Shao-shan Carol Huang

Curriculum Vitae

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Center for Genomics and Systems Biology
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Education and qualifications

2018	**Workshop on Leadership in Biosciences** Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA This intensive, four-day program offered a comprehensive introduction to key strategies for managing scientific research teams and projects in both academic and industry environments.
2011	**Ph.D., Computational and Systems Biology** Massachusetts Institute of Technology (MIT), Cambridge, MA, USA Advisor: Dr. Ernest Fraenkel, Department of Biological Engineering Thesis: A constraint optimization framework for discovery of cellular signaling and regulatory networks
2005	**B.Sc., Combined Honors Computer Science and Biology, Co-op Option** University of British Columbia (UBC), Vancouver, BC, Canada Advisor: Dr. Wyeth Wasserman, Center for Molecular Medicine and Therapeutics Honors thesis: Computational identification of over-represented combinations of transcription factor binding sites in sets of co-expressed genes

Current positions

2025-present	Associate Professor with tenure, Center for Genomics and Systems Biology, Department of Biology, New York University
2019-present	Affiliate Faculty, Center for Data Science, New York University
2020-2024	Mentoring Faculty, NIH Training Grant for the Developmental Genetics PhD Program, NYU School of Medicine
2018-2024	Assistant Professor, Center for Genomics and Systems Biology, Department of Biology, New York University

Past research positions

2011-2017	Postdoctoral associate, Genomic Analysis Laboratory & Plant Biology Laboratory, Howard Hughes Medical Institute (HHMI), Salk Institute for Biological Studies Mentor: Dr. Joseph Ecker Research focus: plant regulatory genomics, epigenome variation, transcriptional regulatory networks in plant hormone responses
2011	Postdoctoral associate, Department of Biological Engineering, MIT Mentor: Dr. Ernest Fraenkel Research focus: computational methods for discovery of signaling and transcriptional regulatory networks in glioblastoma
2005-2011	Ph.D. student, Program in Computational and Systems Biology, MIT Mentor: Dr. Ernest Fraenkel Research focus: computational methods for integrative analysis of phosphoproteome and transcriptome data
2004-2005	Undergraduate research assistant, Center for Molecular Medicine and Therapeutics, UBC Mentor: Dr. Wyeth Wasserman Research focus: identification of conserved regulatory modules in mammalian genomes
2003-2005	Undergraduate research assistant, Department of Mathematics, UBC Mentor: Dr. Leah Edelstein-Keshet

Research focus: mathematical modeling of beta-amyloid plaque formation in Alzheimer's disease brains

Scientific leadership activities

2027, 2029	Vice-Chair and Chair, Gordon Research Conference on Single-Cell Approaches in Plant Biology.
2023-present	Scientific Advisory Board, United States Department of Energy Research Center - BioPoplar: A tunable chassis for diversified bioproduct production.
2022-present	Computation/Modeling/AI Committee Lead, The Plant Cell Atlas Research Coordination Network.
2022-2023	Senior Scientist in MAVEN Institute, an NIH funded mentorship program for woman scientist in science, research, and healthcare.

Funding

Ongoing grant support

DOE - DE-SC0026255 Huang (PI) 2025/09/01 - 2028/08/31

Department of Energy, Office of Biological & Environmental Research
Title: Genome-scale mapping and functional characterization of cis-regulatory networks in cellular reprogramming and regeneration
Investigators: Kenneth Birnbaum (New York University; Co-PI); Miaomiao Li (Oak Ridge National Laboratory; Co-PI)
Total award to NYU: $2,398,000 ($1,511,104 direct costs)
Description: This project aims to enhance the regenerative capacity of certain recalcitrant DOE-target crops by leveraging genomics-enabled approaches to uncover and reprogram the gene regulatory networks (GRNs) governing somatic embryogenesis (SE), a process where plants regenerate from somatic cells. My lab is responsible for inference and modeling of GRNs using single cell genomics and transcription factor binding site data.

NSF - IOS-2414183 Huang (Co-PI) 2024/09/01 - 2028/08/31

National Science Foundation, Integrative Organismal Systems
Title: RESEARCH-PGR: Enhancing grain yield under a changing climate
Investigators: Ron Mittler (University of Missouri-Columbia; PI); Felix Fritschi (University of Missouri-Columbia; Co-PI); Marc Libault (University of Missouri-Columbia; Co-PI)
Total award to NYU: $718,351 ($446,182 direct costs)
Description: This grant aims to enhance crop yields under heat stress and heat stress combined with other stresses like drought, by improving plant cooling processes, particularly in tissues critical for grain production, such as flowers and pods. My lab is responsible for inferring gene regulatory networks in soybean stomatal cells under stress conditions using single-cell RNA-seq and ATAC-seq data, and mapping the binding sites of key transcriptional regulators.

19 Washington Square North Faculty Fellows Huang & Amandine Cornille (PI) 2025/09/01 - 2026/08/31

New York University
Title: Discovery of combinatorial gene regulation from single cell transcriptome datasets
Investigators: Amandine Cornille (NYU Abu Dhabi; PI)
Total award: $30,000 ($30,000 direct costs)
Description: This collaborative project investigates how epigenetic variation can be harnessed to improve the climate resilience of apple trees, a crucial perennial crop facing increasing environmental pressures. My lab is responsible for analyzing the epigenome data and modeling the resulting gene regulatory networks.

