ALEXANDRO E. TREVIÑO, PH. D.

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Location: Lexington, KY

SUMMARY

Multidisciplinary scientist, mentor, and group leader with 15 years of experience studying gene regulation, neural development, and oncology. Consistent high impact at every career stage, including over 12,000 citations from 20+ peer-reviewed articles and directing research for a $200M early stage company. Bridge-builder between research and engineering; laboratory and computational biology; academia and industry. Thought leader and strategist with a special dedication to connecting and motivating technical experts across fields.

EDUCATION

Stanford University, Palo Alto, CA
Ph. D., Department of Bioengineering — December 2020
Thesis: "Gene regulation and the physical genome." Advisor: William J. Greenleaf, Ph. D.
M.S., Department of Bioengineering — June 2017

Harvard College, Cambridge, MA
B.A., *cum laude*, Neurobiology — May 2012
Thesis: "The contribution of secretory leukocyte protease inhibitor to the generation and maintenance of inflammatory pain." Advisor: Clifford J. Woolf, M.D., Ph. D.

AWARDS

Siebel Scholars Award	2019
Weiland Family Fellowship	2016
National Science Foundation Graduate Research Fellowship	2015
Stanford Bioengineering Fellowship	2014
Stanford Office of the Provost EDGE-STEM Fellowship	2014
Most Outstanding Poster, Broad Institute Retreat	2013
Captain Jonathan Fay Prize Nominee	2012
Thomas T. Hoopes Harvard Undergraduate Thesis Prize	2012
Summa Thesis Honors	2012
Plenary Lecture award at National Collegiate Research Conference	2012

EXPERIENCE

Enable Medicine — 2021-present
Head of Research

- Proposed and drove the creation of a cross-functional drug development pipeline, leveraging in situ spatial profiling, human-centric data, and computing infrastructure to derive target hypotheses.
- Planned and began execution of company-level strategy, resource allocation, and scientific roadmap towards establishing multiple drug assets by 2025.

Lead Scientist

- Directed the scientific roadmap for a team of machine learning experts focused on high-parameter data integration techniques, multimodal biological search, and data infrastructure.
- Conceived of original research projects that led to publication in peer reviewed journals and invited talks at biotech and biopharma companies.

- Served as manager and mentor to 15 scientists, including 5 full time employees, 3 doctoral or postdoctoral trainees conducting studies in collaboration with Enable, and 7 summer interns.
- Established and led collaborations with key academic centers towards the goal of demonstrating the value of Enable research and growing a unique atlas of human patient samples.

Scientist

- Designed and developed an R software to retrieve, store, and analyze spatial biology data, including novel tools to study cell-cell interactions, cell neighborhoods, and spatial heterogeneity.
- Applied neural networks to highly multiplexed immunofluorescence image datasets to characterize disease-associated cellular niches and impute protein expression.
- Designed and set up wet lab for generating multiplexed spatial proteomic data at scale. Established and guided best practices in the lab for young team.

William Greenleaf Lab – Stanford Dept. of Genetics 2015-2021
Ph. D. Student
Jointly advised by Howard Chang M.D./Ph. D

- Charted chromatin accessibility and gene expression in long-term, stem cell-derived 3D organoid model of human forebrain development, as well as in primary human cerebral cortex. Leveraged genomics assays and bioinformatic techniques to uncover gene-regulatory relationships and disease risk pathways at difficult-to-study stages of human brain development.
- Advanced new methods to measure physical features of the genome, including DNA structural transitions and unconstrained supercoils, and designed natural and engineered systems to test the effects of torsional strain on chromatin structure and gene expression in living cells.
- Discovered how the chromatin architecture of dinoflagellates is shaped by a fundamental biophysical force, namely, DNA torsional strain induced by transcription.
- Developed and optimized methods for measuring chromatin accessibility in tissues, including fresh and frozen tissues.

Feng Zhang Lab – Broad Institute of MIT and Harvard 2012-2014
Research Associate

- Rationally engineered catalytically inactive Cas9 as a robust transcriptional effector, enabling genome-wide gain-of-function screening in mammalian cells.
- Designed, tested, and optimized light-inducible transcriptional effectors, leveraging sequence-specific DNA-binding proteins and plant signaling proteins to allow optical control of mammalian transcription and epigenetic states at defined endogenous genomic loci.
- Explored strategies to improve the specificity of the RNA-guided CRISPR-Cas9 nuclease for sensitive genome editing applications.
- Participated in the preparation of five manuscripts for peer review and publication
- Performed primary mouse and rat cell cultures and virus production for various lab projects.

