

# Albert Tian Chen

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## EDUCATION

**Harvard University, Harvard Medical School, Division of Medical Sciences** 2022 – Present  
Doctoral (PhD) student in Biological and Biomedical Sciences (BBS)

**Northeastern University, College of Engineering** 2015 – 2020  
Bachelor of Science in Bioengineering 3.73 / 4.0 GPA (3.91 / 4.0 Major GPA)

## RESEARCH EXPERIENCE

**Gu Lab, Harvard Medical School** *Graduate Research Assistant* 7/2023 – Present  
<https://gu.hms.harvard.edu/>

**Vector Engineering Lab** *Senior Computational Associate* 5/2021 – 7/2022  
**Broad Institute of MIT and Harvard** *Associate Computational Biologist* 5/2020 – 5/2021  
<https://vector.engineering> *Bioinformatics Co-op* 5/2019 – 12/2019

- ▶ Author on 2 papers (lead author on 1), author for 2 more manuscripts in preparation. Key contributor of data analysis, figure creation, and manuscript writing for our lab's projects in adeno-associated virus (AAV) capsid engineering for gene therapy in the central nervous system.
- ▶ Initiated, organized, and led a Capstone project with six Northeastern University students. Generated and helped students analyze single-cell transcriptome sequencing (scRNA-seq) data of AAV-producing cells, aiming to identify genes affecting AAV production. Currently exploring dynamics of AAV production, using imaging, fluorescence-activated cell sorting (FACS), qPCR, and bulk RNAseq.
- ▶ Created COVID CG (<https://covidcg.org>), a tool for visualizing, filtering, and downloading mutations in over 10M+ SARS-CoV-2 genomes. COVID CG has been visited 50,000+ times by users from over 180 countries. Fielded questions from news outlets and helped scientists from international government agencies analyze data from our site. Assisted in securing funding from AstraZeneca.
- ▶ Developing a centralized database and analysis engine for querying and analyzing 20 TB+ of AAV library screening next-generation sequencing (NGS) data.

**Slavov Lab, Northeastern University** (<https://slavovlab.net>) *Research Assistant* 7/2016 – 5/2019

- ▶ Lead author on 2 papers, DART-ID (<https://dart-id.slavovlab.net>), a Bayesian framework for increasing peptide identification rates in single cell mass spectrometry proteomics data, and DO-MS (<https://do-ms.slavovlab.net>), a modular, extensible, and automated data analysis/QC platform for rationally optimizing mass spectrometry experiments.
- ▶ Awarded \$8000 in university fellowships support P-SCoPE (Single cell phosphoproteomics by mass spectrometry), a modification of the Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) method (<https://scope2.slavovlab.net>). Designed and ran LC/MS proteomics experiments, from cell culture to instrument operation. Analyzed data and optimized sample prep and mass spectrometer instrument parameters.
- ▶ Organized and ran weekly programming office hours for students and RAs in the lab. Tutored 2 RAs in programming basics, data analysis, and data visualization.

**Waters Corporation, Separations R&D** *Chemistry Co-op* 7/2017 – 12/2017

- ▶ Prototyped high-throughput LC/MS workflow that doubled throughput to 4800 samples/day, through hardware/firmware modifications to existing instrumentation, low-level C++ data processing code, and an online data visualization dashboard.

## PUBLICATIONS

Witte I, Lampe GD, Eitzinger S, ..., **Chen AT**, ..., Sternberg SH, Liu DR. Programmable gene insertion in human cells with a laboratory-evolved CRISPR-associated transposase. *Science* (2025). <https://doi.org/10.1126/science.adt5199>

Huang Q, ..., **Chen AT**, ..., Deverman BE. An AAV capsid reprogrammed to bind human Transferrin Receptor mediates brain-wide gene delivery. *Science* (2024). <https://doi.org/10.1126/science.adm8386>

