

# Riley J. Mangan

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## EDUCATION

**Duke University**, Durham, North Carolina Aug 2018 – Aug 2023

- Ph.D. - Molecular Genetics and Microbiology
  - Graduate Program in Cell and Molecular Biology
  - GPA: 3.98 / 4.0
  - Advised by Craig B. Lowe, Ph.D.
  - Dissertation Title: *Divergence, Mutation, Function, Selection: The Evolution of the Human Genome*
  - Dissertation Committee: Greg Crawford, Tim Reddy, Debby Silver, Greg Wray

**Davidson College**, Davidson, North Carolina Aug 2012 – May 2016

- B.S. - Biology, *Magna Cum Laude*
  - GPA: 3.79 / 4.0

## EXPERIENCE

**Massachusetts Institute of Technology**, Cambridge, Massachusetts Oct 2023 – Present

- Postdoctoral Associate, Laboratory of Manolis Kellis, Ph.D.
  - **Central Focus:** My work integrates deep learning sequence-to-function models and diverse regulatory epigenomic data resources to uncover how genomic changes in human evolutionary history have altered gene regulatory circuitry and ultimately shaped derived phenotypes in anatomically modern humans.
  - Member of the Computational Biology Group at MIT CSAIL, the Computer Science and Artificial Intelligence Laboratory.

**Duke University School of Medicine**, Durham, North Carolina Aug 2018 – Sep 2023

- Ph.D. Candidate, Laboratory of Craig B. Lowe, Ph.D.
  - **Central Focus:** My work combined interdisciplinary tools from computational genomics, neurodevelopment, and molecular evolution to investigate how human-specific gene regulatory innovation led to human-unique disease susceptibility and derived human traits.
  - I identified HAQERs, the fastest-evolved regions of the human genome, many of which encode human-specific functional elements and are associated with human neurodevelopment and disease. *Mangan et al, Cell 2022*.
  - I developed *in vivo* STARR-seq, a high-throughput, single-cell, multiplex enhancer assay to quantify the cell type-specific enhancer activity of DNA sequences in developing brain tissue.
  - As a member of the T2T Consortium, I worked to identify rapidly-evolving regions in the human genome using state-of-the-art telomere-to-telomere primate genome assemblies.

**Duke Human Vaccine Institute**, Durham, North Carolina May 2016 – Jul 2018

- Research Technician II, Laboratory of Sallie R. Permar, MD., Ph.D.
  - **Central Focus:** My work focused on vaccine and non-vaccine strategies for the prevention and elimination of postnatal virus infections, with particular focus on HIV, CMV, and the Zika virus.
  - Characterization of the determinants of interaction between the HIV-1 Env and Tenascin-C, an innate antiviral protein present in breast milk, which is believed to impair postnatal breastmilk transmission of HIV. *Mangan et. al, Mucosal Immunology 2019*.
  - Assay development for the characterization of the HIV-1 Env-specific B cell repertoire by next-generation sequencing of immunoglobulin heavy chains from Env-vaccinated rhesus macaques.
  - Functional characterization of the vaccine elicited antibody repertoire in Env-vaccinated infant rhesus macaques by antigen-specific B cell sorting, monoclonal antibody generation, and ELISA epitope mapping.

**Davidson College Biology Department**, Davidson, North Carolina Aug 2015 – Dec 2015

- Student Research Assistant, Laboratory of Rachid El Bejjani, Ph.D.
  - **Central Focus:** My work identified and characterized a novel function of *Rab-6.2* in cuticle development and skin permeability in *Caenorhabditis elegans*. *Kim et. al, Journal of Cell Science 2019*.

**Department of Medicine, University of Illinois at Chicago**, Chicago, Illinois May 2015 – Aug 2015

**Feinberg School of Medicine, Northwestern University**, Chicago, Illinois May 2012 – Aug 2014

- Summer Research Intern, Laboratory of Paul Grippo, Ph.D.
  - **Central Focus:** My first research experience, here my work focused on signaling in the tumor microenvironment of colorectal cancer and pancreatic ductal adenocarcinoma.
  - We studied TGF- $\beta$  and PEDF in fibrosis, immune evasion, and PDAC tumorigenesis.