NIH - R35 GM138143 (MIRA) Huang (PI) 2020/07/01 - 2025/04/30 (no cost extension to 2026/04/30)

National Institutes of Health, National Institute of General Medical Sciences
Title: Dissecting natural variation in transcription factor - DNA interactions
Total award to NYU: $1,953,975 ($1,250,000 direct costs)
Description: Variable transcription factor-DNA interaction mediates phenotypic variation, including traits and a wide range of human diseases. Using *Arabidopsis* as a model organism, our proposed studies aim to understand how naturally occurring genomic and epigenomic variation gives rise to variation in transcription factor-DNA interactions, and how this variation collectively alters the regulatory networks in the cell. Our research will have the potential to reveal novel principles for predicting the regulatory functions of genomic and genomic variants, a critical element in the development of precision medicine.

Completed or withdrawn grants

NSF - IOS-1916804 Huang (Co-PI) 2019/08/01 - 2023/07/31 (no cost extension to 2025/07/31)

National Science Foundation, Integrative Organismal Systems
Title: TRTech-PGR: Mapping and functional characterization of cis-regulatory module variation in plants
Investigators: Andrea Gallavotti (Rutgers University; PI), Naden Krogan (American University; Co-PI)
Total award to NYU: $752,076 ($485,796 direct costs)
Description: This grant aims to generate high-resolution maps of transcription factor binding sites across multiple genetic backgrounds in *Arabidopsis* and maize, focused on a diverse panel of transcription factors representing major structural families. We will use these maps to identify conserved and population-specific binding site clusters and use genome editing to validate the functions of selected binding sites predicted to impact traits relevant for agricultural productivity. My lab is responsible for developing the binding site mapping methods in *Arabidopsis* to be applied to maize, and for jointly analyzing the resulting data across both species.

Whitehead Fellowship for Junior Faculty in Biomedical and Biological Sciences Huang (PI) 2022/09/01 - 2024/08/31

New York University
Title: Discovery of combinatorial gene regulation from single cell transcriptome datasets
Total award: $30,000 ($30,000 direct costs)
Description: This proposal aims to develop a computational method that leverages single cell RNA-seq datasets to identify combinatorial regulation in gene regulatory networks.

NIH - R01 GM136926 (withdrawn) Huang (PI) 2020/04/01 - 2025/03/31

National Institutes of Health, National Institute of General Medical Sciences
Title: Dissecting natural variation in transcription factor - DNA interactions
Total projected award: $1,957,885 ($1,250,000 direct costs)
This proposal received a fundable score at 17 percentile with Early Stage Investigator status. However, since I was awarded a R35 (MIRA) with a more expansive scope and funding, this R01 was withdrawn to comply with NIGMS policy that limits MIRA recipients to only one NIGMS-funded award at a time.

Publications

Google Scholar: https://scholar.google.com/citations?user=10Fx1a4AAAAJ&hl=en
Total: Citations 6,609; h-index 20; i10-index 24
Since 2020: Citations 4,383; h-index 19; i10-index 23

Notations: * co-first author, ** co-corresponding author, # Huang lab trainee.

Peer-reviewed publications since independence

1. Nguyen, C. C., S. Thibivilliers, Y. Li, **C. Fazekas**#, E. Yang, J. Asiamah, M. Á. Peláez-Vico, N. Castro-Guerrero, D. Mendoza-Cozatl, O. Martin, **S.-S. C. Huang**, R. Mittler, and M. Libault. Uncovering the core genetic programs governing plant guard cell biology. *New Phytologist*, 2025, in press.

   This paper resulted from our collaboration with Marc Libault's group at the University of Missouri. Using single-nucleus RNA-seq, the paper characterized the transcriptome landscape of stomata cells from four different soybean organs and five different plant species. My PhD student Chris Fazekas performed the gene regulatory network inference and interpretation from the single cell data.

2. Galli, M., Z. Chen, **T. Ghandour**#, A. Chaudhry, J. Gregory, F. Feng, **M. Li**#, N. Schleif, X. Zhang, Y. Dong, G. Song, J. W. Walley, G. Chuck, C. Whipple, H. F. Kaeppler, **S.-S. C. Huang****, and A. Gallavotti**. Transcription factor binding divergence drives transcriptional and phenotypic variation in maize. *Nature Plants* 11 (6 2025): 1205–1219. https://doi.org/10.1038/s41477-025-02007-8.

   This paper stems from a collaboration I initiated upon joining NYU. We adapted the DAP-seq and doubleDAP-seq techniques, originally developed in my lab for *Arabidopsis*, to the complex maize genome, creating binding site maps for over 200 transcription factors and heterodimers in two maize inbred lines. We identified cis-regulatory modules and characterized key binding sites regulating gene expression and plant architecture, which we validated through CRISPR genome editing. My lab contributed significantly, with former postdoc Miaomiao Li developing the doubleDAP-seq protocol and research assistant Tara Ghandour analyzing the relationships between binding sites, gene expression, and GWAS data.

