

# BRENT Y. CHICK

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## EDUCATION

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- Ph.D., Biological Sciences, UC San Diego** 2020 – exp. 2027  
*Hargreaves Lab, Salk Institute* · Thesis: Epigenetic mechanisms of ERK signal decoding in cell fate decisions
- M.A., Molecular, Cellular & Developmental Biology, UC Santa Barbara** 2018 – 2020  
*Wilson Lab, optogenetics and signaling dynamics*
- B.S., Molecular Biology, UC San Diego** 2010 – 2015  
*Hedrick Lab, T cell immunology*

## RESEARCH EXPERIENCE

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**Graduate Researcher · Hargreaves Lab, Salk Institute** 2020 – present

- Co-first author on *Immunity* (2023) defining how the canonical BAF complex shapes the enhancer landscape that licenses CD8+ T cell effector and memory fates. Owned ATAC-seq, RNA-seq, and CUT&RUN analyses end-to-end, raw reads to figures.
- Pioneered CUT&RUN in the lab from scratch and redesigned the standard ConA-bead protocol into a 96-well-plate workflow. Now enables routine 48-sample CUT&RUN runs that would be impractical with the conventional protocol; adopted across the group.
- Sole architect and administrator of tanuki, the lab's shared compute server. Designed storage, environments, and pipelines that support all of the group's bioinformatics work.
- Building a high-throughput optogenetics platform with RNA-seq readout (CUT&RUN and ATAC-seq next) to map how dynamic ERK signaling encodes chromatin state, fusing Wilson-lab optogenetics with Hargreaves-lab chromatin profiling.
- Use AI-assisted tools (Claude, Claude Code) routinely for code generation, pipeline scaffolding, and literature triangulation as part of an integrated research workflow.

**Master's Researcher · Wilson Lab, UC Santa Barbara** 2018 – 2020

- Optogenetic perturbation of intracellular signaling. Designed quantitative live-cell imaging experiments and built custom image-analysis and modeling code to extract single-cell signaling dynamics.

**Junior Specialist / Undergraduate Researcher · Crooks Lab (UCLA), Hedrick Lab (UCSD)** 2013 – 2017

- Co-developed the artificial thymic organoid (ATO) system, a foundational platform for *in vitro* human T cell differentiation from pluripotent and hematopoietic stem cells. Co-author on four peer-reviewed papers (*Nature Methods*, *Cell Stem Cell*, *Cell Reports*, *J Immunol*).

## SELECTED PUBLICATIONS (\* = co-first author)

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Chung HK, et al. (incl. Chick B). Atlas-guided discovery of transcription factors for T cell programming. *Nature*, 2026.

Labarta-Bajo L, et al. (incl. Chick BY). The antiviral interferon pathway drives astrocyte aging and motor decline. *bioRxiv*, 2025.

Chick BY, Hargreaves DC. RNA polymerase II promoter-proximal pausing promotes BAF chromatin binding and remodeling. *Nature Genetics*, 2024. Invited News & Views.

McDonald B\*, Chick BY\*, et al. Canonical BAF complex activity shapes the enhancer landscape that licenses CD8+ T cell effector and memory fates. *Immunity*, 2023.

Chick BY, Hargreaves DC. Switching under selection: how CoREST controls endocrine therapy resistance in ER+ breast cancer. *Nature Structural & Molecular Biology*, 2022. Invited News & Views.

Co-authored manuscript in revision, *Cancer Cell*. Five additional peer-reviewed publications including *Nature Methods*, *Cell Stem Cell*, *Cell Reports*. Full list at [brentchick.com](http://brentchick.com).

## TECHNICAL SKILLS

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**Wet-lab:** CUT&RUN, PRO-seq, ATAC-seq, scRNA-seq, primary CD8+ T cell biology, FACS, CRISPR/Cas9, lentiviral engineering, mouse models, protein biochemistry, optogenetic perturbation, high-throughput live-cell imaging

**Computational:** Python, R, bash; ATAC-seq, RNA-seq, CUT&RUN, scRNA-seq, scATAC-seq pipelines; image analysis and signaling-dynamics modeling

**Infrastructure:** Linux server administration; sole architect of shared lab compute (tanuki); Nextflow and Singularity for reproducible bioinformatics pipelines

**Funding & Awards:** NIH T32 Pathways in Biological Sciences Training Grant (5T32GM133351) · UCSD Marguerite Vogt Award (2023) · Mary K. Chapman Foundation Award (2023) · UCSD McElroy Award (2021)