**PUBLICATIONS 17 TOTAL, 3 AS FIRST AUTHOR**

- Singh T, Miller IG, Venkatayogi S, Webster H, Heimsath HJ, Eudailey JA, Dudley DM, Kumar A, **Mangan RJ**, Thein A, Aliota MT, Newman CM, Mohns MS, Breitbach ME, Berry M, Wiehe K, O'Connor DH, and Permar SR. (2023) Prior dengue serotype 3 infection modulates subsequent plasmablast responses to ZIKV infection in a nonhuman primate model. *Submitted*.
- Au EH\*, Fauci C\*, Luo Y\*, **Mangan RJ\***, Snellings DA\*, Shoben CR, Weaver S, Simpson S, Lowe CB. (2023) Genomics: Uniting high performance and readability for genomics with Go. *Bioinformatics*. In Press. \*Co-first author, listed alphabetically.
- Mangan RJ**, Alsina FC\*, Mosti F\*, Sotelo-Fonseca JE, Snellings DA, Au EH, Carvalho J, Sathyan L, Johnson GD, Reddy TE, Silver DL, Lowe CB. (2022) Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. *Cell*. 185: 4587–4603. \*Indicates co-second author.
- Nelson AN, Dennis M, Mangold JF, Li K, Saha PT, Cronin K, Kumar A, **Mangan RJ**, Shaw GM, Bar K, Haynes B, Moody MA, Alam M, Pollara J, Hudgens MG, Van Rompay KKA, De Paris K, Permar SR. (2022) Leveraging antigenic seniority for maternal vaccination to prevent mother-to-child transmission of HIV-1. *NPJ Vaccines*. 7(1): 87.
- Berendam S\*, Morgan-Asiedue PK\*, **Mangan RJ**, Li S, Heimsath H, Luo K, Curtis A, Eudailey J, Faison W, Fox C, Phillips B, Tomai M, Kunz E, Itell H, Hudgens M, Cronin K, Wiehe K, Alam SM, Van Rompay KKA, De Paris K, Permar SR, Moody MA, Fouda GG. (2021) Different adjuvanted pediatric HIV envelope vaccines induced distinct plasma antibody responses despite similar B cell receptor repertoires in infant rhesus macaques. *PLOS One*. 16(12):e0256885. \*Indicates co-first author.
- Itell HL, Berenz A, **Mangan RJ**, Permar SR, Kaufman D. (2021) Systemic and mucosal levels of lactoferrin in very low birth weight infants supplemented with bovine lactoferrin. *Biochemistry and Cell Biology*. 99(1):25-34.
- Martinez DR, Tu JJ, Kumar A, Mangold JF, **Mangan RJ**, Goswami R, Giorgi EE, Chen J, Mengual M, Douglas AO, Heimsath H, Saunders KO, Nicely NI, Eudailey J, Hernandez G, Morgan-Asiedue PK, Wiehe K, Haynes BF, Moody MA, LaBranche C, Montefiori DC, Gao F, Permar SR. (2020) Maternal broadly neutralizing responses select for neutralization-resistant infant transmitted/founder HIV variants. *mBio*. 11(2):e00176-20.
- Goswami R, Nelson AN, Tu JJ, Dennis M, Feng L, Kumar A, Mangold J, **Mangan RJ**, Mattingly C, Curtis AD, Obregon-Perko V, Mavigner M, Pollara J, Shaw GM, Bar K, Chahroudi A, De Paris K, Chan C, Van Rompay KKA, Permar SR. (2019) Analytical treatment interruption of postnatal SHIV infection after short-term anti-retroviral therapy in an infant rhesus macaque model. *mBio*. 10(5): e01971-19.
- Nelson AN, Goswami R, Dennis M, Tu J, **Mangan RJ**, Saha P, Cain DW, Shen X, Bar K, Hudgens M, Pollara J, De Paris K, Van Rompay KKA, and Permar SR. (2019) SHIV CH505 infected infant and adult rhesus macaques exhibit similar HIV Env-specific antibody kinetics, despite distinct T follicular helper (Tfh) and germinal center B cell landscapes. *Journal of Virology*. 93(15): e00168-19.
- Mangan RJ**, Stamper L, Ohashi T, Eudailey JA, Go EP, Jeager F, Itell HL, Watts BE, Fouda GG, Erickson HP, Alam SM, Desaire H, Permar SR. (2019) Determinants of tenascin-C and HIV Env binding and neutralization. *Mucosal Immunology*. 12: 1004-1012.
- Kim J\*, Chun A\*, **Mangan RJ**, Doyle H, Mourao B, and El Bejjani R. (2019) A retromer-independent function for RAB-6.2/RAB6 in *C. elegans* epidermis integrity. *Journal of Cell Science*. 8(3): 3826-2839. \*Indicates co-first author.
- Himes JE, Goswami R\*, **Mangan RJ\***, Kumar A, Jeffries TL, Eudailey JA, Hemsath H, Nguyen QN, Pollara J, LaBranche C, Chen M, Vandergrift NA, Schiro F, Midkiff C, Ferrari G, Montefiori DC, Alvarez-Hernandez X, Aye PP, Permar SR. (2018) Polyclonal anti-HIV envelope breast milk antibodies limit founder SHIV acquisition and cell-associated virus loads in infant rhesus monkeys. *Mucosal Immunology*. 11(6): 1716-1726. \*Co-second author.
- Nguyen QN, Martinez DR, Himes JE, Edwards RW, Han Q, Kumar A, **Mangan R**, Nicely NI, Shen X, Pollara J, Permar SR. (2018) Predominant envelope variable loop 2-specific and antibody-dependent cellular cytotoxicity antibody responses in acutely SIV-infected African green monkeys. *Retrovirology*. 15(1): 24.
- Principe DR, Diaz AM, Torres C, **Mangan RJ**, DeCant B, McKinney R, Tsao MS, Lowy A, Munshi HG, Grippo PJ. (2017) TGF $\beta$  engages MEK/ERK to differentially regulate benign and malignant pancreas cell function. *Oncogene*. 36(30):4336-4348.

