

Poster Board Number	Title	Presenting author	Affiliation	Country
PS2.13.158	<i>A Framework for Accessible Microbiome Analysis: Tutorials, Visualization Tools, and Cross Database Taxonomic Comparison for QIIME 2</i>	Diana Calvo	Northern Arizona University	United States of America
PS2.13.159	<i>A GNN-enhanced framework infers strain-level interactions of Klebsiella and phages</i>	Biffon Manyura Momanyi	Southern University of Science and Technology	China
PS2.13.160	<i>A Statistical Hi-C Framework to Quantify Host-Mobile Genetic Element Networks and Environmental Constraints on Horizontal Gene Transfer</i>	Grace Solini		United States of America
PS2.13.161	<i>Accessible and accurate metagenomic taxonomic profiling with Metabuli and Metabuli App</i>	Jaebeom Kim		Korea, Republic of
PS2.13.162	<i>An integrated framework for giant virus and endogenous viral element discovery, genomics and quality control</i>	Frederik Schulz	Joint Genome Institute (DOE)	United States of America
PS2.13.163	<i>Applications of Long-read Nanopore Sequencing to Drinking Water Microbiota</i>	William Taylor		New Zealand
PS2.13.164	<i>Bias calibration enables robust spike-in-based absolute quantification in metagenomic sequencing</i>	Xianghui Shi	The University of Hong Kong	Hong Kong
PS2.13.165	<i>Biome-specific genome catalogues reveal functional potential of shallow sequencing</i>	Dattatray Mongad	University of Turku	Finland
PS2.13.166	<i>CleanBar: a versatile demultiplexing tool for split-and-pool barcoding in high-throughput microbial single-cell genomics</i>	Mária Džunková	University of Valencia	Spain
PS2.13.167	<i>Clustering Proteomes and Curating References at Scale with MMseqs2-ProteomeCluster</i>	gyuri kim	Seoul National University	Korea, Republic of
PS2.13.168	<i>Comprehensive virome profiling with BAQLaVa reveals viral perturbations in inflammatory bowel disease and colorectal cancer</i>	Kelsey Thompson	Harvard TH Chan School of Public Health	United States of America
PS2.13.169	<i>Creating unity: linking 16S rRNA gene sequence information to the core taxonomy of genomes</i>	Hilde Vinje	Norwegian University of Life Sciences	Norway
PS2.13.170	<i>Detecting natural selection from longitudinal human gut metagenomes</i>	Sur Herrera Paredes	Universidad Nacional Autónoma de México	Mexico

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PS2.13.171	<i>Development of statistical method for identification of important species from complex microbial community</i>	Toshikazu Fukushima	NIPPON STEEL CORPORATION	Japan
PS2.13.172	<i>Diversity of bacterial cellulose gene clusters across the tree of life</i>	Angie Waldisperg	Aalborg University	Denmark
PS2.13.173	<i>DRAM2: A Modular, Multi-Omics-Integrated Platform for Scalable Microbial Genome Annotation</i>	Mikayla Borton	Colorado State University	United States of America
PS2.13.174	<i>From performance to practicality: benchmarking microbial sequencing platforms for genomics, metagenomics and community profiling in academic labs</i>	Kevin Lee	Auckland University of Technology	New Zealand
PS2.13.175	<i>From sequences to traits: An AI-driven AutoML framework for genome-resolved microbial ecology</i>	Breno Livio Silva de Almeida	University of Sao Paulo	Brazil
PS2.13.176	<i>Genomic characterization of the rice paddy methanotroph <i>Methylobacterium fluvii</i> F7 reveals traits supporting methane mitigation and plant-growth promotion</i>	Gi Uk Hong	university	Korea, Republic of
PS2.13.177	<i>Global antimicrobial resistance patterns in human gut metagenomes are structured along socio-economic gradients</i>	Mahkameh Salehi	University of Turku	Finland
PS2.13.178	<i>High-dimensional properties of k-mer frequency data and their relationship to the recoverability of metagenome assembled genomes</i>	Rohan Williams	National University of Singapore	Singapore
PS2.13.179	<i>Improved recovery of insertion sequences in assemblies and metagenome-assembled genomes via Oxford Nanopore Technologies long-read sequencing</i>	Julia Plewka	University of Duisburg-Essen	Germany
PS2.13.180	<i>Inferring gene co-evolution through ancestral state-aware analyses for functional prediction: applications to microbial ecogenomics</i>	Yuki Nishimura	The University of Tokyo	Japan
PS2.13.181	<i>Integrating Read-Based and Assembly-Based Approaches to Recover Non-Bacterial Diversity from Arctic Ocean Metagenomes</i>	Tulika Bhardwaj		Canada
PS2.13.182	<i>Integrative exploration of Earth's viomes through the VIRE platform</i>	Suguru Nishijima	The University of Tokyo	Japan
PS2.13.183	<i>ItBins: Ultrafast MAG refinement</i>	Alexander Probst	University of Duisburg-Essen	Germany