Eid F, **Chen AT**, Chan KY, Huang Q, Zheng Q, Tobey IG, Pacouret S, Brauer PP, Keyes C, Powell M, Johnston J, Zhao B, Lage K, Tarantal AF, Chan YA, Deverman BE. Systematic multi-trait AAV capsid engineering for efficient gene delivery. *Nature Communications* (2024). <https://doi.org/10.1038/s41467-024-50555-y>

Huang Q, **Chen AT**, Chan KY, Sorensen H, Barry AJ, Azari B, Zheng Q, Beddow T, Zhao B, Tobey IG, Moncada-Reid C, Eid F, Walkey CJ, Ljungberg MC, Lagor WR, Heaney JD, Chan YA, Deverman BE. Targeting AAV vectors to the CNS via de novo engineered capsid-receptor interactions. *PLOS Biology* (2023). <https://doi.org/10.1371/journal.pbio.3002112>  
GitHub: [https://github.com/vector-engineering/AAV\\_capsid\\_receptor](https://github.com/vector-engineering/AAV_capsid_receptor)

Wilkins D, ..., **Chen AT**, ..., Yun KW. Nirsevimab binding-site conservation in respiratory syncytial virus fusion glycoprotein worldwide between 1956 and 2021: an analysis of observational study sequencing data. *The Lancet Infectious Diseases* (2023). [https://doi.org/10.1016/S1473-3099\(23\)00062-2](https://doi.org/10.1016/S1473-3099(23)00062-2)

Krolak T, Chan KY, Kaplan L, Huang Q, Wu J, Zheng Q, Kozareva V, Beddow T, Tobey IG, Pacouret S, **Chen AT**, Chan YA, Ryvkin D, Gu C, Deverman BE. A high-efficiency AAV for endothelial cell transduction throughout the central nervous system. *Nature Cardiovascular Research* (2022) <https://doi.org/10.1038/s44161-022-00046-4>

**Chen AT**, Altschuler K, Zhan SH, Chan AY, Deverman BE. COVID-19 CG: Tracking SARS-CoV-2 mutations by locations and dates of interest. *eLife* (2021) <https://doi.org/10.7554/eLife.63409>  
Website: <https://covidcg.org>

**Chen AT**, Franks A, Slavov N. DART-ID increases single-cell proteome coverage. *PLOS Computational Biology* (2019) <https://doi.org/10.1371/journal.pcbi.1007082>  
Website: <https://dart-id.slavovlab.net>

Huffman RG\*, **Chen AT**\*, Specht H\*, Slavov N. DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. *Journal of Proteome Research* (2019) <https://doi.org/10.1021/acs.jproteome.9b00039>  
\*Contributed equally. Website: <https://do-ms.slavovlab.net>

## AWARDS / FELLOWSHIPS

- 2025 Best Poster Award, 2025 Volume Electron Microscopy Gordon Research Conference
- 2024–2026 John S. LaDue Memorial Fellowship in Cardiovascular Medicine / Vascular Biology Research  
Full support for two years + research support
- 2021 Broad Institute Excellence in Science & Engineering Award
- 2021 Broad Institute Spot Award, Student/Employee Recognition Program
- 2020 NSF Graduate Research Fellowships Program (GRFP), Honorable Mention
- 2019 Summer Scholars Independent Research Fellowship, Northeastern University (\$5000)
- 2018 Advanced Research/Creative Endeavor Award, Northeastern University (\$3000)
- 2018 ASBMB Active Site Poster / Travel Award Winner
- 2018 Bioengineering Research Achievement Award, Northeastern University
- 2015–2020 Dean's List, Dean's Merit Scholarship, Northeastern University

