# **Augustine George Chemparathy**

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#### **EDUCATION**

# Stanford University, Stanford, CA

- BS, Bioengineering and Computer Science, Phi Beta Kappa, with Distinction, 2015-2019
- MS, Management Science and Engineering, Health Systems Modeling and Policy track, 2019-2021
- MD, scholarly concentration in Informatics and Data-Driven Medicine, 2021-2025
- Relevant coursework: Precision Practice with Big Data (BIOMEDIN 205), Mathematical Models and Medical Decisions (BIOMEDIN 219), Machine Learning Approaches for Data Fusion in Biomedicine (BIOMEDIN 221), Intermediate Biostatistics: Regression, Prediction, Survival Analysis (EPI 262)

#### **EXPERIENCE**

#### Greicius Lab, Stanford Center for Memory Disorders, Research Assistant

January 2022-Present

- Used computational tools to identify large genetic variants from long-read sequencing of patients at the Stanford Alzheimer's Disease Research Center (ADRC).
- Published two co-first author research papers in Neuron and Neurology Genetics (see Publications)
- Received a Top 10 presentation award at the 2023 Stanford Medical Student Research Symposium

### Qi Lab, Stanford Bioengineering, Research Assistant

September 2019-December 2021

- Used bioinformatic tools to search bacterial and archaeal genomes for novel DNA-cutting enzymes. These enzymes can provide an alternative to CRISPR-Cas for use in gene therapies.
- Developed a bioinformatic method to target a broad spectrum of RNA viruses with a minimal set of Cas13d guides. Created the website crispr-pacman.stanford.edu to make antiviral crRNA sets available to the research community.

#### Systems Utilization Research for Stanford Medicine (SURF), Research intern March 2018-August 2021

Designed and evaluated a electronic health record dashboard at Stanford Children's Hospital to increase
adherence to the central line-associated bloodstream infection (CLABSI) prevention bundle. In the 15
months after the dashboard was deployed, adherence to the entire CLABSI bundle across the hospital
increased from 25% to 44%.

## Dror Lab, Stanford Computer Science, Research intern

June 2017-January 2020

- Developed a data analysis tool to gather insights from noncovalent interaction data from molecular dynamics (MD) simulations. Available at getcontacts github.io.
- Optimized ComBind, a software package for ranking ligand docking poses. Used ligands that do not bind to an enzyme in order to improve pose ranking for ligands that bind to the enzyme.

#### Arbor Biotechnologies, Software engineering intern

June 2019-September 2019

 Identified novel CRISPR/Cas proteins using Arbor's metagenomic database. Developed a machine learning model to predict which computational hits were most likely to function as biologically active CRISPR effectors.

#### **ACTIVITIES**

# Neurology Free Clinic Co-coordinator, Stanford Medical School

March 2024-March 2025

Coordinate Stanford's student-run free Neurology clinic. Developed a referral screener enabling general clinic providers to identify patients who would benefit from referral to Neurology.

Ophthalmology Free Clinic Co-coordinator, Stanford Medical School March 2022-March 2023 Coordinated Stanford's student-run free Ophthalmology clinic. Recruited residents and preclinical volunteers and communicate with patients. Introduced an EHR prompt to encourage providers to refer diabetic patients for retinopathy screening

Writing Tutor, Stanford Hume Center for Writing And Speaking

Assist undergraduate and graduate students at Stanford with all stages of the writing process for conference publications, theses, term papers, applications, and other academic writing pieces.

# **Co-President, Stanford Students in Biodesign (SSB)**May 2017-June 2019 Coordinate recruitment, activities, and club organization for Stanford's largest undergraduate organization for interdisciplinary biosciences.

**Teaching Assistant, Linear Dynamical Systems (EE 263), Stanford University**Sept 2017-Dec 2017
Held office hours, wrote midterm problems, and graded exams for 135 students in Stanford's highest-enrollment electrical engineering course.