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PS2.13.184	<i>Jumbo phages encode diverse mechanisms to manipulate host cell surface interactions</i>	Ling Yuan		China
PS2.13.185	<i>Longitudinal metatranscriptomic analyses of spoilage microbiome of MAP broiler at two temperatures reveals succession of active species</i>	Julia Manninen	University of Helsinki	Finland
PS2.13.186	<i>Machine learning prediction of eukaryotic hosts for giant viruses</i>	Hsin-Ying Chang		Taiwan, Province of China
PS2.13.187	<i>Meta2bSeek: integrated cross-kingdom taxonomic, strain and functional profiling of microbial communities using k-mers at type IIb restriction sites</i>	Shi Huang		Hong Kong
PS2.13.188	<i>MetaCoOc: Global-scale environmental association and co-occurrence of microbial species</i>	Benjamin Coltman		Austria
PS2.13.189	<i>MetaSpicii refines phage-host infection networks generated from meta-HiC data</i>	Zichun Sun		China
PS2.13.190	<i>Microbiome Datahub: An Open-access Platform Integrating Environmental Metadata, Taxonomy, and Functional Annotation for Comprehensive Metagenome-assembled Genome Datasets</i>	Hiroshi Mori	National Institute of Genetics	Japan
PS2.13.191	<i>Modeling Microbiome Time Series for Automated Detection of Significant Community Shifts</i>	Ann-Kathrin Dörr		Germany
PS2.13.192	<i>Modelling the Dynamics of Wolbachia and Viral Infections in Aedes albopictus Mosquitoes</i>	Eve Wood	University of Oxford	United Kingdom
PS2.13.193	<i>Modern genome mining with BiG-SCAPE 2.0 - faster and more accurate sequence clustering of metabolic gene clusters</i>	Catarina Loureiro		Australia
PS2.13.194	<i>Multi-omic evidence reveals a low-abundance Hyphomicrobium as a keystone biodegrader challenging the role of methane-oxidizing bacteria in sulfamethoxazole degradation</i>	Alen Simonic	Technical University of Denmark	Denmark
PS2.13.195	<i>nf-core/funcprofiler: a community-led workflow for metagenomic functional classification profiling</i>	Vinícius Werneck Salazar		Australia
PS2.13.196	<i>OmniCorr: A multi-omics integration tool for exploring host-microbiome interactions</i>	Veronica Quarato	Norwegian University of Life Sciences	Norway

