Alison Tang

Curriculum Vitae

San Mateo, CA 94401
alisondtang.github.io

Education

2016–2022 **Ph.D. Biomolecular Engineering and Bioinformatics**, *UC Santa Cruz*.

2012–2016 **B.A. Molecular and Cell Biology**, *UC Berkeley*.

Experience

Industry

2022–Present **Senior Computational Biologist, Translational Sciences**, *Freenome*, Brisbane.

- Trained machine learning models with plasma multiomics data for breast cancer detection in partnership with SIEMENS Healthineers.
- In a Genentech partnership involving multiple indications (IMpower133 and IMvigor130) and plasma analytes, I performed single-analyte and additive multi-analyte analyses for optimizing multi-class classification tasks, tumor burden estimation, and analysis of plasma biomarkers associated with tumor subtypes (posters presented by colleagues at 2025 AACR and 2025 ESMO)
- Adapted Freenome's early CRC detection ML models to monitor minimal residual disease after curative-intent surgery using measures of cfDNA methylation (2024 AACR and 2026 SDDS poster)

Academic

2016–2022 **Graduate Student Researcher**, *Department of Biomolecular Engineering*, Santa Cruz, Angela Brooks Lab.

- Analyzed long nanopore sequencing of CLL patients with recurrent splicing factor mutations to characterize mutant- and cancer-specific RNA isoforms. I developed FLAIR, a leading tool for analyzing long-read cDNA/direct RNA data that summarizes noisy reads into high-confidence isoforms, in addition to a suite of downstream analysis tools (github.com/BrooksLabUCSC/flair)
- Interrogated the regulatory mechanisms connecting A-to-I RNA editing, RNA splicing, and lung adenocarcinoma progression. I knocked down ADAR in lung ADC cells and developed FLAIR2 to analyze the cis-effects of variants on splicing changes
- Worked in highly collaborative settings, from single lab collaborations to large consortiums. I also mentored several bioinformatics undergraduate students on research projects

2015–2016 **Undergraduate Researcher**, *Integrated Biology Department*, Berkeley, Rasmus Nielsen Lab.

- Modeled inversion polymorphism F_{ST} and performed GO permutation analysis to investigate selective bias for SNPs with large divergence between subpopulations of *D. melanogaster* genomes with and without inversions

2014–2016 **Undergraduate Researcher**, *Children's Hospital Oakland Research Institute*, Oakland, Dario Boffelli Lab.

- Studied AID-promoted EMT in breast cancer cell lines using CRISPR/Cas9 to knock out AID. I performed the wet lab experiments and then applied standard NGS differential expression workflows to the RNA-Seq data

Skills

Dry lab PYTHON programming/bioinformatics tools development and use of popular packages such as pysam, pandas, sklearn, seaborn; R programming and use of popular packages such as DESeq2, glmnet; INKSCAPE for vector figure creation; GIT; SNAKEMAKE for workflows involving common tools such as bedtools, picard, aligners, variant callers

Wet lab Molecular biology techniques starting from cell culture to sequencing *e.g.* siRNA treatment of cells, extraction of RNA/proteins, PCR, running low-melt gels for size selection, library preparation, Western blotting

Awards

2022 Darrell Long and Elaine Long Prize in Experimental Engineering for Ph.D. Dissertations

2020-2023 F-31 Ruth L. Kirschstein Predoctoral Individual National Research Service Award

2017-2018 T-32 Genome Sciences NIH Training Grant

Publications

2024 GENOME BIOLOGY. **Alison D. Tang**, Colette Felton, Eva Hrabeta-Robinson, Roger Volden, Christopher Vollmers, Angela N. Brooks. *Detecting haplotype-specific transcript variation in long reads with FLAIR2.*

2020 NATURE COMMUNICATIONS. **Alison D. Tang**, Cameron M. Soulette, Marijke J. Van Baren, Kevyn Hart, Eva Hrabeta-Robinson, Catherine J. Wu, Angela N. Brooks. *Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia reveals downregulation of retained introns.*