- Principe DR, **Mangan RJ**, Grippo PJ. (2017) Transforming Growth Factor  $\beta$ . *Cancer Therapeutic Targets*, pp.503-516. (Textbook Chapter)
- Principe DR, DeCant B, Staudacher J, Vitello D, **Mangan RJ**, Wayne E, Mascariñas E, Diaz AM, Bauer J, McKinney RD, Khazaie K, Pasche B, Dawson DW, Munshi HG, Grippo PJ, Jung B. (2016) Loss of TGF $\beta$  signaling promotes colon cancer progression and tumor-associated inflammation. *Oncotarget*. 8(3):3826-3839.
- Principe DR, Decant B, Diaz AM, **Mangan RJ**, Hwang R, Lowy A, Shetuni BB, Sreekumar BK, Chung C, Bentrem DJ, Munshi HG, Jung B, Grippo PJ, Bishehsari F. (2016) PEDF inhibits pancreatic tumorigenesis by attenuating the fibroinflammatory reaction. *Oncotarget*. 7(19): 28218-28234.

**TEACHING AND PRESENTATIONS**

**POSTER PRESENTATIONS**

- 2023 The Biology of Genomes, Cold Spring Harbor Laboratories
- 2019 Duke University Division of Human Genetics Retreat
- 2017 and 2018 Duke University Department of Pediatrics Research Retreat
- 2016, 2017, and 2018 Center for AIDS Research (CFAR) Retreat, Duke University
- 2016 Math and Science Research Symposium, Davidson College Biology Department
- 2016 Community-Based Learning Poster Session, Davidson College Department of Mathematics and Computer Science

**INVITED TALKS**

- 2023 Invited Guest Lecture, course in Cell and Molecular Neuroscience, Davidson College **“Human Evolutionary Neuroscience: Genomic Insights.”**
- 2022 Annual Meeting, American Society of Human Genetics **“Adaptive sequence divergence forged new neurodevelopmental enhancers in humans.”**
- 2020 Duke University Division of Human Genetics Retreat. **“High-throughput functional analysis of the fastest evolving regions of the human genome.”**
- 2019 Duke University Department of Molecular Genetics and Microbiology Research Retreat. **“Exploring the fastest evolving regions of the human genome.”**

**MENTORING**

I was the primary mentor to two undergraduate students when I was a graduate student. One student, under my mentorship, completed an Honor’s thesis, which was awarded the “Best Undergraduate Thesis” in Evolutionary Anthropology at Duke University.

Extensive experience mentoring rotation students, graduate students, and research staff in the lab.

**AWARDS & SCHOLARSHIPS**

- Triangle Center for Evolutionary Medicine Graduate Student Award Fall 2020
- Sigma Xi Grants-In-Aid of Research. 2019  
Matching contribution from the Duke Graduate School.
- Steinway Piano Gallery-Charlotte Award May 2016  
For pianistic excellence and academic achievement.  
2016 Davidson College Honoree.
- Donald B. Plott and J. Estes Millner Scholarship, Davidson College 2012–2016  
For students with exceptional talent and passion for music.

**RESEARCH SKILLS**

- In Vivo Research  
Mouse handling and husbandry, genotyping, survival surgery, behavior, tissue resection, and perfusion. Human and non-human primate blood and tissue sample processing. C. elegans colony maintenance, Mendelian genetics, behavioral and pharmacological assays.
- Molecular Biology  
Western blotting, immunoprecipitation, histology, flow cytometry, ELISA, cell culture, plasmid production and cloning, monoclonal antibody production, next-generation sequencing, confocal and super-resolution microscopy.
- Mathematics and Statistics  
Experience and knowledge of statistical modeling and Bayesian inference, calculus, linear algebra, machine learning, and numerical analytic methods.

- Software Engineering
  - Lead developer on Gonomics, an open-source genomics software platform for the Go programming language.
  - Proficiency in Go, Python, R, bash/csh, HTML/CSS, and  $\text{\LaTeX}$  with previous experience in Java and Matlab.
  - Extensive experience with cluster computing environments (slurm) and Git version control.
  - Extensive knowledge and development of open-source bioinformatic pipelines for phylogenetics, comparative genomics, bulk and single-cell RNA sequencing.