3. **Li**, **M.** #, T. Yao, **W. Lin**#, **W. E. Hinckley**#, M. Galli, W. Muchero, A. Gallavotti, J.-G. Chen, and **S.-S. C. Huang**. Double DAP-seq uncovered synergistic DNA binding of interacting bZIP transcription factors. *Nature Communications* 14, no. 1 (2023): 2600. https://doi.org/10.1038/s41467-023-38096-2.

   This paper introduces doubleDAP-seq, a technique developed in our lab to map the genome-wide binding sites of interacting transcription factor pairs. Using doubleDAP-seq, we identified unique binding sites for heterodimers between Group C/S1 bZIP transcription factors in *Arabidopsis*, uncovering new motifs and shedding light on the functional specificity of the heterodimers versus homodimers. This work was solely conducted in my NYU lab, led by our former postdoc, Miaomiao Li, with assistance from NYU PhD student Will Hinckley and MS student Wanru Lin.

4. **Shojaee**, **A.** #, and **S.-S. C. Huang**. Robust discovery of gene regulatory networks from single-cell gene expression data by Causal Inference Using Composition of Transactions. *Briefings in Bioinformatics* 24 (6 2023). https://doi.org/10.1093/bib/bbad370.

   This paper describes CICT, a machine learning algorithm for inferring gene regulatory networks from single-cell gene expression data. We demonstrated that CICT outperformed alternative methods while maintaining robust performance across varying network complexities and experimental conditions. This work was solely conducted in my NYU lab and led by our former postdoc, Abbas Shojaee.

5. Zhang, C., Z. Dai, T. Ferrier, L. Orduña, A. Santiago, A. Peris, D. C. J. Wong, C. Kappel, S. Savoi, R. Loyola, A. Amato, B. Kozak, **M. Li**#, A. Liang, D. Carrasco, C. Meyer-Regueiro, C. Espinoza, G. Hilbert, R. Figueroa-Balderas, D. Cantu, R. Arroyo-Garcia, P. Arce-Johnson, P. Claudel, D. Errandonea, M. Rodríguez-Concepción, E. Duchêne, **S.-S. C. Huang**, S. D. Castellarin, G. B. Tornielli, F. Barrieu, and J. T. Matus. MYB24 orchestrates terpene and flavonol metabolism as light responses to anthocyanin depletion in variegated grape berries. *The Plant Cell* 35 (12 2023): 4238–4265. https://doi.org/10.1093/plcell/koad228.

   This work resulted from a collaboration I started at NYU with the lab of Tom Matus at the University of Valencia in Spain. A key finding is that the transcription factor MYB24 in grapevine regulates terpene and flavonol synthesis in response to light stress in variegated grape berries. Led by former postdoc Miaomiao Li, my lab conducted the MYB24 DAP-seq experiment and data analysis, which provided crucial evidence supporting this key finding.

6. Orduña, L., M. Li, D. Navarro-Payá, C. Zhang, A. Santiago, P. Romero, Ž. Ramšak, G. Magon, J. Höll, P. Merz, K. Gruden, A. Vannozzi, D. Cantu, J. Bogs, D. C. J. Wong, **S.-s. C. Huang**, and J. T. Matus. Direct regulation of shikimate, early phenylpropanoid and stilbenoid pathways by Subgroup 2 R2R3-MYBs in grapevine. *The Plant Journal* 110, no. 2 (2022): 529–547. https://doi.org/10.1111/tpj.15686.

   This paper resulted from a collaboration I started at NYU with Tom Matus's lab at the University of Valencia in Spain, where we used DAP-seq to identify genome-wide binding sites of the R2R3 MYB transcription factors MYB13, MYB14, and MYB15 in grapevine, revealing their roles in regulating key genes in the stilbenoid pathway. Our lab's work was led by our former postdoc Miaomiao Li and involved conducting the grapevine DAP-seq experiments and trained the collaborating lab in data analysis, helping to uncover new regulatory targets, including stilbene synthase genes and resveratrol-modifying gene candidates.

7. **Li**, **M.** #, and **S.-S. C. Huang**. "DNA Affinity Purification Sequencing (DAP-Seq) for Mapping Genome-Wide Transcription Factor Binding Sites in Plants." In *Accelerated Breeding of Cereal Crops*, edited by A. Bilichak and J. D. Laurie, 293–303. New York, NY: Springer US, 2022. https://doi.org/10.1007/978-1-0716-1526-3_15.

   This methods book chapter provides an updated DAP-seq protocol with specialized instructions and tips for working with plant samples. It was written by our former postdoc Miaomiao Li.

8. Plant Cell Atlas Consortium, S. Ghosh Jha*, A. T. Borowsky*, B. J. Cole*, N. Fahlgren*, A. Farmer*, **S.-s. C. Huang***, P. Karia*, M. Libault*, N. J. Provart*, S. L. Rice*, M. Saura-Sanchez*, P. Agarwal, A. H. Ahkami, C. R. Anderton, S. P. Briggs, J. A. Brophy, P. Denolf, L. F. Di Costanzo, M. Exposito-Alonso, S. Giacomello, F. Gomez-Cano, K. Kaufmann, D. K. Ko, S. Kumar, A. V. Malkovskiy, N. Nakayama, T. Obata, M. S. Otegui, G. Palfalvi, E. H. Quezada-Rodríguez, R. Singh, R. G. Uhrig, J. Waese, K. Van Wijk, C. R. Wright, D. W. Ehrhardt, K. D. Birnbaum, and S. Y. Rhee. Science Forum: Vision, challenges and opportunities for a Plant Cell Atlas. *eLife* 10 (2021): e66877. https://doi.org/10.7554/eLife.66877.

