

THE 23<sup>rd</sup> INTERNATIONAL  
LAKE ARROWHEAD MICROBIAL GENOMICS CONFERENCE

**LIST OF CONFIRMED SPEAKERS**

September 11-15, 2022  
UCLA Conference Center  
Lake Arrowhead, California  
909 / 337-2478

Kjersti Marie Aagaard, Baylor College of Medicine Houston, TX

“Womb with a View: Importance of Maternal-Fetal Communication in Heritability and Adaptation”

Rosie Alegado, University of Hawaii at Manoa, Honolulu, HI

“Systems microbial ecology: resistance and resilience patterns of subtropical island estuarine microbial assemblages in response to seasonal forcing”

Eric Alm, Massachusetts Institute of Technology, Cambridge, MA

“Gene Transfer and Other Mechanisms of evolution in the Human Microbiome”

Jeffrey E. Barrick, University of Texas at Austin, Austin, TX

“Unintentional Laboratory Evolution of Plasmids and Microbes”

Ilana Brito, Cornell University, Ithaca, NY

“Mechanisms Underlying Microbiome Impacts Across Diseases”

Gina Chaput, University of California Davis, Davis, CA

“Under the Sea: Exploring Plant-Microbe Interactions of Seagrass”

Gautam Dantas, Washington University School of Medicine in St. Louis, St. Louis, MO

“Understanding, Predicting, And Remediating Perturbations To Diverse Microbiomes”

Carrie Ann Eckert, University of Colorado, Boulder, CO

“Development of synthetic biology toolkits for genotype to phenotype evaluation in non- model microbes”

Cesar de la Fuente, University of Pennsylvania, Philadelphia, PA

“Machine Biology for Infectious Diseases”

Joanne B. Emerson, University of California, Davis, CA

“Exploring the soil virosphere”

Anthony Fodor, University of North Carolina, Charlotte, NC

“Adventures with the Poisson distribution: The limitations and surprising power of independence assumptions in microbiome algorithm design”

Alexandra Grote, Broad Institute of MIT and Harvard, Cambridge, MA

“Using genomics and transcriptomics to uncover mechanisms of bacterial persistence”

Katherine Paige Lemon, Baylor College of Medicine, Houston, TX

"In the search for beneficial bacteria, follow your nose!"

Asaf Levy, The Hebrew University of Jerusalem, Jerusalem, Israel

"Systematic Discovery and Characterization of Microbial Toxins"

Tami Lieberman, Massachusetts Institute of Technology, Cambridge, MA

"De Novo Mutations in Human Microbiomes"

Xiaoxia (Nina) Lin, University of Michigan, Ann Arbor, MI

"Microdroplet enabled cultivation and dissection of bacterial communities"

Allison J. Lopatkin, Barnard College of Columbia University, New York, NY

"Genetic determinants of acquiring antibiotic resistance genes"

Hosein Mohimani, Carnegie Mellon University, Pittsburgh, PA

"Computational methods for natural product discovery from microbial communities by integrating mass spectrometry and metagenome mining"

Aindrilla Mukhopadhyay, Lawrence Berkeley Laboratory, Berkeley, CA

"Systems Biology Approaches to Scalable Bioproduction Hosts"

Trent Northen, Lawrence Berkeley Laboratory, Berkeley, CA

"Feeding My Friends: Examining Metabolite Exchange in the Rhizosphere"

Connie Rojas, University of California - Davis, Davis, CA

"Microbiome variation and function in wild and domestic mammals"

Jason Stajich, University of California, Riverside, CA

"Volatile Messages: Fungal-Bacterial Communication"

Cameron Thrash, University of Southern California, Los Angeles, CA

"Illuminating bacterioplankton evolution and function through genomics"

Paul Turner, Yale School of Medicine, New Haven, CT

"Predicting evolutionary genetics of virus-bacteria interactions in patients receiving phage therapy"

Daria Van Tyne, University of Pittsburgh, Pittsburgh, PA

"Adaptation of Multidrug-Resistant Bacteria During Human Infection"

Jean-Marie Volland, Joint Genome Institute, Berkeley, CA

"Crossing bacterial boundaries. Larger and more complex than ever"

Harris Wang, Columbia University College of Physicians and Surgeons, New York, NY

"High-throughput Characterization and Engineering of the Gut Microbiome"

Peter R. Weigle, New England Biolabs, Ipswich, MA

"Genome chemistry: DNA hypermodification in viruses of bacteria."