

CAREER OPPORTUNITIES

We are looking for a postdoc scientist and a technician to join Carol Huang's lab at New York University (huanglab.rbind.io) in the heart of Manhattan.

ABOUT THE LAB

Our lab uses both “dry”- and “wet”-lab genomics methods to study gene regulation at the systems level. Specifically, we are interested in understanding how the repertoire of genome and epigenome variations at the levels of individual and population give rise to phenotypic variations in realistic environment. The extensive intra-specific genome and epigenome variation and adaptability to the environment found in the plant kingdom provide rich resources to investigate this question. Working with the reference plant *Arabidopsis* and extending to agriculturally and ecologically important plants, we focus on three related topics:

- identifying genomic and epigenomic determinants of intra-specific transcriptional variation;
- using single cell sequencing methods to characterize cell type-specific responses;
- mapping population- and cell type-specific regulatory networks in hormone responses.

We aim to build a highly interdisciplinary and collaborative lab, and are committed to provide a supportive environment for lab members to achieve scientific excellence and gain expertise in both computational and experimental skills. The lab space is centrally located in the Washington Square campus of NYU, in a six-year-old building that houses the Center for Genomics and Systems Biology.

ABOUT THE POSITIONS

Postdoc scientist

We are looking for a motivated scientist with expertise in any of the areas listed below, as evidenced by first-author or co-first-author publications. We seek candidates with PhD training in plant biology, molecular biology, genetics/genomics, ecology/evolution, or computational biology. Experience with *Arabidopsis* and/or plant hormone biology is a plus. Relevant skills and experience include work on molecular cloning, protein expression and purification, single cell genomics, comparative genomics, analysis of high-throughput sequencing data, basic statistics, computer programming and/or machine learning. The position is expected to continue for multiple years contingent on satisfactory performance.

Applying: To apply, please send a brief description of research interests and accomplishments, CV, contact information for three references, and a publication representative of your work to s.c.huang@nyu.edu. We encourage candidates to identify potential funding sources for which they may be eligible and interested in applying for. Applications will be considered until the position is filled. Informal inquiries are welcome.

Technician

We are looking for a motivated and organized individual with training in molecular biology, biochemistry, or plant biology with prior laboratory experiences. The technician will work with the PI to assist with multiple research projects. Responsibilities may include molecular cloning, protein expression and purification, high-

throughput sequencing library preparations, FACS, common molecular biology techniques focused on *Arabidopsis* or other plants such as transformation, as well as managing purchases. Being able to work a flexible schedule based on research needs and deadlines is a plus. The position is expected to continue for one or more years contingent on satisfactory performance.

Applying: To apply, please send a cover letter, resume and contact information for three references to s.c.huang@nyu.edu. Applications will be considered until the position is filled. Informal inquiries are welcome.

SELECTED PUBLICATIONS

- **S. C. Huang**, J. R. Ecker. Piecing together cis-regulatory networks: insights from epigenomics studies in plants. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, 2017.
- T. Kawakatsu*, **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. 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, J. R. Ecker. Epigenomic Diversity in a Global Collection of *Arabidopsis thaliana* Accessions. *Cell*, 2016. *co-first authors
- R. O'Malley*, **S. C. Huang***, L. Song, M. Lewsey, A. Bartlett, J. Nery, M. Galli, A. Gallavotti, J. R. Ecker. Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell*, 2016. *co-first authors.
- L. Song, **S. C. Huang**, A. Wise, R. Castanon, J. R. Nery, H. Chen, M. Watanabe, J. Thomas, Z. Bar-Joseph, J. R. Ecker. A transcription factor hierarchy defines an environmental stress response network. *Science*, 2016.