   This paper presents the vision for the Plant Cell Atlas (PCA), a framework to map all plant cell types and comprehensively annotate molecular localization and organization at cellular and tissue levels. As the Computation/Modeling/AI Committee lead of the PCA Research Coordination Network, I contributed to writing the challenges and knowledge gaps sections, which highlight current limitations and how the PCA can address them.

9. Scherma, M., J. S. Qvist, A. Asok, **S.-s. C. Huang**, P. Masia, M. Deidda, Y. B. Wei, R. K. Soni, W. Fratta, P. Fadda, E. R. Kandel, D. B. Kandel, and P. A. Melas. Cannabinoid exposure in rat adolescence reprograms the initial behavioral, molecular, and epigenetic response to cocaine. *Proceedings of the National Academy of Sciences* 117, no. 18 (2020): 9991–10002. https://doi.org/10.1073/pnas.1920866117.

   This work is part of our long-term collaboration with Philippe Melas at the Karolinska Institute in Sweden. Using a multiomics approach in a rat model, this study demonstrates that adolescent exposure to synthetic cannabinoids induces molecular and epigenetic changes in the prefrontal cortex, potentially mediating an enhanced response to cocaine's stimulatory effects, including alterations in histone acetylation, chromatin accessibility, mRNA response, and protein phosphorylation. My lab contributed by performing the computational analysis of the ATAC-seq and RNA-seq data.

10. Procko, C., S. Morrison, C. Dunar, S. Mills, B. Maldonado, C. Cockrum, N. E. Peters, **S.-s. C. Huang**, and J. Chory. Big Data to the Bench: Transcriptome Analysis for Undergraduates. *CBE–Life Sciences Education* 18, no. 2 (2019): ar19. https://doi.org/10.1187/cbe.18-08-0161.

    This paper describes a semester-long undergraduate course that integrates RNA-seq analysis with wet-lab experiments to investigate plant responses to light, helping students develop computational skills and bioinformatics self-efficacy. I contributed by reviewing the code and statistics of the RNA-seq analysis.

Invited reviews since independence

11. Sinha, R., M. Á. Peláez-Vico, L. S. Pascual, S. Thibivilliers, M. Libault, **S.-S. C. Huang**, F. B. Fritschi, S. I. Zandalinas, and R. Mittler. The differential transpiration response of plants to stress. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* 380 (1927 2025): 20240241. https://doi.org/10.1098/rstb.2024.0241.
12. **Hajheidari**, **M.** #, and **S.-s. C. Huang**. Elucidating the biology of transcription factor–DNA interaction for accurate identification of cis-regulatory elements. *Current Opinion in Plant Biology* 68 (2022): 102232. https://doi.org/10.1016/j.pbi.2022.102232.
13. **Shojaee**, **A.** #, **M. Saavedra**#, and **S.-s. C. Huang**. Potentials of single-cell genomics in deciphering cellular phenotypes. *Current Opinion in Plant Biology* 63 (2021): 102059. https://doi.org/10.1016/j.pbi.2021.102059.
14. **Qian**, **Y.** #, and **S.-s. C. Huang**. Improving plant gene regulatory network inference by integrative analysis of multi-omics and high resolution data sets. *Current Opinion in Systems Biology* 22 (2020): 8–15. https://doi.org/10.1016/j.coisb.2020.07.010.

15. **Huang**, **S.-s. C.**, and J. R. Ecker. Piecing together cis-regulatory networks: insights from epigenomics studies in plants. *WIREs Systems Biology and Medicine* 10, no. 3 (2018): e1411. https://doi.org/10.1002/wsbm.1411.

Preprints and manuscripts under preparation

16. **Hinckley**, **W. E.** #, J. Swift, F. Romei, J. P. Muschietti, **S. S. C. Huang**, G. M. Coruzzi, and M. Obertello. HHO5: A key orchestrator of dose-dependent nitrogen signaling pathways in Arabidopsis. *bioRxiv*, August 2025. https://doi.org/10.1101/2025.07.31.667803.

    This manuscript reports that the Arabidopsis thaliana transcription factor HRS1 HOMOLOG 5 (HHO5) exhibits N-dose–dependent expression and functions as both an activator and repressor in plant nitrogen dose signaling. The project was led by Will Hinckley, a Ph.D. student jointly advised by Coruzzi and me.
17. Sinha, R., S. I. Zandalinas, M. Á. Peláez-Vico, A. Ghani, M. A. Khan, S. P. Induri, A. Bereimipour, **T. Ghandour**#, A. Ogden, **S.-S. C. Huang**, R. K. Azad, D. Mendoza-Cózatl, T. Joshi, F. B. Fritschi, and R. Mittler. bHLH35 mediates specificity in plant responses to multiple stress conditions. *bioRxiv*, May 2025. https://doi.org/10.1101/2025.05.07.652729.

