

Department Seminar Series

UCDAVIS
**FOOD SCIENCE AND
TECHNOLOGY**

4:10 PM, Wednesday June 1st, 2022

Attend in person in room 1207 RMI-South, or remotely by Zoom:

<https://ucdavis.zoom.us/j/98032142511>



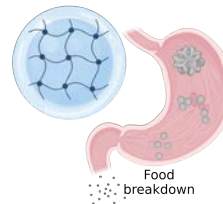
Hop Creep: Quantified, Understood, Solved.

Jessica Young
First Year M.S. Student
Fox lab

*Jessica Young received her B.S. in cell and molecular biology from Armstrong State University in Savannah, Ga. After several years in the brewing industry, Jessica now works in the Anheuser-Busch endowed brewing and malting science lab. She studies the activity of enzymes associated with *Humulus lupulus* that cleave dextrins, better known as hop creep. The focus of her research is to gain a better understanding of hop creep in order to reclaim control over fermentation for brewers.*

SUMMARY: Hop creep continues to thwart the brewing industry. The impacts are not only financial, but also degradative to beer quality. This presentation aims to give an outline of hop creep and the experimental design to hopefully understand and provide a practical solution for industry.

Food structure



Effect of processing on the structure and breakdown of food proteins

Alisha Kar
First Year Ph.D. Student
Bornhorst lab

Alisha received her M.S in Food Science and Technology from University of Nebraska, Lincoln, where she worked on radiofrequency processing of egg white powder to study structural and functional effects. Then, she joined Givaudan as a Sensory analyst focusing on finished flavors used in beverages. The focus of her current research is developing a predictive model for protein breakdown using in vitro, in vivo studies and non-invasive methods.

SUMMARY: Protein structures have a significant impact on protein digestion and functionality. Therefore, the development of any protein-based novel product relies on its initial properties as well as breakdown properties. These in turn affect the biological implications associated with the product. This presentation aims to give an overview of the food breakdown classification system in context of proteins, and the methods that could be implemented to develop a predictive model to assess protein breakdown.