Yu Zhang, Ph.D.

Postdoctoral Research Fellow
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Focus: Genome-to-Drug: rapid, genome-guided antibiotic discovery that outputs synthesis-ready candidates with early toxicity risk control.
Selected Impact: 17 peer-reviewed journal articles (7 first-author), spanning AI drug discovery and systems pharmacology.

Research Experience

Postdoctoral Research Fellow — **2024 – Present**
Collins Lab, Wyss Institute (Harvard), MIT, and Broad Institute — *Cambridge, MA*

- **Multitask Learning Architect:** Designed and led the development of multitask toxicity prediction models and filtering rules that prioritize non-toxic antibiotic candidates for experimental follow-up (under review).
- **Generative Antibiotic Design:** Contributed to the generative design and experimental validation pipeline for *de novo* antibiotics; performed bacterial cytological profiling (microscopy) and image/data analysis to quantify antibiotic stress phenotypes.

Ph.D. Candidate — **2017 – 2024**
Popel Systems Biology Laboratory, Johns Hopkins University — *Baltimore, MD*

- **Mechanistic Modeling Lead:** Conceived and led the development of mechanistic ODE models of VEGF, Ang-Tie, and integrin signaling to reveal non-intuitive therapeutic targets for vascular stability.
- **QSP Platform Development:** Built and deployed multi-scale biophysical platforms that predict drug efficacy and guide dosing strategies for sickle cell anemia and ischemic diseases.

Industry QSP Intern — **Summer 2022**
CytomX Therapeutics — *South San Francisco, CA*

- **Clinical Translation:** Developed clinical QSP models for Probody™ therapeutics used to support dose selection and define safety margins in immuno-oncology trials.

Education

Ph.D. in Biomedical Engineering (GPA: 4.0/4.0) — **2017 – 2024**
Johns Hopkins University School of Medicine — *Baltimore, MD*

B.S. in Biomedical Engineering & Applied Mathematics — **2013 – 2017**
Johns Hopkins University — *Baltimore, MD*
(*Minor: Spanish, GPA: 3.96/4.0; General & Departmental Honors*)

Selected Publications & Manuscripts

A generative deep learning approach to de novo antibiotic design. *Cell* (2025)
Krishnan A*, Anahtar MN*, Valeri JA*, ..., **Zhang Y**, ... and Collins JJ.
Impact: First demonstration of generative deep learning yielding experimentally validated antibiotic candidates.
Role: Performed bacterial cytological profiling (microscopy) and image-based analysis.

Multitask learning enables discovery of nontoxic antibiotics. (in peer review at *Nature Biotechnology*, 2025)
Zhang Y*, Hennes A*, Krishnan A* ... and Collins JJ.
Impact: Establishes a multitask model for toxicity prediction to overcome a primary bottleneck in drug discovery.

Deep learning-enabled discovery of antibiotics effective against *Neisseria gonorrhoeae*. (provisionally accepted at *Science Translational Medicine*, 2024)
Anahtar MN*, Valeri JA*, Modaresi SM*, ..., **Zhang Y**, ... and Collins JJ.
Impact: Demonstrates a deep learning–guided discovery that delivers antibiotics against drug-resistant *N. gonorrhoeae*.

* indicates co–first authors.

Full Publication List

Peer-reviewed articles

[1] **Yu Zhang**, Christopher D Kontos, Brian H Annex, and Aleksander S Popel. Promoting vascular stability through Src inhibition and Tie2 activation: A model-based analysis. *iScience* **28**.6 (**2025**).

[2] Alberto Ippolito, Hanwen Wang, **Yu Zhang**, Vahideh Vakil, Hojjat Bazzazi, and Aleksander S Popel. Eliciting the antitumor immune response with a conditionally activated PD-L1 targeting antibody analyzed with a quantitative systems pharmacology model. *CPT: Pharmacometrics & Systems Pharmacology* **13**.1 (**2024**), pp. 93–105.

[3] Alberto Ippolito, Hanwen Wang, **Yu Zhang**, Vahideh Vakil, and Aleksander S Popel. Virtual clinical trials via a QSP immuno-oncology model to simulate the response to a conditionally activated PD-L1 targeting antibody in NSCLC. *Journal of Pharmacokinetics and Pharmacodynamics* **51**.6 (**2024**), pp. 747–757.

[4] Geli Li, Yuchen Ma, Sujie Zhang, Wen Lin, Xinyi Yao, Yating Zhou, Yanyong Zhao, Qi Rao, Yuchen Qu, Yuan Gao, Lianmin Chen, **Yu Zhang**, et al. A mechanistic systems biology model of brain microvascular endothelial cell signaling reveals dynamic pathway-based therapeutic targets for brain ischemia. *Redox Biology* **78** (**2024**), p. 103415.

[5] **Yu Zhang**, Yuhao Qiang, He Li, Guansheng Li, Lu Lu, Ming Dao, George E Karniadakis, Aleksander S Popel, and Chen Zhao. Signaling-biophysical modeling unravels mechanistic control of red blood cell phagocytosis by macrophages in sickle cell disease. *PNAS nexus* **3**.2 (**2024**), pgae031.