Clifford J. Woolf Lab – Dept. of Neurobiology, Harvard University 2010-2012
Student Researcher

- Researched the role of an endogenous protease inhibitor in the generation and maintenance of inflammatory pain during wound healing; investigated its mechanism in mouse sensory neurons and immune cells using molecular and behavioral tests
- Prepared results as an award-winning undergraduate honors thesis.

Richard R. Burgess Lab – Dept. of Oncology, University of WI-Madison 2009
Research Assistant

- Assisted investigation of treatment-resistant breast cancer using biochemical and genetic techniques; specifically, optimized quantitative protein immunoassays, made and ran nucleotide gels, and carried out site-directed mutagenesis experiments in bacterial cultures.

SELECTED PUBLICATIONS

As corresponding author:

Wu Z*, Boen JT*, Jindal S, Basu S, He S, Zou J, Sharma P, **Trevino AE.** Predictive and mechanistic signatures of immunotherapy response in hepatocellular carcinoma. (In preparation).

Wu E, Wu Z, Charville GW, Mayer AT, Trevino AE, Zou J. In silico multiplexed immunofluorescence staining from histopathology images. (In preparation).

Wu Z, Kondo A, McGrady M, Baker EAG, Wu E, Rahim MK, Bracey NA, Charu V, Cho RJ, Cheng JB, Afkarian M, Zou J, Mayer AT, **Trevino AE.** Discovery and generalization of tissue structures from spatial omics data. Cell Reports Methods. (In press).

Yu J, Wu Z, Mayer AT, **Trevino AE**, Zou J. A Multi-Granularity Approach to Similarity Search in Multiplexed Immunofluorescence Images. *Machine Learning in Computational Biology*. 2024 Jan. PMLR 240:135-147, 2024.

Baker EAG, Huang M-Y, Lam A, Rahim MK, Bieniosek MF, Wang B, Zhang NR, Mayer AT, **Trevino AE.** emObject: domain specific data abstraction for spatial omics. *BioRxiv*. 2023.06 07.543950.

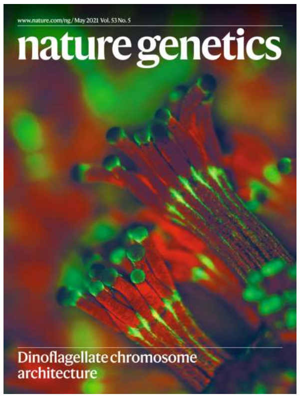
As co-first or second author:

Wu E*, **Trevino AE***, Wu Z, Swanson K, Kim HJ, D'Angio HB, Preska R, Chiou AE, Charville GW, Dalerba PD, Duvvuri U, Colevas AD, Levi J, Bedi N, Chang S, Sunwoo J, Egloff AM, Uppaluri R, Mayer AT, Zou J. 7-UP: Generating in silico CODEX from a small set of immunofluorescence markers. *PNAS Nexus*. 2023 June. 2(6)

Dayao MT, **Trevino AE**, Kim HJ, Ruffalo M, D'Angio HB, Preska R, Duvvuri U, Mayer AT, Bar-Joseph Z. *Bioinformatics*. 2023 June; 39(Supplement 1), i140-148.

Wu Z*, **Trevino AE***, Wu E, Swanson K, Kim HJ, D'Angio HB, Preska R, Charville GW, Dalerba PD, Egloff AM, Uppaluri R, Duvvuri U, Mayer AT, Zou J. Graph deep learning for the characterization of tumor microenvironments from spatial protein profiles in tissue specimens. *Nature Biomedical Engineering*. 2022 December; 6(12), 1435-1448.

Trevino AE*, Müller F*, Andersen J*, Sundaram L*, Kathiria A, Shcherbina A, Farh K, Chang HY, Pașca AM, Kundaje A, Pașca SP, Greenleaf WJ. Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. *Cell*. 2021 September; *184*, 1-17.



Marinov GK*, **Trevino AE***, Xiang T*, Kundaje A, Grossman AR, Greenleaf WJ. Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate *Brevium minutum*. *Nature Genetics*. 2021 April; **53**, 613-617

Trevino AE*, Sinnott-Armstrong NA*, Andersen J*, Yoon S-J, Huber N, Pritchard JK, Chang HY, Greenleaf WJ, Pasca SP. Chromatin accessibility dynamics in a model of human forebrain development. *Science*. 2020 Jan 24;367(6476). pii: eaay1645.

