Thomas A. Sasani, Ph.D

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Research Summary

I use cutting-edge DNA sequencing technologies and innovative computational approaches to study the origins and consequences of germline and somatic mutation. I am particularly interested in discovering and characterizing *mutation rate modifiers* in eukaryotic genomes.

Education

University of Utah — Salt Lake City, UT, USA
Ph.D in Human Genetics, advised by Dr. Aaron Quinlan — *2015 — 2019*

Lawrence University — Appleton, WI, USA
B.A. in Biochemistry, summa cum laude — *2011 — 2015*

Experience

Staff Research Scientist — Oct 2022 — Present
Quinlan Lab, Department of Human Genetics, University of Utah — *Atlanta, GA, USA (remote)*

Senior Data Scientist — May 2021 — Oct 2022
Recursion Pharmaceuticals — *Salt Lake City, UT, USA*

Postdoctoral Fellow — March 2020 — May 2021
Harris Lab, Department of Genome Sciences, University of Washington — *Seattle, WA, USA*

Graduate Research Assistant — Aug 2015 — March 2020
Quinlan Lab, Department of Human Genetics, University of Utah — *Salt Lake City, UT, USA*

Preprints

2025

- Happ HC, **Sasani TA**, Warner D, Neklason DW, Quinlan AR. AVITI sequencing of a four-generation CEPH/Utah pedigree confirms low mutation rates at homopolymer loci despite their low sequence complexity. ***bioRxiv***.
- Kunisaki J, Goldberg ME, Lulla S, **Sasani TA**, Hiatt L, Nicholas TJ, Liu L, Torres-Arce E, Guo Y, James E, Horns JJ, Ramsay JM, Chen W, Hotaling JM, Aston KI, Quinlan AR. Sperm from infertile, oligozoospermic men have elevated mutation rates. ***medRxiv***.

2024

- Mokveld T, Dolzhenko E, Dashnow H, Nicholas TJ, **Sasani TA**, van der Sanden B, Jadhav B, Pedersen B, Kronenberg S, Tucci A, Sharp AJ, Quinlan AR, Gilissen C, Hoischen A, Eberle MA. TRGT-denovo: accurate detection of *de novo* tandem repeat mutations. ***bioRxiv***.
- Xu K, Zhang Y, Baldwin-Brown J, **Sasani TA**, Phadnis N, Miller MP, Rog O. Decoding chromosome organization using CheC-PLS: chromosome conformation by proximity labeling and long-read sequencing. ***bioRxiv***.
- Ashbrook DG, **Sasani TA**, Maksimov M, Gunturkun MH, Ma N, Villani F, Ren Y, Rothschild D, Chen H, Lu L, Colonna V, Dumont B, Harris K, Gymrek M, Pritchard JK, Palmer AA, Williams RW. Private and sub-family specific mutations of founder haplotypes in the BXD family reveal phenotypic consequences relevant to health and disease. ***bioRxiv***.

Peer-reviewed manuscripts

Also see Google Scholar

2025

- Porubsky D, Dashnow H*, **Sasani TA***, Logsdon GA*, Hallast P*, Noyes MD*, Kronenberg ZN*, Mokveld T*, Koundinya N, Nolan C, Steely CJ, Guarracino A, Dolzhenko E, Harvey WT, Rowell WJ, Grigorev K, Nicholas TJ, Goldberg ME, Oshima KK, Lin J, Ebert P, Watkins WS, Leung TY, Hanlon VCT, McGee S, Pedersen BS, Happ HC, Jeong H, Munson KM, Hoekzema K, Chan DD, Wang Y, Knuth J, Garcia GH, Fanslow C, Lambert C, Lee C, Smith JD, Levy S, Mason CE, Garrison E, Lansdorp PM, Neklason DW, Jorde LB, Quinlan AR, Eberle MA & Eichler EE. Human *de novo* mutation rates from a four-generation pedigree reference. ***Nature***.

2024

- **Sasani TA**, Quinlan AR, Harris K. Epistasis between mutator alleles contributes to germline mutation spectrum variability in laboratory mice. ***eLife***. *Code.*

2022

- Fixsen SM, Cone KR, Goldstein SA, **Sasani TA**, Quinlan AR, Rothenburg S, Elde NC. Poxviruses capture host genes by LINE-1 retrotransposition. ***eLife***.
- **Sasani TA**, Ashbrook DG, Beichman AC, Lu L, Palmer AA, Williams RW, Pritchard JK, Harris K. A natural mutator allele shapes mutation spectrum variation in mice. ***Nature***. *Code.*

2021

- Belyeu JR*, **Sasani TA***, Pedersen BS, Quinlan AR. Unfazed: parent-of-origin detection for large and small *de novo* variants. ***Bioinformatics***. *Code.*

2020

- Wallace AD, **Sasani TA**, Swanier J, Gates B, Greenland J, Pedersen BS, Varley KT, Quinlan AR. CaBagE: a Cas9-based Background Elimination strategy for targeted, long-read DNA sequencing. ***PLoS One***.
- Cawthon RM, Meeks HD*, **Sasani TA***, Smith KR, Kerber RA, O'Brien E, Baird L, Dixon MM, Peiffer AP, Leppert MF, Jorde LB, Quinlan AR. Germline mutation rates in young adults predict longevity and reproductive lifespan. ***Scientific Reports***.