    This paper resulted from our collaboration with Ron Mittler's group at the University of Missouri. It identifies the transcription factor bHLH35 in Arabidopsis thaliana as a key regulator of plant survival under combined salinity, excess light, and heat stress. My lab contributed the co-expression and regulatory network analyses, as well as the correlation between natural genetic variation and climate variables, led by former M.S. student Tara Ghandour.
18. **Hinckley**, **W. E.** #, A. Jack, **A. Li**#, S. Frangos, A. Pasquino, **S.-S. C. Huang****, and G. M. Coruzzi**. Transcription Factor (TF) validation using Dam-IT simultaneously captures genome-wide TF-DNA binding, direct gene regulation, and chromatin accessibility in plant cells. *bioRxiv*, May 2025. https://doi.org/10.1101/2025.05.06.652526.

    This paper introduces Dam-IT (DamID-seq Incorporating Transcriptomics), a technique co-developed by our lab and the lab of Gloria Coruzzi at NYU, that simultaneously captures TF-DNA binding, direct TF-gene regulation, and chromatin accessibility in the same batch of cells. The project was led by Will Hinckley, a PhD student jointly advised by Coruzzi and myself.
19. **Ghandour**, **T.** #, J. R. Glausier, A. Asok, M. R. Doyle, P. Campo, L. Colnaghi, D. A. Lewis, D. B. Kandel, E. R. Kandel, G. de Guglielmo, **S.-S. Carol Huang****, and P. A. Melas**. CircRNA hypomethylation in the human amygdala implicates FKBP5 in alcohol use disorder. *bioRxiv*, May 2025. https://doi.org/10.1101/2025.05.04.652083.

    This work is part of our long-term collaboration with Philippe Melas at the Karolinska Institute in Sweden. Analyzing postmortem human basolateral amygdala (BLA) tissue from alcohol use disorder patients, we found extensive m (6)A hypomethylation uniquely affecting circular RNAs (circRNAs), notably at the FKBP5-hosted circRNAs. My former MS student Tara Ghandour performed all the data analysis and made the key discoveries presented in the manuscript.
20. **Li**, **M.** #, T. Yao, M. Galli, **W. Lin**#, **Y. Zhou**#, J.-G. Chen, A. Gallavotti, and **S.-s. C. Huang**. Diversification and conservation of DNA binding specificities of SPL family of transcription factors. *bioRxiv*, 2024. https://doi.org/10.1101/2024.09.13.612952.

    This study used DAP-seq to map the genome-wide binding profiles of all 16 transcription factors in the *Arabidopsis* SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) family, revealing distinct DNA motif preferences that may explain functional differences between paralogs SPL9 and SPL15. By comparing the DAP-seq identified binding sites in *Arabidopsis* to those in maize and wheat, we characterized the conservation and divergence of SPL DNA binding targets across species, highlighting the utility of DAP-seq in investigating the evolutionary trajectories of transcription factor networks. This work is solely conducted in my NYU lab.
21. Yin, L., M. Zander, **S.-s. C. Huang**, M. Xie, L. Song, J. P. S. Guzmán, E. Hann, B. K. Shanbhag, S. Ng, S. Jain, B. J. Janssen, N. M. Clark, J. W. Walley, T. Beddoe, Z. Bar-Joseph, M. G. Lewsey, and J. R. Ecker. Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways. *bioRxiv*, 2023, 2023.03.07.531630. https://doi.org/10.1101/2023.03.07.531630.

    This work is part of our long-term collaboration with the labs of Mat Lewsey at La Trobe University (Australia) and Joe Ecker at the Salk Institute (USA). It reveals how multiple hormone signaling pathways are integrated in *Arabidopsis* seedlings, identifying shared transcription factors among the hormones and MPK6 as a key regulator. It also highlights the role of alternative splicing in early hormone responses. My lab's contribution includes the design and implementation of data processing pipeline and analysis strategies.