Corces RM, **Trevino AE**, Hamilton EG, Sinnott-Armstrong NA, Satpathy AT, Rubin AJ, Montine KS, Wu B, Cho SW, Mumbach MR, Carter AC, Kasowski M, Vesuna S, Orloff LA, Khavari PA, Montine TJ, Greenleaf WJ, Chang HY. Optimized ATAC-seq for chromatin accessibility in archival human tissues with sub-millimeter resolution. *Nature Methods*. 2017 Aug 28; 14:959-962.

Konermann S*, Brigham MD*, **Trevino AE**, Joung J, Abudayyeh OO, Barcena C, Hsu PD, Habib N, Gootenberg JS, Nishimasu H, Nureki O, Zhang F. Genome-scale transcriptional activation by an engineered CRISPR/Cas9 complex. *Nature*. 2015 Jan 29; 517(7536):583-8.

Trevino AE, Zhang F. Genome Editing Using Cas9 Nickases. *Methods in Enzymology*. 2014; 546:161-74.

Konermann S*, Brigham MD*, **Trevino AE**, Hsu PD, Heidenreich M, Cong L, Platt RJ, Scott DA, Church GM, Zhang F. Optical control of endogenous mammalian transcription and epigenetic states. *Nature*. 2013 Aug 22; 500(7463):472-6.

Other notable contributions:

Lemaitre L, Adeniji N, Suresh A, Reguram R, Zhang J, Park J, Reddy A, **Trevino AE**, Mayer AT, Deutzmann A, Hansen A, Tong L, Arjunan V, Kambham N, Visser B, Dua M, Bonham A, Kothary N, D'Angio HB, Preska R, Rosen Y, Zou J, Charu V, Felsher DW, Dhanasekaran R. *Nature Cancer*. (In press).

Balood M, Ahmadi M, Eichwald T, Ahmadi A, Majdoubi A, Roversi K, Roversi K, Lucido CT, Restaino AC, Huang S, Ji L, Huang K-C, Semerena E, Thomas SC, **Trevino AE**, Merrison H, Parrin A, Doyle B, Vermeer DW, Spanos WC, Williamson CS, Seehus CR, Foster SL, Dai H, Shu CJ, Rangachari M, Thibodeau J, Del Rincon SV, Drapkin R, Rafei M, Ghasemlou N, Vermeer PD, Woolf CJ, Talbot S. Nociceptor neurons affect cancer immunosurveillance. *Nature*. 2022 November; 611(7935):405-412

Tycko J, Wainberg M, Marinov GK, Ursu O, Hess GT, Ego BK, Aradhana, Li A, Truong A, **Trevino AE**, Spees K, Yao D, Kaplow IM, Greenside PG, Morgens DW, Phanstiel DH, Snyder MP, Bintu L, Greenleaf WJ, Kundaje A, Bassik MC. Identification and mitigation of pervasive off-target activity in CRISPR-Cas9 screens for essential non-coding elements. *Nature Communications*. 2019 Sep 6; 10(1):4063.

Wu X, Scott DA*, Kriz AJ*, Chiu AC, Hsu PD, Dadon DB, Cheng AW, **Trevino AE**, Konermann S, Chen S, Jaenisch R, Zhang F, Sharp PA. Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells. *Nature Biotechnology*. 2014 Jul; 32(7):670-6.

Ran FA*, Hsu PD*, Lin CY, Gootenberg JS, Konermann S, **Trevino AE**, Scott DA, Inoue A, Matoba S, Zhang Y, Zhang F. Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. *Cell*. 2013 Sep 12; 154(6):1380-9.

** = equal contribution*

PATENTS

Konermann S, **Trevino AE**, Brigham MD, Ran FA, Hsu PD, Lin CY, Nureki O, Nishimasu H, Ishitani R, Zhang F. Systems, methods and compositions for sequence manipulation with optimized functional crispr-cas systems. US Patent Application 15/179,912. Jun 2016.