2019

- **Sasani TA**, Pedersen BS, Gao Z, Baird L, Przeworski M, Quinlan AR, Jorde LB. Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. ***eLife***. *Code.*
  - ▸ Listen to my interview on the Naked Scientists podcast.
- Gao Z, Moorjani P, **Sasani TA**, Pedersen BS, Quinlan AR, Jorde LB, Amster G, Przeworski M. Overlooked roles of DNA damage and maternal age in generating human germline mutations. ***PNAS***.

2018

- **Sasani TA***, Cone KR*, Quinlan AR, Elde NC. Long read sequencing reveals poxvirus evolution through rapid homogenization of gene arrays. ***eLife***. *Code.*
- Belyeu JR, Nicholas TJ, Pedersen BS, **Sasani TA**, Havrilla JM, Kravitz SN, Conway ME, Lohman BK, Quinlan AR, Layer RM. SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. ***GigaScience***.
- Jain M*, Koren S*, Miga KM*, Quick J*, Rand AC*, **Sasani TA***, Tyson JR*, Beggs AD, Dilthey AT, Fiddes IT, Malla S, Marriott H, Nieto T, O'Grady J, Olsen HE, Pedersen BS, Rhie A, Richardson H, Quinlan AR, Snutch

TP, Tee L, Paten B, Phillippy AM Simpson JT, Loman NJ, Loose M. Nanopore sequencing and assembly of a human genome with ultra-long reads. ***Nature Biotechnology***.

2017

- Feusier J, Witherspoon DJ, Watkins WS, Goubert C, **Sasani TA**, Jorde LB. Discovery of rare, diagnostic Alu Yb8/9 elements in diverse human populations. ***Mobile DNA***.
- Piasecki BP, **Sasani TA**, Lessenger AT, Huth N, Farrell S. MAPK-15 is a ciliary protein required for PKD-2 localization and male mating behavior in *Caenorhabditis elegans*. ***Cytoskeleton.***

* indicates equal contribution

Awards and Fellowships

NIH T32 Postdoctoral Genome Sciences Training Grant 2020 — 2021
University of Washington

NIH T32 Predoctoral Genetics Training Grant 2017 — 2019
University of Utah

Charles J. Epstein Trainee Award for Excellence in Human Genetics 2017 & 2018
Semifinalist, American Society for Human Genetics

Lassonde Institute Student Innovator 2017
University of Utah

Howard and Helen Russell Award for Excellence in Biological Research 2015
Lawrence University

Invited Seminars

Discovering epistasis between germline mutator alleles in mice 2023
University of Utah Bioscience Annual Retreat *Alta, UT, USA*

Mapping mutator alleles in mice 2021
Recent Advances in Biology Lecture Series *Lawrence University, USA (Virtual)*

Mapping mutator alleles in mice 2021
Pritchard Lab Mini-Conference *Stanford University, USA (Virtual)*

A wild-derived antimutator drives mutation spectrum differences in mice 2021
Przeworski Lab Meeting *Columbia University, USA (Virtual)*

A short tale of viral evolution told with long reads 2019
Society for Molecular Biology and Evolution (SMBE) Annual Meeting *Manchester, UK*

Human immune defense mechanisms drive rapid genome evolution in vaccinia virus 2017
London Calling, Oxford Nanopore Technologies Annual Meeting (**viewable here**) *London, UK*

Contributed Presentations

Fast and furious mutation at tandem repeats in a four-generation human family 2025
The Biology of Genomes *Cold Spring Harbor, NY, USA*

Discovering epistasis between germline mutator alleles in mice 2023
The Biology of Genomes *Cold Spring Harbor, NY, USA*

Directly measuring the human mutation rate by sequencing large pedigrees 2018
American Society of Human Genetics (ASHG) Annual Meeting *San Diego, CA, USA*

Human immune defense mechanisms drive rapid genome evolution in vaccinia virus 2017
American Society of Human Genetics (ASHG) Annual Meeting *Orlando, FL, USA*

Mentorship

Graduate students

Taeho K. Aug 2024 — Oct 2024
Accuracy of Element AVITI sequencing at homopolymer loci in the human genome *University of Utah*

Candice Y. Sep 2020 — Dec 2020
Identifying structural variants in a recombinant inbred mouse cross *University of Washington*

Erica H. Jan 2020 — Mar 2020
Regional variation in mutation rates and spectra *University of Utah*

Bianca A. Oct 2019 — Dec 2019
Patterns of recombination in large Utah pedigrees *University of Utah*

Undergraduate students

Julia O. Jul 2025 — Sep 2025
Detecting *de novo* mutations in large pedigrees *University of Utah*

High School Students

Myles F. Jul 2020 — Sep 2020
Variation in mutation rates and spectra in a recombinant inbred mouse cross *University of Washington*

Teaching Experience

University of Utah

Instructor 2019 & 2024
Applied Computational Genomics, Salt Lake Learners of Biostatistics

Teaching Assistant 2016 — 2017
Programming for Biomedical Science, Applied Computational Genomics

Guest Lecturer 2016
Summer Data Science Bootcamp

Cold Spring Harbor Laboratory

Teaching Assistant 2016 & 2017
Advanced Sequencing Technologies and Applications

Reviewing

Nature, Genome Biology, Genome Medicine, Molecular Biology and Evolution, Bioinformatics, eLife, Science, Nature Communications, PNAS

Courses and Professional Development

Leena Peltonen School of Human Genomics 2018
Les Diablerets, CHE