

## **CSBC Investigator Highlight**

### ***Dr. Melissa Kemp Uses Computational Models to Understand Redox Metabolism in Cancer***

Melissa Kemp, Ph.D., a CSBC investigator at the Georgia Institute of Technology, studies the metabolic state of cells and how it affects cell signaling pathways.

During her postdoc, she trained with several current CSBC members, including [Doug Lauffenburger](#), [Peter Sorger](#), and [Forest White](#), at the [Massachusetts Institute of Technology \(MIT\) Cell Decision Process Center](#). Now, she uses systems biology approaches to understand redox metabolism in tumors.



In this interview, she discusses her career journey in engineering, her views on cancer systems biology, and her CSBC research focused on head and neck cancer.

- **Why did you choose to study engineering?**

After my freshman year of college, I struggled to find a summer job. Even though I started as a biology major, I didn't have any relevant coursework or lab experience to get a research position. I also got back home later than other students, so all the retail jobs were taken. I ended up volunteering at the Cleveland Clinic in a protein crystallography lab. It was really eye opening for me because I was in a clinical research setting where everyone had a Ph.D. in physics. It helped me see that I didn't need to be a biology major to do biomedical research. I came back to the MIT for my sophomore year and decided to get an engineering degree. I started looking into relevant engineering majors and stumbled upon the radiation sciences and medical physics track within the nuclear engineering program. It was a perfect fit for me, and included classes in biology, organic chemistry, and quantitative physiology. At the time, there was interesting research going on in the department using computational modeling. That is how I ended up going into computational biology, which has been a common thread throughout my research career.

- **Why is it important to encourage the next generation of scientists to develop and use systems approaches for cancer research?**

Scientists can characterize cancer cells in such incredible detail that traditional biology approaches are overwhelmed with the amount of data that's being collected. Training students and postdocs in systems biology really sets them up to get new insights about patient variability and unknown mechanisms. I think there's a lot to be learned from using systems approaches. It's incredibly important to teach the next generation of scientists how to use systems biology tools and how to develop their own tools early on in their careers.

- **Why does your lab do both experiments and computational work?**

I think it's important in systems biology to really understand where your data is coming from. If my lab was just a modeling resource for crunching the data that's being generated at other sites, then we would be at a disadvantage in the biological interpretation. Since we're also doing some of the experiments, we have an understanding of the cell lines the other labs

are using, why certain techniques are good or not so good for the questions we're asking, and more. This gives us a stronger ability to integrate all this biological information into comprehensive models.

- **Why is your CSBC project focused on understanding redox metabolism in head and neck cancer?**

My collaborator, [Cristina Furdulj](#), has a lot of expertise in head and neck cancer. Until we started working on this project together, I knew very little about this type of cancer. The initiation of head and neck tumors is often related to oxidative stress through tobacco, alcohol, and human papillomavirus exposures. Also, the primary ways in which people treat head and neck cancers, specifically ionizing radiation and platinum-based drugs, are related to the induction of reactive oxygen species. We felt that by tackling redox metabolism in head and neck cancer and its role in the actions of new cancer drugs, we could make significant research progress on this type of cancer.

- **Can you describe a computational model being used in your CSBC project?**

I think that flux balance analysis modeling is going to be useful for the development of personalized models for cancer patients. This approach leverages transcriptomic data to make predictions about the metabolic activity in a patient. By looking at different enzymes that are contributing to the overall production of a single metabolite, the model predicts how quickly a patient is going to metabolize a chemotherapeutic drug. Ideally, we want to use these types of models to come up with a handful of biomarkers for predicting the potency of a drug without having to do huge transcriptomic-wide analyses.

### ***Links***

[Georgia Tech Profile of Melissa Kemp](#)

[Kemp Laboratory Website](#)