Science Foundation
- 2022 College of Expert Reviewers, European Science Foundation
- 2022 Ad Hoc Reviewer, Kleberg Foundation Scholars Program Internal Competition, Johns Hopkins University
- 2022 Outside Reviewer, Medical Research Council, United Kingdom Research and Innovation
- 2022 Ad Hoc Reviewer, NHGRI Genomic Data Science AnVIL Cloud Credits Continued Program (AC3)
- 2021 Outside Reviewer, Independent Research Fund Denmark, Danish Agency for Higher Education and Science
- 2018–2019, 2021 Outside Reviewer, Biological Anthropology Program, National Science Foundation

Education, volunteering & outreach

- 2018, 2021–2026 Mock F31 Panelist, Communicating Science, Johns Hopkins University
- 2020, 2024 Representative of JHU CMDB, NIH Graduate & Professional School Fair, Bethesda, MD

- 2024 Speaker, Faculty Salon Career Mentorship Series, Department of Biology, Johns Hopkins University
- 2024 Keynote Speaker, Northeast District 2 Annual Convention, TriBeta Biological Honors Society, Johns Hopkins University
- 2022-2024 Virtual Training Program Mentor, Society for Molecular Biology & Evolution
- 2023 Judge, Postdoctoral Conference Poster Session, Johns Hopkins University
- 2023 Co-author, [cloud-based modules for interactive exploration of human genomic variation](#)
- 2023 South Asian Students at Hopkins Faculty Panelist, Johns Hopkins University
- 2022 Ingenuity Speaker Series, Baltimore Polytechnic Institute, Baltimore, MD
- 2020 Visiting Fellow in Biology Assessment, AP Higher Education, The College Board
- 2019 Undergraduate Mentor, Society for Molecular Biology & Evolution, Manchester, England
- 2018-2019 Senior Project Mentor, School Without Walls, Washington, DC
- 2018 Bioethics Panelist, Biology Club, University of Maryland, Baltimore County, Catonsville, MD

Prior to faculty position

- 2017, 2018 Education Outreach Volunteer, University Prep Middle School, Seattle, WA
- 2018 Judge, NWABR Middle School Essay Contest, Seattle, WA
- 2017 Session Moderator, Detection and Interpretation of Structural Variation, Annual Meeting of the American Society of Human Genetics, Orlando, FL
- 2017 Invited Speaker, Emerald City Rotary, Seattle, WA
- 2016 Volunteer, University of Washington Paws-On Science, Pacific Science Center, Seattle, WA
- 2016 Invited Speaker, Open Mic Science, Treehouse Cafe, Bainbridge Island, WA
- 2014 AP Biology E-mentor, Arroyo High School, San Lorenzo, CA
- 2012-2013 Copy Editor, *Six Degrees: The Stanford Journal of Human Rights*
- 2012 Judge, Synopsys Silicon Valley Science and Technology Championship, San Jose, CA
- 2012 PhD Interview Visit Committee, Department of Biology, Stanford University
- 2011 New PhD Student Orientation Committee, Department of Biology, Stanford University

Selected Media

- 2026 Genetic basis of aneuploidy, which often causes pregnancy loss, revealed. [The Scientist](#)
- 2026 Study reveals genetic factors influencing pregnancy loss. [Johns Hopkins University Hub](#)
- 2026 Meiotic gene variants linked to recombination, pregnancy loss-related aneuploidy. [GenomeWeb](#)
- 2025 Human genome sequencing powers personalized, precision medicine. [Johns Hopkins University Hub](#)
- 2024 Gene expression, underlying genetic variation profiled in diverse human populations. [GenomeWeb](#)
- 2024 New study addresses long-standing diversity bias in human genetics. [Johns Hopkins University Hub](#)
- 2024 Many pregnancy losses are caused by errors in cell division. [Scientific American](#)
- 2023 Study on chromosomal abnormalities sheds light on early embryo development in human reproduction and IVF. [The Johns Hopkins News-Letter](#)
- 2023 Why the human genome was never completed. [BBC](#)
- 2023 Researchers assemble the first complete sequence of a human Y chromosome. [NHGRI Press Release](#)
- 2023 Male sex chromosome, missing piece in human genome, finally decoded. [Johns Hopkins University Hub](#)

- 2022 Link between long telomeres and long life is a tall tale, study finds. [The New York Times](#)
- 2022 Long telomeres may heighten cancer risks. [NIH Research Matters](#)
- 2022 The human genome is finally fully sequenced. [TIME](#)
- 2022 Genome defined as human genetic blueprint fully sequenced for first time. [Newsweek](#)
- 2022 Hopkins team plays a role in sequencing complete human genome. [The Johns Hopkins News-Letter](#)
- 2022 Johns Hopkins scientists contribute to the first complete sequence of human genome. [Johns Hopkins University Hub](#)
- 2021 Scientists finish the human genome at last. [The New York Times](#)
- 2020 Aneuploidy common in early-stage human embryos, single-cell RNA-seq study reveals. [GenomeWeb](#)
- 2020 Abnormal cells in embryos might not prevent IVF success. [Johns Hopkins University Hub](#)

Prior to faculty position

- 2018 A new genetic study suggests modern Flores island pygmies and ancient hobbits are unrelated. [Smithsonian Magazine](#)
- 2018 Small height evolved twice on 'Hobbit' island of Flores. [BBC](#)
- 2018 Bodies keep shrinking on this island, and scientists aren't sure why. [The New York Times](#)
- 2017 What Neanderthal DNA is doing to your genome (video). [SciShow](#)
- 2017 How ancient Neanderthal DNA still influences our genes today. [Smithsonian Magazine](#)
- 2015 A scrambled mess. [The Scientist](#)