

# Tynan Gardner

tynangardner@gmail.com · linkedin.com/in/tynangardner · github.com/tynangardner

## EDUCATION

### University of Texas at Austin

Ph.D. Candidate in Cell and Molecular Biology | Bioinformatics Track

*Expected 06/28*

### Princeton University

B.A. in Molecular Biology | Certificate in Engineering Biology

*May 2020*

## RESEARCH EXPERIENCE

### University of Texas at Austin

*Graduate Research Assistant, Marcotte and Wallingford Labs*

*Aug 2022 - Present*

- Integrate deep-learning protein structure prediction, proteomics, and experimental cell biology to discover and characterize protein interactions governing ciliogenesis and human genetic disease
- Conduct proteome-scale AlphaFold/AlphaFold-Multimer screens to identify candidate protein interactions and interpret predicted interfaces, integrating structural confidence metrics with proteomic and evolutionary evidence to prioritize experimental targets
- Discovered and characterized a functional interaction between the ciliopathy-associated CPLANE protein Jbts17 and the distal appendage kinase Ttbk2, combining structure prediction with *Xenopus* functional experiments; work forms the basis of a first-author manuscript
- Design and execute experimental validation of computational predictions using molecular cloning, CRISPR/morpholino perturbation, mRNA overexpression, quantitative fluorescence microscopy, and protein interaction assays in *Xenopus* embryos
- Develop computational workflows in Python, R, and Bash for large-scale structural-model analysis, proteomics, and quantitative imaging on high-performance computing systems

### The University of Pennsylvania

*Research Specialist A, DiNardo Lab*

*Jul 2020 – May 2022*

- Identified *org-1* (Tbx1 ortholog) as a regulator of *Drosophila* testis stem cell niche development, demonstrating severe niche disorganization and loss of cell-identity markers in *org-1* mutants; work contributed to a 2026 *Development* publication
- Used endogenous fluorescent reporters, immunofluorescence, and quantitative microscopy to show reduced Islet expression and complete loss of FasIII in *org-1* mutant niches

### Princeton University

*Undergraduate Researcher, Avalos Lab*

*Dec 2018 – May 2020*

- Engineered a fluorescent biosensor-based screen using inhibitory camelid nanobodies to identify regulators of endogenous isopentanol and isobutanol biosynthesis in *S. cerevisiae*

## SELECTED COMPUTATIONAL PROJECTS

**Proteome-Aware Peptide Design** — Developing a computational framework for proteome-scale off-target screening of designed peptide binders to improve specificity and prioritize candidates for experimental validation

**CZI CELLxGENE Protein Interaction Screen** — Screening several thousand co-expressed protein pairs selected from single-cell transcriptomic data using AlphaFold and Boltz to identify candidate physical protein interactions for experimental follow-up.

**Bits to Binders | BioML Society** — Developed a Boltz-based structural modeling workflow to predict ~12,000 submitted binder-CD20 complexes for large-scale evaluation of AI-designed CAR-T candidates

## PUBLICATIONS

---

1. **Gardner TP**, Prolomova A, Lee C, Marcotte EM, Wallingford JB. Predicted structure of the complete CPLANE complex reveals novel interactors and mechanisms of Jbts17 during ciliogenesis. *bioRxiv*. 2026. doi:10.64898/2026.10.05.756796. In revision at *Molecular Biology of the Cell*.
2. Cox RM, Papoulas O, Shril S, Lee C, **Gardner TP**, Ansari ZT, Battenhouse AM, Lee M, Drew K, McWhite CD, Yang D, Leggere JC, Durand D, Hildebrandt F, Wallingford JB, Marcotte EM. A protein interactome for the last eukaryotic common ancestor illuminates the biochemical basis of modern genetic diseases. *Cell Genomics*. 2026;6(6):101254. doi:10.1016/j.xgen.2026.101254.
3. Kosonocky CW, Abel AM, Feller AL, Cifuentes Rieffer AE, Woolley PR, Lála J, Barth DR, **Gardner T**; Bits to Binders Competitors; Ekker SC, Ellington AD, Wierson WA, Marcotte EM. Validation and analysis of 12,000 AI-driven CAR-T designs in the *Bits to Binders* competitions. *bioRxiv*. 2026. doi:10.64898/2026.03.03.709355.
4. Hofe P, Harrington A, **Gardner T**, DiNardo S, Anllo L. The Tbx1 ortholog *org-1* is required to establish testis stem cell niche identity in *Drosophila*. *Development*. 2026;153(1). doi:10.1242/dev.204914.
5. Vazquez N, Lee C, Valenzuela I, Phan TP, Derderian C, ... **Gardner TP**, ... Wallingford JB. The human ciliopathy protein RSG1 links the CPLANE complex to transition zone architecture. *Nature Communications*. 2025;16(1):5701. doi:10.1038/s41467-025-61005-8.

## LEADERSHIP

---

### Nucleate

Jan 2024 - Present

Regional Director, Texas; Co-Managing Director, Austin

- Lead Nucleate's Texas region, coordinating ~50 student leaders across Austin, Dallas, Houston, and San Antonio to operate biotech venture-building programs, founder programming, and ecosystem partnerships
- Direct the Austin chapter and the **Activator**, Nucleate's equity-free accelerator for academic biotechnology ventures, recruiting scientific founders and interdisciplinary contributors and connecting teams with investors, industry experts, and entrepreneurial resources
- Develop statewide **fundraising and strategic partnerships** with universities, foundations, biotechnology companies, investors, and service providers to support accelerator programming and Texas-wide initiatives
- Organize major ecosystem programs and events, including **Texas Demo Day, SXSW programming, the Nucleate Global Summit, and undergraduate entrepreneurship initiatives**, connecting researchers, founders, investors, and industry leaders across the Texas biotechnology ecosystem

## AWARDS & FELLOWSHIPS

---

NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award (F31) NIGMS — 2026-Present

UT Austin Graduate Dean's Prestigious Fellowship Supplement — 2025

NSF Graduate Research Fellowship Program, Honorable Mention — 2024

## SKILLS

---

**Computational:** Python, R/tidyverse, Bash, Linux, Git, HPC/SLURM, AlphaFold/AlphaFold-Multimer, structural bioinformatics, proteomics, quantitative image analysis

**Experimental:** Molecular cloning, CRISPR/Cas9, co-IP/MS, proximity labeling, confocal microscopy, *Xenopus laevis*, *Tetrahymena thermophila*, *Drosophila melanogaster*