Peer-reviewed publications prior to independence

22. Ursu, O., S. J. C. Gosline, N. Beeharry, L. Fink, V. Bhattacharjee, **S.-s. C. Huang**, Y. Zhou, T. Yen, and E. Fraenkel. Network modeling of kinase inhibitor polypharmacology reveals pathways targeted in chemical screens. *PLOS ONE* 12, no. 10 (October 2017): 1–22. https://doi.org/10.1371/journal.pone.0185650.
23. Trigg, S. A., R. M. Garza, A. MacWilliams, J. R. Nery, A. Bartlett, R. Castanon, A. Goubil, J. Feeney, R. O'Malley, **S.-s. C. Huang**, Z. Zhang, M. Galli, and J. R. Ecker. CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nature Methods* 14, no. 8 (2017): 819. https://doi.org/10.1038/nmeth.4343.
24. Bartlett, A., R. C. O'Malley, **S.-s. C. Huang**, M. Galli, J. R. Nery, A. Gallavotti, and J. R. Ecker. Mapping genome-wide transcription-factor binding sites using DAP-seq. *Nature Protocols* 12, no. 8 (2017): 1659–1672. https://doi.org/10.1038/nprot.2017.055.
25. Song, L., **S.-s. C. Huang**, A. Wise, R. Castanon, J. R. Nery, H. Chen, M. Watanabe, J. Thomas, Z. Bar-Joseph, and J. R. Ecker. A transcription factor hierarchy defines an environmental stress response network. *Science* 354, no. 6312 (2016). https://doi.org/10.1126/science.aag1550.
26. Kawakatsu, T. *, **S.-s. C. Huang***, F. Jupe*, E. Sasaki*, R. J. Schmitz, M. A. Urich, R. Castanon, J. R. Nery, C. Barragan, Y. He, H. Chen, M. Dubin, C.-R. Lee, C. Wang, F. Bemm, C. Becker, R. O'Neil, R. C. O'Malley, D. X. Quarless, The 1001 Genomes Consortium, N. J. Schork, D. Weigel, M. Nordborg, and J. R. Ecker. Epigenomic Diversity in a Global Collection of *Arabidopsis thaliana* Accessions. *Cell* 166, no. 2 (2016): 492–505. https://doi.org/10.1016/j.cell.2016.06.044.
27. O'Malley, R. C. *, **S.-s. C. Huang***, L. Song, M. G. Lewsey, A. Bartlett, M. Galli, J. R. Nery, A. Gallavotti, and J. R. Ecker. Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell* 165, no. 5 (2016): 1280–1292. https://doi.org/10.1016/j.cell.2016.04.038.
28. Pedmale, U. V., **S.-s. C. Huang**, M. Zander, B. J. Cole, J. Hetzel, K. Ljung, P. A. Reis, P. Sridevi, K. Nito, J. R. Nery, J. R. Ecker, and J. Chory. Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. *Cell* 164, nos. 1-2 (2016): 233–245. https://doi.org/10.1016/j.cell.2015.12.018.
29. Chang, K. N., S. Zhong, M. T. Weirauch, G. Hon, M. Pelizzola, H. Li, **S.-s. C. Huang**, R. J. Schmitz, M. A. Urich, D. Kuo, et al. Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. *eLife* 2 (2013): e00675. https://doi.org/10.7554/eLife.00675.
30. **Huang**, **S.-s. C.**, D. C. Clarke, S. J. Gosline, A. Labadorf, C. R. Chouinard, W. Gordon, D. A. Lauffenburger, and E. Fraenkel. Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling. *PLoS Computational Biology* 9, no. 2 (2013): e1002887. https://doi.org/10.1371/journal.pcbi.1002887.
31. Tuncbag, N., A. Braunstein, A. Pagnani, **S.-S. C. Huang**, J. Chayes, C. Borgs, R. Zecchina, and E. Fraenkel. Simultaneous reconstruction of multiple signaling pathways via the Prize-Collecting Steiner Forest problem. *Journal of Computational Biology* 20, no. 2 (2013): 124–136. https://doi.org/10.1089/cmb.2012.0092.
32. Qiao, H., Z. Shen, **S.-s. C. Huang**, R. J. Schmitz, M. A. Urich, S. P. Briggs, and J. R. Ecker. Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. *Science* 338, no. 6105 (2012): 390–3. https://doi.org/10.1126/science.1225974.
33. Tuncbag, N., S. McCallum, **S.-s. C. Huang**, and E. Fraenkel. SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. *Nucleic Acids Research* 40, no. W1 (2012): W505–W509. https://doi.org/10.1093/nar/gks445.
34. **Huang**, **S.**, and E. Fraenkel. Swimming upstream: identifying proteomic signals that drive transcriptional changes using the interactome and multiple '-omics' datasets. *Computational Methods in Cell Biology* 110 (2012): 57. https://doi.org/doi:10.1016/B978-0-12-388403-9.00003-5.
35. **Huang**, **S.-s. C.**, and E. Fraenkel. Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. *Science Signaling* 2, no. 81 (2009): ra40. https://doi.org/10.1126/scisignal.2000350.

Patent

1. Fraenkel, E., **S.-S. C. Huang**, D. R. Karger, L. Riva, and E. Yeger-Lotem. *Identifying biological response pathways*. US Patent No. 8612160. December 2013.

Conference and Seminar Talks

Invited national and international conference talks since independence

1. 35th International Conference on Arabidopsis Research. Gent, Belgium. June 20, 2025.
2. Workshop on Plant Cistromics in the 32nd Plant & Animal Genome Conference. San Diego, CA. January 14, 2025.
3. Workshop on Systems Biology and Machine Learning in the 32nd Plant & Animal Genome Conference. San Diego, CA. January 10, 2025.
4. 34th International Conference on Arabidopsis Research. San Diego, USA. July 17, 2024.
5. Cold Spring Harbor Laboratory Meeting in Plant Genomes, Systems Biology & Engineering. Cold Spring Harbor, NY. November 30, 2023.
6. 2023 Gordon Research Conference Single-Cell Approaches in Plant Biology. Ventura, CA. August 3, 2023.
7. 19th Annual NYU Center for Genomics and Systems Biology Symposium. New York, NY. June 7, 2023.
8. 2023 Society of Developmental Biology Mid-Atlantic Regional Meeting. Princeton, NJ. April 21, 2023.
9. 32nd International Conference on Arabidopsis Research. Belfast, Northern Ireland. Presented virtually. June 23, 2022.
10. Annual Meeting of Mid-Atlantic section of the American Society of Plant Biologists (ASPB). College Park, MD. May 24, 2022.
11. European Cooperation in Science and Technology: INTERGRAPE 3rd Annual Meeting. Virtual. Presented virtually. July 28 and 30, 2021.
12. Annual Meeting of Mid-Atlantic section of the American Society of Plant Biologists (ASPB). College Park, MD. Cancelled due to COVID-19. May 2020.
13. CNRS - Jacques Monod Conference: First International Plant Systems Biology Meeting. Roscoff, France. September 12, 2018.
14. Workshop on Construction of Gene Regulatory Networks in Arabidopsis in the 29th International Conference on Arabidopsis Research. Turku, Finland. June 26, 2018.

