Full-length Alternative Transcript Isoform Analysis Using Long-read Nanopore Sequencing

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Location: **COB1 113**

Angela Brooks

Assistant Professor, Biomolecular Engineering
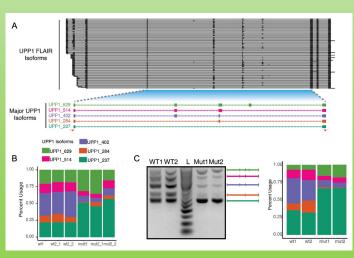
University of California, Santa Cruz

For more information, contact : **Anna Beaudin**

abeaudin@ucmerced.edu

Abstract

Our group aims to understand the mechanisms of alternative RNA splicing regulation and splicing dysregulation in cancer. Short-read, high-throughput cDNA sequencing (RNA-Seq) has revolutionized our ability to profile RNA splicing; however, this approach cannot capture the full complexity of RNA transcripts. First, "RNA-Seq" should, more appropriately, be called cDNA-Seq—it is not sequencing RNA directly. Second, short-reads limit our ability to accurately identify and quantify full-length RNA isoforms. For a more comprehensive characterization of alternative transcript isoform expression, we have been developing computational approaches to analyze long-read nanopore sequencing data. I will present a study to identify differentially expressed isoforms from nanopore cDNA sequencing of isogenic cell lines with and without a mutation in U2AF1, which is a recurrently mutated splicing factor in cancer. I will also present our analysis of native RNA sequencing of the GM12878 cell line, as part of the Nanopore RNA Consortium. Utilizing the full benefit of directly sequencing full-length RNA transcripts, we identified alternative transcript isoforms and their association with allele expression, RNA modifications, and poly(A) tail length.

About the Speaker

Angela Brooks is an Assistant Professor of Biomolecular Engineering at the University of California, Santa Cruz. She is also an Affiliated Faculty of the UC Santa Cruz Genomics Institute and the Center for Molecular Biology of RNA. Angela joined UC Santa Cruz in 2015, after completing her Postdoctoral Fellowship at the Dana-Farber Cancer Institute/Broad Institute. She completed her Ph.D. in Molecular and Cell Biology with a Designated Emphasis in Computational and Genomic Biology in 2011 at UC Berkeley. In 2018, she was named a Pew Scholar in the Biomedical Sciences and was selected for the Women in Science and Engineering Award as part of the UC Santa Cruz Chancellor's Achievement Awards for Diversity. The Brooks lab works on developing computational and experimental approaches to study cancer mutations that cause changes in the transcriptome, particularly through RNA splicing.