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PS2.13.197	<i>Optimal Transport-Based Recasting of Beta Diversity for Microbiome Data</i>	Yu Nakajima	Japan Agency for Marine-Earth Science and Technology	Japan
PS2.13.198	<i>Optimization of microbial function through environmental manipulations</i>	Jaewook Lee	University of California Irvine	United States of America
PS2.13.199	<i>Orchestrating Microbiome Analysis with Bioconductor</i>	Tuomas Borman	University of Turku	Finland
PS2.13.200	<i>Pilea: profiling bacterial growth dynamics from metagenomes with sketching</i>	Xi Chen		Hong Kong
PS2.13.201	<i>Predicting water quality through microbial community shift in New Zealand groundwater</i>	Louise Weaver	PhF Science	New Zealand
PS2.13.202	<i>Prevalence-based core microbiomes are robust across environments but method-dependent across kingdoms</i>	Camilo Andres Quiroga Gonzalez	Helmholtz-Centre for Environmental Research	Germany
PS2.13.203	<i>PyamilySeq: exposing the fragility of conventional gene (re)clustering and prokaryotic pangenomic inference methods</i>	Nicholas Dimonaco	Queen's University Belfast	United Kingdom
PS2.13.204	<i>rescomp: An R package for resource competition modelling</i>	Christopher Brown		Australia
PS2.13.205	<i>rRNA-ops pipeline for the analysis of long-read rRNA operon Nanopore data of microbial communities</i>	Anil Kumar	Rutgers University, New Brunswick	United States of America
PS2.13.206	<i>Rsearch: A user-friendly R interface to VSEARCH with data-driven parameter tuning for streamlined metabarcoding data processing and analysis</i>	Cassandra Stamsaas	Norwegian University of Life Sciences	Norway
PS2.13.207	<i>SAR11 Genome Atlas: An interactive web interface navigating from genetic potential to global biogeochemistry</i>	Satoshi Nishino	The University of Tokyo	Japan
PS2.13.208	<i>Selecting the right metagenomes: Improving genome recovery through targeted co-assembly</i>	Rebecca Freitag	Technical University of Denmark	Denmark
PS2.13.209	<i>Shotgun metagenomic profiling reveals foodborne fungal and viral communities associated with pathogenicity and spoilage in ready-to-eat foods</i>	Thendo Mafuna	University of Johannesburg	South Africa

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PS2.13.210	<i>Stability of functional gene dynamics inferred from genome and functional gene level network structures and high-frequency temporal dynamics in the mouse gut microbiome</i>	Musashi Arakawa	Institute of Science Tokyo	Japan
PS2.13.211	<i>The Other Microbial Dark Matter: the hidden structure below the species level in metagenomic datasets</i>	Arthur Solano	University of Sao Paulo	Brazil
PS2.13.212	<i>Towards microbial dark matter-inspired synthetic metabolic networks for biotechnology</i>	Pranas Grigaitis	Karlsruhe Institute of Technology	Germany
PS2.13.213	<i>Trait-based ecology reveals microbial alkaline adaptive strategies</i>	Minglei Ren		China
PS2.13.214	<i>Tree of life scale analyses of protein families and their genomic context with AASTK</i>	Daan Speth		Austria
PS2.13.215	<i>Unsupervised Anomaly Detection with Flow Cytometric 2D Histogram Data Identifies Possible Origins for Anomalous Changes in Microbial Communities in Drinking Water</i>	Isabel Erb		Sweden
PS2.13.216	<i>Unveiling a Mobile Saxitoxin Biosynthetic Gene Cluster through Protein Domain Mapping and Customized Detection rules</i>	Marcele Laux	University of São Paulo	Brazil
PS2.13.217	<i>Urban freshwater viromes from four wastewater treatment plants reveal host-linked viral dynamics and resistance gene potential</i>	Kira Moon	Hankuk University of Foreign Studies	Korea, Republic of
PS2.13.218	<i>Vitamin A deficiency induces sex-specific ecological convergence of the gut microbiome</i>	IWIN JOSEPH	National Agri-Food Biotechnology Institute	India
PS2.13.219	<i>Wagtail: A hybrid QIIME 2 and Minimap2 Snakemake pipeline for accurate and scalable 16S RNA profiling</i>	Rizky Nurdiansyah	Queensland University of Technology	Australia