

Poster Board Number	Title	Presenting author	Affiliation	Country
PS2.26.289	<i>10-HDA Inhibits Bacterial Biofilm, Iron Uptake and Drug Resistance by Regulating Small RNA Expression</i>	Yue Hao	Chinese Academy of Agricultural Sciences	China
PS2.26.290	<i>Acalypha australis L. extract reduces antibiotic resistance gene dissemination and reshapes the gut resistome in weaned piglets</i>	Xinyi Yang	Nanjing Agricultural University	China
PS2.26.291	<i>Antibiotic Pollution Weakens Passive Wastewater Treatment and Ecosystem Health: Insights from a Low-Cost Multi-Stage Lab-Scale Constructed Wetland</i>	Mikołaj Wołacewicz		Poland
PS2.26.292	<i>Antibiotic resistance gene carriage is associated with an elevated mortality risk in the general Finnish population</i>	Sanni Haahti		Finland
PS2.26.293	<i>Antimicrobial Resistance and One Health: It's not just the selection pressure from the use of antimicrobials, it's also the human-caused environmental changes</i>	Sonja Johanna Muurinen	University of Helsinki	Finland
PS2.26.294	<i>Antimicrobial Resistance by metaGenomics Overview in a Sewage system (ARGOS)</i>	Víctor López Maroto	National Museum of Natural Science	Spain
PS2.26.295	<i>Antimicrobial resistance dissemination potential of bio-based fertilizers according to field trials</i>	Marko Virta	University of Helsinki	Finland
PS2.26.296	<i>Antimicrobial resistance in remote lakes: metagenomic and phenotypic insights</i>	Giulia Borgomaneiro		Italy
PS2.26.297	<i>Antimicrobial resistance in the marine environment in Norway - Need for surveillance</i>	Nachiket Marathe		Norway
PS2.26.298	<i>Artificial sweetener diversity drives oxidative stress mediated evolution of antibiotic resistance in soil animal gut microbiomes</i>	Yi-Fei Wang	Chinese Academy of Sciences	China
PS2.26.299	<i>Bacterial vesicle encapsulation confers resilience to plasmid transfer against UV radiation and oxidative stress</i>	Stelios Chatzimichail	University of Cyprus	Cyprus
PS2.26.300	<i>Characterization, Antagonistic Effect and Antibiotic Sensitivity Pattern:</i>	Timothy O. Adejumo	Precious Cornerstone University	Nigeria
PS2.26.301	<i>Chlorine disinfection drives evolutionary dynamics of antibiotic resistance in waterborne pathogens</i>	Zhigang Yu		Australia

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PS2.26.302	<i>Comparative analysis of contamination rates by plasmid-mediated antibiotic resistant bacteria in dried fish products in Japan and Vietnam</i>	Tatsuya Nakayama		Japan
PS2.26.303	<i>Complete genomic sequencing and characterization of an ESBL-producing Escherichia coli sequence type 8211 isolated from the fecal material of an Eastern Bongo</i>	Richard McLaughlin	Gateway Technical College	United States of America
PS2.26.304	<i>Comprehensive analysis of air hospital microbiomes uncovers potential hotspots and avenues for transmission of diverse pathogens linked to hospital-acquired infections</i>	Pedro Lebre		United Kingdom
PS2.26.305	<i>Deciphering Phenotypic Antimicrobial Resistance and Transfer Dynamics in the Plastisphere via Single-cell Techniques</i>	Kai Yang	Institute of Urban Environment, Chinese Academy of Sciences	China
PS2.26.306	<i>Development of a pipeline for the characterisation of primordial antibiotic resistance elements to the candidate antibacterial, niclosamide</i>	Hannah Lee-Harwood		New Zealand
PS2.26.308	<i>Environmental filtering shapes human-associated faecal markers and resistome persistence across wastewater-river networks</i>	John Paul Makumbi	Stellenbosch University	South Africa
PS2.26.309	<i>Evidence of antimicrobial resistance in the gut microbiota of children from informal settlements in South Africa</i>	Nobuhle Kambunga		South Africa
PS2.26.310	<i>Experimental evolution of copper resistance in plant-associated pseudomonads</i>	Hema Rallapati		New Zealand
PS2.26.311	<i>Farming Practices Shape Microbiomes and Resistomes across Pigs, Soil, and Farm workers</i>	Cuipeng Zhu		China
PS2.26.312	<i>From resistance to resilience: uncovering how sludge microbes evolve to destroy sulfonamides</i>	Mengyan Li	New Jersey Institute of Technology	United States of America
PS2.26.313	<i>Genome Guided Discovery of RiPP Biosynthesis Relevant to Antimicrobial Resistance</i>	Arjun Nagarajan	The University of Auckland	New Zealand
PS2.26.315	<i>Genome-Resolved Local Community Surveillance Reveals Ecological Structuring and Mobility-Enabled Connectivity of Antimicrobial Resistance</i>	Soyeon Kim	Chung-Ang University	Korea, Republic of
PS2.26.316	<i>Genomic Convergence and Synergistic Co-occurrence of Virulence and Resistance in Salmonella enterica from Swine and Poultry Food Chains in Metro Manila, Philippines</i>	Jonah Feliza Mora	University of the Philippines Diliman	Philippines