[6] Samira Anbari, Hanwen Wang, **Yu Zhang**, Jun Wang, Minu Pilvankar, Masoud Nickaeen, Steven Hansel, and Aleksander S Popel. Using quantitative systems pharmacology modeling to optimize combination therapy of anti-PD-L1 checkpoint inhibitor and T cell engager. *Frontiers in Pharmacology* **14** (**2023**), p. 1163432.

[7] **Yu Zhang**, Aleksander S Popel, and Hojjat Bazzazi. Combining multikinase tyrosine kinase inhibitors targeting the vascular endothelial growth factor and cluster of differentiation 47 signaling pathways is predicted to increase the efficacy of antiangiogenic combination therapies. *ACS Pharmacology & Translational Science* **6**.5 (**2023**), pp. 710–726.

[8] **Yu Zhang**, Hanwen Wang, Rebeca Hannah M Oliveira, Chen Zhao, and Aleksander S Popel. Systems biology of angiogenesis signaling: Computational models and omics. *WIREs mechanisms of disease* **14**.4 (**2022**), e1550.

[9] Chen Zhao, Joshua L Heuslein, **Yu Zhang**, Brian H Annex, and Aleksander S Popel. Dynamic multiscale regulation of perfusion recovery in experimental peripheral arterial disease: a mechanistic computational model. *Basic to Translational Science* **7**.1 (**2022**), pp. 28–50.

[10] **Yu Zhang**, Christopher D Kontos, Brian H Annex, and Aleksander S Popel. A systems biology model of junctional localization and downstream signaling of the Ang–Tie signaling pathway. *npj Systems Biology and Applications* **7**.1 (**2021**), p. 34.

[11] Mohammad Jafarnejad, Richard J Sové, Ludmila Danilova, Adam C Mirando, **Yu Zhang**, Mark Yarchoan, Phuoc T Tran, Niranjan B Pandey, Elana J Fertig, and Aleksander S Popel. Mechanistically detailed systems biology modeling of the HGF/Met pathway in hepatocellular carcinoma. *npj Systems Biology and Applications* **5**.1 (**2019**), p. 29.

[12] **Yu Zhang**, Christopher D Kontos, Brian H Annex, and Aleksander S Popel. Angiopoietin-Tie signaling pathway in endothelial cells: a computational model. *iScience* **20** (**2019**), pp. 497–511.

[13] Chen Zhao, **Yu Zhang**, and Aleksander S Popel. Mechanistic computational models of microRNA-mediated signaling networks in human diseases. *International Journal of Molecular Sciences* **20**.2 (**2019**), p. 421.

[14] Hojjat Bazzazi, **Yu Zhang**, Mohammad Jafarnejad, Jeffrey S Isenberg, Brian H Annex, and Aleksander S Popel. Computer simulation of TSP1 inhibition of VEGF–akt–eNOS: an angiogenesis triple threat. *Frontiers in physiology* **9** (**2018**), p. 644.

[15] Hojjat Bazzazi, **Yu Zhang**, Mohammad Jafarnejad, and Aleksander S Popel. Computational modeling of synergistic interaction between $\alpha V\beta 3$ integrin and VEGFR2 in endothelial cells: Implications for the mechanism of action of angiogenesis-modulating integrin-binding peptides. *Journal of theoretical biology* **455** (**2018**), pp. 212–221.

[16] **Yu Zhang**, Hojjat Bazzazi, Raquel Lima e Silva, Niranjan B Pandey, Jordan J Green, Peter A Campochiaro, and Aleksander S Popel. Three-dimensional transport model for intravitreal and suprachoroidal drug injection. *Investigative Ophthalmology & Visual Science* **59**.12 (**2018**), pp. 5266–5276.

Book chapters

[1] **Yu Zhang**, Chen Zhao, and Aleksander S. Popel. "Systems biology modeling of endothelial cell and macrophage signaling in angiogenesis in human diseases". *The Vasculome*. Academic Press, **2022**, pp. 163–172.

Manuscripts under review

[1] **Yu Zhang**, Hanwen Wang, Natsuki Furukawa, Akash Patil, Theinmozhi Arulraj, and Aleksander S. Popel. Quantitative systems pharmacology model predicts enhanced antitumor efficacy of anti-CTLA-4 when combined with anti-PD-1 in syngeneic mouse model of breast cancer. *Under Review* (**2025**).

Selected Presentations

ACS Spring 2025 – Multitask Learning Enables Discovery of Nontoxic Antibiotics **2025**
Session speaker (Symposium on AI in Drug Discovery), San Diego, CA

NAVBO In-Focus Webinar – Endothelial Regulation of Microvascular Permeability **2024**
Invited webinar speaker, Virtual

Foundations of Systems Biology in Engineering (FOSBE) **2022**
Session speaker, Boston, MA

Leadership, Service & Recognition

Organizing Committee **2024 – Present**
Broad Institute Machine Learning for Drug Discovery Symposium *Cambridge, MA*
Co-design program and recruit speakers for an annual AI-for-drug-discovery symposium.

Review Editor **2023 – Present**
Frontiers in Pharmacology

Lead Teaching Assistant **2016, 2020**
JHU: Models and Simulations (EN.580.223) *Baltimore, MD*

Benjamin Zweifach Student Travel Award **2022**
The Microcirculatory Society (Travel Award)

Richard J. Johns Award for Outstanding Academic Achievement **2017**
JHU Dept. of Biomedical Engineering *Baltimore, MD*