#### **HONORS AND AWARDS**

#### **PUBLICATIONS**

- Chemparathy, A.\*, Le Guen, Y.\*, Zeng, Y., Gorzynski, J., Jensen, T., Yang, C., Kasireddy, N., Talozzi, L., Belloy, M., Stewart, I., et al. (2024). A 3 UTR insertion is a candidate causal variant at the TMEM106B locus associated with increased risk for FTLD-TDP. *Neurology: Genetics*. (\*these authors contributed equally)
- Chemparathy, A.\*, Le Guen, Y.\*, Chen, S., Lee, E., Leong, L., Gorzynski, J., Jensen, T., Ferrasse, A., Xu, G., Xiang, H., et al. (2024). APOE loss-of-function variants: Compatible with longevity and associated with resistance to Alzheimer's Disease pathology. *Neuron*. (\*these authors contributed equally)
- Ward, A., Chemparathy, A., Seneviratne, M., Gaskari, S., Mathew, R., Wood, M., Donnelly, L., Lee, G., Scheinker, D., Shin, A., et al. (2023). The Association Between Central Line-Associated Bloodstream Infection and Central Line Access. *Critical Care Medicine*.
- Lin, X., Liu, Y., Liu, S., Zhu, X., Wu, L., Zhu, Y., Zhao, D., Xu, X., **Chemparathy, A.**, Wang, H., et al. (2022). Nested epistasis enhancer networks for robust genome regulation. *Science*.
- Zeng, L., Liu, Y., Nguyenla, X., Abbott, T., Han, M., Zhu, Y., Chemparathy, A., Lin, X., Chen, X., Wang, H., et al. (2022). Broad-spectrum CRISPR-mediated inhibition of SARS-CoV-2 variants and endemic coronaviruses in vitro. *Nature Communications*.
- Guo, L., Bian, J., Davis, A., Liu, P., Kempton, H., Zhang, X., Chemparathy, A., Gu, B., Lin, X., Rane, D., et al. (2022). Multiplexed genome regulation in vivo with hyper-efficient Cas12a. *Nature Cell Biology*.
- Paggi, J., Belk, J., Hollingsworth, S., Villanueva, N., Powers, A., Clark, M., Chemparathy, A., Tynan, J., Lau, T., Sunahara, R., et al. (2021). Leveraging nonstructural data to predict structures and affinities of protein–ligand complexes. *Proceedings of the National Academy of Sciences*.
- Xu, X., Chemparathy, A., Zeng, L., Kempton, H., Shang, S., Nakamura, M., Qi, L., et al. (2021). Engineered miniature CRISPR-Cas system for mammalian genome regulation and editing. *Molecular Cell*.
- Chemparathy, A., Seneviratne, M., Ward, A., Mirchandani, S., Li, R., Mathew, R., Wood, M., Shin, A., Donnelly, L., Scheinker, D., et al. (2021). Development and implementation of a real-time bundle-adherence dashboard for central line-associated bloodstream infections. *Pediatric Quality & Safety*.

- Lin, X.\*, Liu, Y.\*, Chemparathy, A.\*, Pande, T., La Russa, M., Qi, L., et al. (2021). A comprehensive analysis and resource to use CRISPR-Cas13 for broad-spectrum targeting of RNA viruses. *Cell Reports Medicine*. (\*these authors contributed equally)
- Lin, X., Chemparathy, A., La Russa, M., Daley, T., Qi, L., et al. (2020). Computational methods for analysis of large-scale CRISPR screens. *Annual Review of Biomedical Data Science*.
- Abbott, T., Dhamdhere, G., Liu, Y., Lin, X., Goudy, L., Zeng, L., **Chemparathy, A.**, Chmura, S., Heaton, N., Debs, R., et al. (2020). Development of CRISPR as an antiviral strategy to combat SARS-CoV-2 and influenza. *Cell*.
- Venkatakrishnan, A., Fonseca, R., Ma, A., Hollingsworth, S., **Chemparathy, A.**, Hilger, D., Kooistra, A., Ahmari, R., Babu, M., Kobilka, B., et al. (2019). Uncovering patterns of atomic interactions in static and dynamic structures of proteins. *BioRxiv*.