

Justin Cha

Education

Cornell University

November 2026 (Expected)

PhD candidate

Computational Biology

Georgia Institute of Technology

May 2018

BS with Highest Honors

Major in Biomedical Engineering; Minor in Physics

Experience

Cornell University – Ithaca, NY

PhD candidate

August 2021 – Present

Dr. Frank Pugh Laboratory

The Pugh Lab is a leader in developing protocols for high-resolution chromatin immunoprecipitation (ChIP-exo) sequencing. I am currently involved in several projects investigating the fundamental characteristics of chromatin. I have investigated the roles of specific components in the SWR1 chromatin remodeler complex in yeast. I have also developed GenoCLAMP, a software to merge highly similar sequence motifs, and GenoPlotter, a browser tool to plot quantitative data on arrays of genomic loci. Currently I am developing a software method for deconvolving DNA sequence motifs according to bound protein configurations using ChIP-exo data.

Broad Institute of Harvard and MIT – Cambridge, MA

Associate Computational Biologist II

September 2018 – July 2021

Dr. Gad Getz Laboratory

At the Broad Institute, I was a member of the Getz Lab, one of the world's leading labs for cancer genomics. I have worked on several exciting projects pushing at the forefront of the field. One was an analysis of genomic progression in head and neck squamous cell carcinoma (HNSCC). For this project, I made use of a novel set of computational methods to reconstruct the trajectory of genomic events from exome sequencing data. This allowed us to see which mutations and other variants tend to occur early on in the progression of cancer, which will be useful in treatment development and prognosis.

Publications

*These authors contributed equally

- **Cha, J.**, Pugh, B. F., and Lai, W. K. (2026) "GenoCLAMP: consolidation of sequence motifs from genomic-scale data," *Genome Biology* (Accepted).
- Leshchiner, I.*, Medford, A.*, **Cha, J.***, *et al.* (2026) "Actionable genetic landscape and dynamics in circulating DNA from 12,827 patients with metastatic breast cancer," *Nature Communications* (Accepted).
- Kübler, K. *et al.* (2025) "Tamoxifen induces PI3K activation in uterine cancer," *Nature Genetics*. Available at: <https://doi.org/10.1038/s41588-025-02308-w>.

- Ranjan, A. *et al.* (2025) “Histone acetylation readers Bdf1 and Yaf9 direct SWR1 remodeler to +1 nucleosome,” *Science Advances*. Available at: <https://doi.org/10.1126/sciadv.adt2002>.
- Louder, R. *et al.* (2024) “Molecular basis of global promoter sensing and nucleosome capture by the SWR1 chromatin remodeler,” *Cell*. Available at: <https://doi.org/10.1016/j.cell.2024.09.007>.
- Burr, R. *et al.* (2024) “Developmental mosaicism underlying EGFR-mutant lung cancer presenting with multiple primary tumors,” *Nature Cancer*. Available at: <https://doi.org/10.1038/s43018-024-00840-y>.
- Naeem, A. *et al.* (2023) “Pirtobrutinib targets BTK C481S in ibrutinib-resistant CLL but second-site BTK mutations lead to resistance,” *Blood Advances*. Available at: <https://doi.org/10.1182/bloodadvances.2022008447>.
- Khalsa, J.*, **Cha, J.***, Utro, F.*, Naeem, A.*, Murali, I.*, *et al.* (2023) “Genetic events associated with venetoclax resistance in CLL identified by whole exome sequencing of patient samples,” *Blood*. Available at: <https://doi.org/10.1182/blood.2022016600>.
- Leshchiner, I.*, Mroz, E.*, **Cha, J.***, *et al.* (2023) “Inferring early genetic progression in cancers with unobtainable premalignant disease,” *Nature Cancer*. Available at: <https://doi.org/10.1038/s43018-023-00533-y>.
- Bustoros, M. *et al.* (2020) “Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression,” *Journal of Clinical Oncology*, 38(21), pp. 2380–2389. Available at: <https://doi.org/10.1200/jco.20.00437>.

Presentations

- “Characterizing Genomic Protein Complex Binding in *S. Cerevisiae* Using Shared Motif Enrichment,” Cornell Computational Biology student seminar, 2023
- “Mutating the intrinsically disordered region of LGE1 in yeast impacts H2B ubiquitination,” Cornell Computational Biology student seminar, 2022
- “Mechanisms of Primary and Acquired Resistance to Venetoclax in Chronic Lymphocytic Leukemia (CLL),” American Association for Cancer Research, 2020
- “Genomic landscape of metastatic breast cancer (MBC): comprehensive cell-free DNA analysis from over 10,000 patients and comparison with primary breast cancer,” San Antonio Breast Cancer Symposium, 2020

Posters

- “CLAMP: identification of consensus sequence motifs from genomic-scale data,” Cold Spring Harbor meeting: Systems Biology: Global Regulation of Gene Expression, 2026
- “Characterizing Genomic Protein Complex Binding in *S. Cerevisiae* Using Shared Motif Enrichment,” American Society for Biochemistry and Molecular Biology, 2024
- “High-resolution characterization of transcription factor binding in *S. Cerevisiae*,” Great Lakes Bioinformatics, 2023
- “Inferring early genetic progression in cancers with unobtainable premalignant disease,” Massachusetts General Hospital Center for Cancer Research, 2019

Volunteering

- African Society for Bioinformatics and Computational Biology (ASBCB) omics codeathon judge and panelist (2023-2026)

Mentoring

- Mentored undergraduate researchers: students have gotten accepted to graduate programs at institutions including the University of Chicago and Rice University

Training

- INTERSECT (2024); Princeton, NJ; all expenses paid
- Open Science Grid (OSG) User School (2022); Madison, WI; all expenses paid

Skills

Programming Languages: Python, JavaScript, Julia, Rust, SQL, Matlab

Quantitative: Data analysis, Statistics, Genomics

Communication: Technical presentation/writing, Data visualization, Web development, Teaching

Links

- jcha40.github.io
Personal website
- <https://orcid.org/0000-0001-6026-2211>
ORCID
- <https://github.com/CEGRcode/GenoPlotter>
GenoPlotter: A browser tool for plotting composite quantitative data over many analogous genomic loci
- <https://github.com/CEGRcode/GenoCLAMP>
GenoCLAMP (Genomic CLustered Alignment of Motif Profiles): A tool for clustering sequence motifs into aligned consensus sequences
- <https://github.com/broadinstitute/PhylogicNDT>
PhylogicNDT: A tool for clustering mutations, inferring tumor phylogeny, and inferring the order of mutations in cancer
- <https://github.com/broadinstitute/getzlab-SignatureAnalyzer>
SignatureAnalyzer: A tool for identifying mutational signatures in a cohort of tumor samples