## PRESENTATION HIGHLIGHTS

- Poster* **Chen AT**, ..., Hess H, Bleck C, Weigel A, Gu C, Pedram K. Optimized rapid high pressure freezing of mouse tissue for the preservation of physiological extracellular space. Presented at 2025 Volume Electron Microscopy Gordon Research Conference/Seminar
- Presentation* **Chen AT**, Altschuler K, Favela D, Zhan SH, Chan AY, Deverman BE. COVID CG: SARS-CoV-2 mutation tracking and genomic data visualization. Presented at PyData Boston April 2021 (Virtual - Online)  
Video: <https://www.youtube.com/watch?v=G744eRCdAYo>
- Oral Abstract* **Chen AT**, Altschuler K, Zhan SH, Chan AY, Deverman BE. COVID-19 CG: Tracking SARS-CoV-2 by Mutation, Location, and Date of Interest. Presented at ASGCT COVID-19 Symposium, September 2020 (Online).
- Presentation* **Chen AT**, Franks A & Slavov N. DART-ID Increases Single-Cell Proteome Coverage. Presented at Single Cell Proteomics (SCP) Conference, June 2019, Boston MA  
Video: <https://www.youtube.com/watch?v=IW easlXs5F0>  
Slides: [https://atchen.me/images/DART\\_SCP\\_v3.pptx](https://atchen.me/images/DART_SCP_v3.pptx)
- Poster* **Chen AT**, Franks A & Slavov N. DART-ID Increases Single-Cell Proteome Coverage. Presented at Experimental Biology (EB) as part of ASBMB, April 2019, Orlando FL  
PDF: [https://atchen.me/images/DART\\_poster\\_v6.pdf](https://atchen.me/images/DART_poster_v6.pdf)

## TECHNICAL SKILLS

### Programming

- Advanced* Python, R, Vega, JavaScript, HTML/CSS
- Proficient* MATLAB, LaTeX, SQL, PL/pgSQL, bash

### Software / Libraries

- Python* multiprocessing, numpy, scipy, pandas, scikit-learn, matplotlib, snakemake, networkx, flask
- R* dplyr/tidyverse ecosystem, ggplot, shiny, LIGER, Seurat
- Sequencing* bcl2fastq, fastqc, bowtie2, minimap2, STAR, kallisto, samtools, pysam, IGV, cellranger
- JavaScript* node.js, React, MobX, Vega, Webpack, Vue.js
- HPC* Google Cloud (Compute Engine, Storage, SQL, Run, Functions), Slurm, UGE
- Other* PyMOL, SnapGene, Fiji (ImageJ), CellProfiler, Ilastik, MaxQuant, Adobe Photoshop, Adobe Illustrator, git, Linux (Ubuntu, CentOS), Docker, STAN, PostgreSQL

### Laboratory

Basic mouse handling, Injections (TV, Stereotax), Mammalian cell culture (suspension and adherent), HPF/FS operation (Leica), TEM operation (JEOL 1200), EM sample preparation (embedding, sectioning), Vector assembly + cloning, Transfection, PCR, FACS (Sony SH800z, MA900), IF/IHC, Tissue sectioning, Illumina sample prep, RNAseq (Bulk, 10X), Proteomics sample prep, LC/MS operation + maintenance

### Hands-On

Shop and hand tools, Basic bench electronic equipment, Computer building and repair

## OTHER EXPERIENCE

### Journal of Medical Insight (<https://jomi.com>)

*Lead Web Developer* 6/2014 – 9/2016

- ▶ In 3 months and with no prior web development experience, created journal website for viewing instructional surgical videos and managing article content.
- ▶ Assisted in filming live surgeries with video team.

### Bikeway Source

*Sales Associate / Bike Mechanic* 8/2012 – 6/2014

- ▶ Performed bike repair, facility construction, sales, and customer service.

## ***RELEVANT COURSEWORK***

### **Biology & Chemistry**

HMS: Genetics, Molecular Biology, Cell Biology, Experimental Design

NEU: Organic Chem. 1+2, Biochem., Molecular Engineering, Cellular Engineering, Tissue Engineering

### **Math / Statistics**

Statistical Inference (Harvard, STAT 111), Supervised Machine Learning (Audited), Unsupervised Machine Learning (Audited), Dynamic Modeling in Systems Biology, Differential Equations, Statistics (MIT OCW 18.05), Linear Algebra (MIT OCW 18.06)

### **Physics**

Physics 1 & 2, Statics and Dynamics, Transport and Fluids, Circuits and Signal Processing