# 24ᵀᴴ Biotechnology Congress: Research & Innovations

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Annual Congress on

# CRISPR Cas9 Technology and Genetic Engineering

October 24-25, 2018 | Boston, USA

## CRISPRseek and GUIDE-seq for design of target-specific guide RNAs in CRISPR-Cas9 genome-editing systems

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The most recently developed genome editing system, CRISPR-Cas9 has greater inherent flexibility than prior programmable nuclease platforms. Because of its simplicity and efficacy, this technology is revolutionizing biological studies and holds tremendous promise for therapeutic applications. However, imperfect cleavage specificity of CRISPR-Cas9 nuclease within the genome is a cause for concern for its therapeutic application. To facilitate the adoption and improvement of this technology, we have developed CRISPRseek for designing target-specific gRNAs, and GUIDE-seq for identifying genome-wide off-target sites from GUIDE-seq and CIRCLE-seq experiments to assess the precision of engineered CRISPR-Cas9 nucleases. In this talk, I will give an introduction to the CRISPR genome editing, GUIDE-seq and CIRCLE-seq technologies, followed by an overview of the functionalities of CRISPRseek and GUIDE-seq. By the end of the talk, the participants should be able to design target-specific gRNAs for various cas9 nucleases and genomes using CRISPRseek and analyze GUIDE-seq and CIRCLE-seq data using GUIDE-seq.

### Biography

Lihua Julie Zhu is a research professor and the head of Bioinformatics Core in the Department of Molecular, Cell and Cancer Biology at University of Massachusetts Medical School. Prior to joining UMASS, she served as the Director of Bioinformatics Consulting Core and the Director of Clinical Informatics Group of the Robert H. Lurie Comprehensive Cancer Center (RHLCCC) at Northwestern University. Her work is devoted to the understanding of gene regulation and cancer biology, biomarker discovery, and development and application of genome editing technology. Her expertise is algorithms and computational tool development. Her group is an active contributor to the open-source open-development Bioconductor project. They have developed a dozen packages with various utilities, ranging from gRNA design, machine learning, peak calling, annotation, data integration to visualization. Among them, two packages are for designing and evaluating gRNAs for the genome editing technology using engineered CRISPR-Cas9 nucleases: CRISPRseek is for designing target-specific and efficient gRNAs, and GUIDE-seq is for evaluating the specificity of gRNAs using GUIDE-seq and CIRCLE-seq technologies. Among her 76 publications

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