2019 NATURE METHODS. Rachael E. Workman*, **Alison D. Tang***, Paul S. Tang*, Miten Jain*, John R. Tyson*, Roham Razaghi*, Philip C. Zuzarte, Timothy Gilpatrick,Joshua Quick, Norah Sadowski, Nadine Holmes, Jaqueline Goes de Jesus, Karen L. Jones, Cameron M. Soulette, Terrance P. Snutch, Nicholas Loman, Benedict Paten, Matthew Loose, Jared T. Simpson, Hugh E. Olsen, Angela N. Brooks, Mark Akeson, Winston Timp. *Nanopore native RNA sequencing of a human poly(A) transcriptome.*

2024 NATURE METHODS. Francisco Pardo-Palacios, ..., **Alison Tang**, ..., Christopher Vollmers, Gloria Sheynkman, Adam Frankish, Kin Fai Au, Ana Conesa, Ali Mortazavi, Angela N. Brooks. *Systematic evaluation of long-read RNA-seq methods for transcript identification and quantification.*

2023 LIFE SCIENCE ALLIANCE. Cameron M. Soulette, Eva Hrabeta-Robinson, Carlos Arevalo, Colette Felton, **Alison D. Tang**, Maximillian G. Marin, Angela N. Brooks. *Nanopore sequencing reveals U2AF1 S34F-associated full-length isoforms.*

2022 Developmental Cell. Tingsheng Yu, Oscar Cazares, **Alison D. Tang**, Hyun-Yi Kim, Tomas Wald, Adya Verma, Qi Liu, Mary Helen Barcellos-Hoff, Stephen N. Floor, Han-Sung Jung, Angela N. Brooks, and Ophir D. Klein. *SRSF1 governs progenitor-specific alternative splicing to maintain adult epithelial tissue homeostasis and renewal.*

2016 Molecular Biology and Evolution. Justin B. Lack, Jeremy D. Lange, **Alison D. Tang**, Russell B. Corbett-Detig, and John E. Pool. *A Thousand Fly Genomes: An Expanded Drosophila Genome Nexus.*

In review

2022 BioRxiv. Colette Felton, **Alison D. Tang**, Binyamin Knisbacher, Catherine J. Wu, Angela N. Brooks. *Detection of alternative isoforms of gene fusions from long-read RNA-seq with FLAIR-fusion.*

Select presentations

2026 SDDS. *Tumor-naive cfDNA methylation monitoring of patients with colorectal cancer.* Stanford. Poster Presentation.

2024 AACR. *Noninvasive longitudinal monitoring of residual disease in chemotherapy-treated colorectal cancer patients.* San Diego. Poster Presentation.

2021 CSHL Eukaryotic mRNA Processing Meeting. *Detecting haplotype-specific RNA variation in long reads.* Poster Presentation.

2021 NHGRI Annual Meeting. *Detecting allele-specific isoform variation in long reads.* Poster Presentation.

2020 Bay Area RNA Club. *Interrogating the role of ADAR1 in lung adenocarcinoma through identification of A-to-I editing in long reads.* Poster Presentation.

2019 Nanopore Community Meeting. *Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia.* New York, NY. Oral Presentation and Panelist.

2019 ENCODE Long-Read RNA-Seq Meeting. *FLAIR: Full-length alternative isoform analysis of RNA.* Barcelona, Spain. Oral Presentation.

2019 Workshop on Splicing Factor Mutations and RNA Biology in Cancer. *Full-length Alternative Isoform analysis of RNA (FLAIR) for nanopore reads.* New Haven, CT. Poster Presentation.

2018 Nanopore Community Meeting. *Full-Length Alternative Isoform analysis of RNA for noisy nanopore reads.* San Francisco, CA. Oral/Poster Presentation.

2018 RNA Society. *Full-length characterization of transcript isoforms to investigate cancer-associated mutations.* Berkeley, CA. Oral Presentation.

2018 AACR Annual Meeting. *Full-length characterization of transcript isoforms to investigate cancer-associated mutations.* Chicago, IL. Poster Presentation.