Zhang F, Konermann S, Brigham MD, **Trevino AE**. Functional screening with optimized crispr-cas systems. US Patent Application 15/469,081. Mar 2017

INVITED TALKS

Bristol Myers Squibb, Cambridge MA	July 2024
Novartis Institutes for Biomedical Research, Cambridge MA	July 2024
James P. Allison Institute, MD Anderson Cancer Center, Houston TX	May 2024
International Society for Autism Research Annual Meeting, Austin TX	May 2022
Cell Circuits Seminar, The Broad Institute	March 2021

RESULTS PRESENTED

Trevino AE, Mueller F, Andersen JA, Sundaram L, Yoon S-J, Huber N, Pritchard JK, Chang HY, Greenleaf WJ, Pasca SP. Interpreting non-coding de novo variants in autism spectrum disorder. *International Society for Autism Research 2022*.

Trevino AE, Sinnott-Armstrong NA, Andersen JA, Yoon SE, Huber N, Pritchard JK, Chang HY, Greenleaf WJ, Pasca SP. Mapping chromatin accessibility dynamics in human forebrain development. *Cold Spring Harbor Labs: Development & 3-D Modeling of the Human Brain 2019*, *Centers for Excellence in Genomic Science 2019*.

Trevino AE, Sinnott-Armstrong NA, Andersen JA, Yoon SE, Pasca SP, Greenleaf WJ. Chromatin dynamics in a 3D organoid model of human forebrain development. *Society for Neuroscience 2019*.

Trevino AE, Sinnott-Armstrong NA, Greenleaf WJ. DNA Supercoiling as a Gene Regulatory Mechanism. *Stanford Bioengineering Retreat 2017*.

Konermann S*, **Trevino AE**, Brigham MD*, Hsu PD, Heidenreich M, Cong L, Platt RJ, Scott DA, Church GM, Zhang F. Optical control of endogenous mammalian transcription and epigenetic states. *American Society of Human Genetics, 2014.*

Trevino AE, Konermann S*, Brigham MD*, Hsu PD, Heidenreich M, Cong L, Platt RJ, Scott DA, Church GM, Zhang F. Optical control of endogenous mammalian transcription and epigenetic states. Most Outstanding Poster *at Broad Retreat, 2013.*

Trevino A, Robson V, Cobos EJ, Ma CH, Ding A, Ghasemlou N, Woolf CJ. The contribution of secretory leukocyte protease inhibitor to the generation and maintenance of inflammatory pain. *Plenary Lecture, National Collegiate Research Conference, 2012.*

Robson V, **Trevino A**, Ma CH, Cobos EJ, Ding A, Ghasemlou N, Woolf CJ. Behavioral and histological characterization of pathogen- and sterile tissue injury-based inflammatory pain. *Poster, Harvard Immunology Summer Program, 2011.*

TEACHING & MENTORSHIP

Direct Mentorship at Enable Medicine 2020-2024

- Zhenqin Wu (Scientist)
- Ethan AG Baker (Scientist)
- Benjamin Chidester (Scientist)
- Monee McGrady (Associate Scientist)
- Meng-Yao Rita Huang (Associate Scientist)
- Monica Dayao (Graduate Student, Carnegie Mellon University)
- Siyu He (Postdoctoral Scholar, Stanford University)
- Eric Wu (Graduate Student, Stanford University)
- Rishabh Sharma (Intern)
- Jairam Hathwar (Intern)
- Jennifer Yu (Intern)
- Nirva Vakharia (Intern)
- Julia Wang (Intern)
- Nicolas Nitko (Intern)
- Kalyan Palepu (Intern)

Direct Mentorship at Stanford University 2016-2019

- Michaela Hinks (Graduate Student, Bioengineering)
- Samuel Kim (Graduate Student, Genetics)
- Nasa Sinnott-Armstrong (Graduate Student, Genetics)
- Olivia Gautier (Rotation Graduate Student, Neuroscience)
- Robin Meyers (Rotation Graduate Student, Genetics)
- David Yao (Rotation Graduate Student, Genetics)
- Josh Tycko (Rotation Graduate Student, Genetics)
- Hanalei Pham (High School Student, SIMR Program)
- Shalin Shah (High School Student, Independent)
- Rajiv Movva (High School Student, Independent)

Teaching Assistant 2015-2017

- BioE 80 – Introduction to Bioengineering
- BioE 301A – Molecular and Cellular Engineering Lab

Peer Tutor – Harvard Bureau of Study Council 2011-2012

- Molecular & Cellular Biology 115 – Cellular Basis of Neuronal Function
- Life Sciences 1a – An Integrated Introduction to the Life Sciences

ADDITIONAL

- Fluent in Mexican Spanish
- Touring performer and musician

REFERENCES

William J. Greenleaf
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