



SPEECH INFORMATION (For Conference Program Book)

Topic	Multi-Omics Tools Decipher Human Microbiome Biomarkers and Therapeutic Potentials
Abstract	<p>Using multi-omics approaches to study the human microbiome fundamentally connects genetic potential (metagenomics) to active gene expression (metatranscriptomics), functional machinery (metaproteomics), and the ultimate biological outcomes (metabolomics). This integration capacity is essential for delineating complex disease mechanisms, yielding mechanistic biomarkers capable of stratifying heterogeneous conditions, such as cancer, metabolic syndrome, social behaviours, and neurological disorders. The translational impact is profound, steering therapeutic development from broad interventions toward individually tailored strategies. To fully realize the potential of omics-informed personalized medicine, the scientific community must overcome computational hurdles through standardization, conduct robust longitudinal cohort studies to establish reliable causality, and strategically leverage advanced computational frameworks and AI tools. These integrated methods are translating dynamic, high-dimensional biological complexity into clinically actionable strategies for patient management.</p>