Invited seminars and symposium talks since independence

15. Academia Sinica Biotechnology Center in Southern Taiwan. Tainan, Taiwan. June 26, 2025.
16. Academia Sinica Institute of Plant and Microbial Biology. Taipei, Taiwan. June 24, 2025.
17. Donald Danforth Plant Science Center. St. Louis, MO. March 26, 2025.
18. Michigan State University Genetics and Genome Sciences Day. East Lansing, MI. May 7, 2024.
19. University of British Columbia Centre for Molecular Medicine and Therapeutics. Vancouver, BC, Canada. April 5, 2024.
20. University of British Columbia Department of Botany. Vancouver, BC, Canada. April 2, 2024.
21. Cincinnati Children’s Hospital Research Foundation. Cincinnati, OH. March 6, 2024.
22. University of Texas Austin Department of Molecular Biosciences. Austin, TX. March 22, 2023.
23. University of Georgia Department of Genetics. Athens, GA. March 15, 2023.
24. University of Florida Department of Horticultural Sciences, October 31, 2022.
25. University of Cambridge Sainsbury Laboratory. Cambridge, UK. November 27, 2019.
26. University of Maryland Department of Cell Biology and Molecular Genetics. College Park, MD. September 20, 2019.
27. Iowa State University Bioinformatics and Computational Biology Symposium. Ames, IA. April 29, 2019.
28. Boyce Thompson Institute. Ithaca, NY. May 8, 2018.

Teaching at NYU

CAS undergraduate courses

Spring 2025	BIOL-UA 124. Fundamentals of Bioinformatics. Sole instructor of record. 22 students; 14/14 lectures.
Spring 2023	BIOL-UA 124. Fundamentals of Bioinformatics. Sole instructor of record. 20 students; 14/14 lectures.
Spring 2021	BIOL-UA 124. Fundamentals of Bioinformatics. Sole instructor of record. 11 students; 14/14 lectures.
Spring 2020	BIOL-UA 124. Fundamentals of Bioinformatics. Sole instructor of record. 10 students; 14/14 lectures.
Spring 2020	BIOL-UA 560. Plant Science and Biotechnology. Co-instructor of record with Ken Birnbaum. 13 students; 3/14 lectures.
Spring 2019	BIOL-UA 124. Fundamentals of Bioinformatics. Co-instructor of record with Manpreet Katari. 11 students; 6/14 lectures.

Graduate courses

Spring 2025	BIOL-GA 2004. BioCore IV: Bio Core IV: Genes, Systems & Evolution. Course Coordinator.
2025	BIOL-GA 2004. BioCore IV: Bio Core IV: Genes, Systems & Evolution. 1 class/year.
2018-2024	BIOL-GA 2003. BioCore III: Molecules and Cells. 1 class/year.
Fall 2021, 2022, 2023, 2024	BIOL-GA 2130. Developmental and Stem Cell Systems. 2 classes/year.
Fall 2020	BIOL-GA 2130. Developmental and Stem Cell Systems I. 2 classes/year.
Spring 2018, 2019, 2020	BIOL-GA 2131. Developmental and Stem Cell Systems II. 1 class/year.

Supervision and training

Postdoctoral scholars [Position upon departure]

2025-present	Sonal Sachdev
2018-2024	Miaomiao Li [R&D Associate Staff Member (Principal Investigator), Oak Ridge National Laboratory].
2020-2023	Abbas Shojaee [Research Principal Consultant, Cytel].
2021-2022	Mohsen Hajheidari [Geneticist, U of Cologne Cluster of Excellence on Plant Sciences]
2020	Yichun Qian

Graduate students [Position upon graduation]

Total: 4 Ph.D., 11 M.S.

2025-present	Christopher Fazekas, Ph.D. in Biology, NYU.
2024-present	Kamal Radharamanan, Ph.D. in Biology, NYU. Joint with Joy Bergelson.
2022-present	Graeme Vissers, Ph.D. in Biology, NYU. Joint with Ken Birnbaum.
2021-present	Will Hinckley, Ph.D. in Biology, NYU. Joint with Gloria Coruzzi.
2024-2025	Tara Ghandour, M.S. in Biology, NYU.
2024	Faiza Rafi, M.S. in Bioinformatics, NYU.
2023-2024	José A. Galván, M.S. in Biology, NYU [High school science teacher, NYC].
2023-2024	Aurelia Li, B.S. and M.S. in Biology, NYU [Clinical Research Assistant, Weill Cornell Medicine].
2021-2022	Wanru Lin, M.S. in Biology, NYU [Ph.D. student at U of Maryland].
2020-2021	Michelle Saavedra, M.S. in Biology, NYU [Scientist at Visikol].
2020-2021	Nabilla Zaman, M.S. in Biology, NYU [Associate Researcher, Mount Sinai Hospital].
2018-2019	Ziyan Lin, M.S. in Biology, NYU [Bioinformatics Analyst, NYU Langone Health].
2018-2019	Ruxin Dai, M.S. in Biology, NYU [Statistical Programmer, Pfizer China].

