

Poster Board Number	Title	Presenting author	Affiliation	Country
PS2.27.355	<i>Application of 10x Genomics and Synthetic Community to Characterize Antagonistic Bacteria and Sclerotia Microbiome of Sclerotinia sclerotiorum</i>	Zong Han Shie	National Taiwan University	Taiwan, Province of China
PS2.27.356	<i>BaseData: An Ethical Global Biodiscovery Network</i>	Emma Bolton		United Kingdom
PS2.27.358	<i>Breaking DNA Restriction Barriers: Enabling Transformation in Diverse Bacterial Species</i>	Acil Will		Denmark
PS2.27.359	<i>Cross-scale correlations in forest health data</i>	Ren Wenzhi		Finland
PS2.27.360	<i>Deep Mediterranean Mysteries: Novel Method, New Microbes, No Money</i>	Grace Tay		Singapore
PS2.27.361	<i>Discovery of Efficient Cell-Penetrating Peptides for Gram-Positive Bacteria: From Translation Inhibition to Spore-Selective Targeting</i>	Kentaro Kurihara		Japan
PS2.27.362	<i>Dual-chamber bioaerosol system for evaluating airborne pathogen survival and disinfection in controlled environments</i>	Fumito MARUYAMA	HIROSHIMA UNIVERSITY	Japan
PS2.27.363	<i>Emulsion-based culture enrichment for isolation of uncultured bacteria from activated sludge</i>	STEFANIA ANDREA ROSSO-VILLANELO		Denmark
PS2.27.364	<i>Enhancing multi-domain metagenomics with long-read sequencing methodologies</i>	Olga Shopina		Australia
PS2.27.365	<i>Evaluation of microbial cultivation method combining DHS reactor and iChip method</i>	Manami Iino	Tohoku University	Japan
PS2.27.366	<i>Genome-resolved ecological synchronization in the mouse gut microbiome revealed by high-resolution automated sampling</i>	Rina Kurokawa	Laboratory for Symbiotic Microbiome Sciences, RIKEN	Japan
PS2.27.367	<i>Going Native: Harnessing Cell-Penetrating Peptides (CPPs) for Direct Functional Characterization of Wild-Type Bacteria</i>	Tetsushi Mori	Center for Integrative Tokyo University of Agriculture and Technology	Japan
PS2.27.368	<i>HiFi long-read metagenomics reveals mobilome diversity beyond short-read cohorts and reference databases</i>	Hoon Je Seong	Jeonbuk National University	Korea, Republic of
PS2.27.369	<i>Hydrogen isotopes of fatty acids as a proxy for carbon use efficiency in soil microbes</i>	Nathalie Amacker	University of Basel	Switzerland

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PS2.27.370	<i>Integrated Host-Microbe Profiling to De-Risk Respiratory Probiotic Candidates</i>	Gwyneth Hutchinson	University of California, Berkeley	United States of America
PS2.27.371	<i>Investigating the endospore-specific portion of wastewater microbiomes</i>	Amelia Danzinger		Canada
PS2.27.372	<i>Live-FISH sorting in wastewater microbiology</i>	Priscila Carlon	Newcastle University	United Kingdom
PS2.27.373	<i>Metabolic and Genetic Framework for Studying the Airway Commensal <i>Selenomonas sputigena</i></i>	Sang Ho Choi		Korea, Republic of
PS2.27.374	<i>Microbial $\delta^{18}\text{O}(\text{PO}_4^{3-})$ as a Dynamic Indicator of Metabolic Responses to Environmental Stressors in Soil Ecosystems</i>	M. Elena Evertz		Switzerland
PS2.27.375	<i>Nano-scale topomimetic leaf surfaces to investigate microbial phyllosphere colonisation</i>	Evan Kear	Freie Universität Berlin	Germany
PS2.27.376	<i>New genotyping method for <i>Escherichia coli</i> Using RSXC Repeat Polymorphism and Gene-Neighborhood Architecture</i>	Dong Suk Park		Korea, Republic of
PS2.27.377	<i>New sequence barcode system allows tracking horizontal gene transfer from multiple origins simultaneously</i>	Veera Partanen	University of Helsinki	Finland
PS2.27.378	<i>Parallel analysis of diverse soil microbes exposed to a microbial inoculant using w/o droplet co-encapsulation</i>	Sumire Kobayashi	The University of Tokyo	Japan
PS2.27.379	<i>Protein Language Models and CRISPR-Transposon Genetic Engineering Guide Identification of Functionally Deterministic Residues In the Nitrogenase Superfamily</i>	Zahra Shivji	California Institute of Technology	United States of America
PS2.27.380	<i>Proteomic Stable Isotope Probing Reveals Prebiotic Utilization Patterns in a Simulated Human Gut Microbiome</i>	Emilee Lance	Oregon State University	United States of America
PS2.27.381	<i>Quantitative metagenomics provides accurate cell counts validated by epifluorescence microscopy, with high taxonomic resolution</i>	Qicheng Bei	University of Southern California	United States of America
PS2.27.382	<i>Quantitative single-cell imaging of microbial trophic interactions using stable isotope probing and Raman microspectroscopy</i>	Gordon Taylor	Stony Brook University	United States of America
PS2.27.383	<i>Raman-Activated cell sorting for targeted isolation of unculturable rumen microorganisms</i>	Katie Lawther	Wageningen University	Netherlands

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PS2.27.384	<i>Reverse Methods Discovery: A Tool for Accessible Microbial Ecology Research</i>	Marianne Haines	University of Calgary	Canada
PS2.27.385	<i>RNA interference may be a promising method to reduce enteric methane emissions</i>	Mi Zhou		Canada
PS2.27.386	<i>Statistical exploration of keystone taxa that reorganize assembly rules in forest root microbiomes</i>	Noguchi Mikihiro		Japan
PS2.27.387	<i>Targeted Protein Translation Suppression in the Dinoflagellate, <i>Prorocentrum lima</i>, using Cell-Penetrating Peptides (CPP)</i>	Qisya M. Amirul	Tokyo University of Agriculture and Technology	Japan
PS2.27.388	<i>The dynamic state of S-layer liquid condensates affects microbial biofilm ecology and biogenesis</i>	Staffan Kjelleberg	Nanyang Technological University	Singapore
PS2.27.389	<i>The potential of Cell-Penetrating Peptide-Conjugated Peptide Nucleic Acids (CPP-PNA) for functional characterization in <i>Streptomyces</i></i>	Suzune HONDA		Japan
PS2.27.390	<i>Towards Identifying Membrane Vesicle Recipients in Bacterial Communities</i>	Masahito Kataoka		Japan
PS2.27.391	<i>Understanding Metabolic Pathways Using Cell-Penetrating Peptide-“Peptide Nucleic Acid (CPP-PNA) Conjugates in Cyanobacteria</i>	Yuka Kikuyama	Tokyo University of Agriculture and Technology	Japan
PS2.27.392	<i>Validating quantitative SIP-Raman-CARD-FISH: Single Cell Chemoautotrophic Rates from Key Taxa in the ETNP ODZ</i>	Natalie Butkevich		United States of America
PS2.27.393	<i>Visualization of functional gene in microorganisms by using click chemistry and HCR-FISH</i>	Tsuyoshi Yamaguchi		Japan
PS2.27.394	<i>Wastewater-based Epidemiology Provides Spatiotemporal SARS-CoV-2 and Influenza Virus Infection Dynamics</i>	Xiawan Zheng	The University of Hong Kong	Hong Kong