Justin Cha

Education

Cornell University December 2026 (Projected)
PhD candidate
Dr. Frank Pugh Laboratory; Computational Biology

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. Currently I am developing a software method for deconvolving DNA sequence motifs according to bound protein configurations using ChIP-exo data.

Georgia Institute of Technology May 2018
BS with Highest Honors
Major in Biomedical Engineering; Minor in Physics

Experience

Broad Institute of Harvard and MIT – Cambridge, MA
Associate Computational Biologist II September 2018 – July 2021

At the Broad Institute, I am 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

- 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 (2023-2025)

Training

- INTERSECT; Princeton, NJ; all expenses paid
- Open Science Grid (OSG) User School; 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/CLAMP

CLAMP (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