2018-2019	Diogo Mesquita, M.S. in Data Science, NYU [Data Scientist, Apple].
2018-2019	Yuhan Wang, M.S. in Biology, NYU [Computational Biologist, Memorial Sloan Kettering Cancer Center].

Research assistants [**Position upon departure**]

2024-2025	Naomi Bak
2023-2025	Tara Ghandour
2024	Sean Doyle [Data Consultant, the Kubrick Group].
2022-2023	Yilin Zhou [MS student in Data Science at Harvard University]
2018-2019	Nathaniel Angeles

Undergraduate students [**Position upon graduation**]

2023-present	Vera Vecherskaia, research assistant, B.S. in Chemical and Biomolecular Engineering, NYU.
2024-2025	Stella Zhang, research assistant, B.A. in Computer Science, NYU [Software Developer, Morgan Stanley].
2023-2024	Sean Doyle, research assistant, B.S. in Computer Science, NYU [Junior Research Associate, NYU].

High school intern [**Position upon graduation**]

2021-2023	Hannah Will, The Packer Collegiate Institute, Brooklyn, NY [Undergraduate student at McGill University].

PhD Thesis Committees

Total: 11 in progress, 10 graduated

Noha Ismail (NYU Abu Dhabi), 2025-present
Amari Hill, 2024-present
Shaili Regmi, 2024-present
Isabel Bojanini, 2024-present, chair
Omar Qassab, 2023-present
Eric Laderman, 2023-present
Wells Burrell, 2023-present
Dylan Fitzmaurice, 2023-present
Mary Galli (Rutgers University), 2022-present, external member
Maggie Beheler-Amass, 2022-2025, chair
Julie Chuong, 2022-present
Yingzhen Pei, 2021-2025, chair
Ornob Alam, 2021-2025
Jose Salome-Correa, 2020-present
Xinyi (Cathy) Guo, 2020-2024
Xinhe Xue, 2020-2023
Yuhan Hao, 2020-2023, chair
Cassandra Buzby, 2020-2025
Akash Sookdeo, 2019-2022
Victoria Le, 2019-2022
Chang Wang, 2019-2021

Service at NYU

Service for the Biology Department

AY2025/26	Co-chair (with Ildar Gainetdinov), PhD Admissions Committee.

AY2024/25, AY2025/26	Institutional Biosafety Committee.
AY2024/25, AY2025/26	Department representative, Faculty of Arts and Sciences Faculty Assembly.
AY2023/24	Alternate, Faculty of Arts and Sciences Faculty Assembly.
2020, 2021, 2023	Department representative at the Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS) Conference.
AY2018/19-2019/20, AY2021/22-2024/25	Member, PhD Admissions Committee.
AY2021/22	Organizer, Biology Faculty Exchange Seminar Series.
AY2020/21	Co-chair (with Enrique Rojas), PhD Admissions Committee.
AY2019/20, AY2020/21	Organizer, Biology Postdoc Seminar Series
2018, 2019	Biology Summer Undergraduate Research Program Selection Committee.
2018	Department representative at SACNAS National Diversity in STEM Conference.

Service for the university

2020	CAS Women In Science (WINS) Selection Committee.

Peer review activities

Journal review (selected)	BMC Biology, BMC Bioinformatics, Current Opinion in Plant Biology, eLife, Frontiers in Plant Science, Genome Biology, Genome Research, IEEE Transactions on Biomedical Engineering, iScience, Molecular Cell, Nature, Nature Communications, Nature Plants, npj Systems Biology and Applications, Nucleic Acids Research, The Plant Journal, The Plant Cell, Plant Communications, PLoS Computational Biology, PLoS ONE, PNAS, Science.
Grant review	National Sciences and Engineering Research Council of Canada Discovery Grant.

Honors and awards

2022	NYU Whitehead Fellowship for Junior Faculty in Biomedical and Biological Sciences
2014	Pioneer Fund Fellow, Salk Institute for Biological Studies
2007-2011	Graduate Fellowship, NCI Center for Cancer Systems Biology at MIT
2011	Scholar-in-Training Award, AACR-NCI Conference on Systems Biology
2005-2009	Post-graduate Scholarship at Foreign Universities, Natural Sciences and Engineering Research Council of Canada (NSERC)
2005	Amy E. Sauder Scholarship and Jean Craig Smith Scholarship, UBC
2004, 2005	Undergraduate Student Research Award in Industry and University, NSERC
2004	Wesbrook Scholar, UBC
2004	AstraZeneca Undergraduate Scholarship, UBC
2002-2003	Women in Engineering and Science Program, National Research Council of Canada
2000-2004	Chancellor’s Entrance Scholarship, UBC
2000-2004	IBM Canada Pacific Development Center Scholarship