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PS2.26.317	<i>Genomic insight into the antibiotic-resistant determinants of Escherichia coli from small ruminants and manure in North West Province, South Africa</i>	Jody Howard		South Africa
PS2.26.318	<i>Genomic insights into Shigella species isolated from small ruminants and manure in the North West Province, South Africa</i>	Tshepang Motlhaping		South Africa
PS2.26.319	<i>Identification of Shared Accessory Genes in Escherichia coli in the Lake Biwa Basin, Japan</i>	Yu Tang	Tsinghua University	China
PS2.26.320	<i>Improvement and application of inverse PCR-approach for analyzing genetic environment of antibiotic resistance genes</i>	Veronika Lyasnikova	University of Helsinki	Finland
PS2.26.321	<i>Insects as vectors for antimicrobial resistance in urban landscapes</i>	Pilar Lopez Hernandez	Uppsala University	Sweden
PS2.26.322	<i>Integrating air quality, microbiome, and ARG metrics reveal season-dependent occupational risks in swine farm aerosols</i>	Gihan Lee		Korea, Republic of
PS2.26.323	<i>Investigating the in vivo efficacy of a novel antimicrobial agent</i>	Stella Colquhoun	The University of Auckland	New Zealand
PS2.26.324	<i>Linking cyanobacterial blooms to the environmental resistome: microbial interactions and gene flow</i>	Seungjun Lee	Kyungpook National University	Korea, Republic of
PS2.26.325	<i>Long-term Impact of Biocide Exposure on Resistance Development of Microbes in Intensive Care Units</i>	Shijiao Qi	Xi'an Jiaotong-Liverpool University	China
PS2.26.326	<i>Mapping the evolutionary and functional landscape of broad-spectrum antibiotic degrading metallo-β-lactamases: environmental reservoirs and pathways to clinical resistance</i>	Georgina Joyce	The University of Queensland	Australia
PS2.26.327	<i>Mapping the hidden reservoir: Nationwide pollution of ARG-carrying pathogens in urban wetland parks</i>	Binhao Wang	Hangzhou Normal University	China
PS2.26.328	<i>Mechanisms and evolution of resistance to antimicrobial biocides and consequences for antibiotic resistance</i>	Frank Schreiber	Federal Institute for Materials Research and Testing	Germany
PS2.26.329	<i>Meta-epigenetics reveals the gut microbiome adaptation in response to antibiotic stress</i>	Han Na Oh		Korea, Republic of

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PS2.26.330	<i>Microbiome-Informed Risk Modelling Reveals Emerging AMR Hotspots and High-Risk Pathogen Lineages Across Asia-Pacific Food Supply Chains</i>	Barbara Drigo	Adelaide University	Australia
PS2.26.331	<i>Mobile Genetic Element-Mediated Transmission Mechanisms of Antibiotic Resistance Genes in Vibrio</i>	Xiaofeng Dai	Shenzhen University	China
PS2.26.332	<i>Mutations associated with streptomycin resistance predicted to be highly prevalent and evolvable across bacteria</i>	Le Na Ngo	University of Queensland	Australia
PS2.26.333	<i>Nanoscale Microbiomes as Key Mediators in Antibiotic Resistance Dissemination Across Ecosystems</i>	Jian-Qiang Su	Institute of Urban Environment, Chinese Academy of Sciences	China
PS2.26.334	<i>Non-enzymatic ciprofloxacin inactivation mediated by metabolic conditions in Microbacterium sp. CJ48 isolated from river</i>	Miryung Kim	Chung-Ang University	Korea, Republic of
PS2.26.337	<i>PanRes2: A database of latent and acquired antimicrobial resistance, allowing for 3D based protein homology search</i>	Martina Vojtkova	Technical University of Denmark	Denmark
PS2.26.338	<i>Phages in urban invasive snail guts bundle resistance and metabolic genes in pathogenic Enterobacteriaceae</i>	Yi-Yue Zhang	Institute of Urban Environment, Chinese Academy of Sciences	China
PS2.26.339	<i>Pioneer colonizers on microplastics govern the enrichment and succession of antibiotic resistance genes</i>	Wenxuan Li	Beijing Forestry University	China
PS2.26.340	<i>Poultry gut is a reservoir of antibiotic resistance genes with global spread to humans</i>	Yasmine Eddoubaji	University of Helsinki	Finland
PS2.26.341	<i>Predicting evolution: Quantifying the emergence of antibiotic resistance in diverse environmental strains of E. coli</i>	Stella Pearlless		New Zealand
PS2.26.342	<i>Production and consumption environments shape the health risk of vegetable-associated resistomes</i>	Wen-Jing Li		China
PS2.26.343	<i>Promiscuous family VIII esterases in the plastisphere: bridging plastic biodegradation and antibiotic resistance?</i>	Harry Lerner		Belgium
PS2.26.344	<i>Protistan predation accelerates plasmid-mediated dissemination of antibiotic resistance in soil microbial communities</i>	Qinglin Chen		China

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PS2.26.345	<i>Protozoan predation promotes bacterial plasmid transfer in aquatic ecosystems</i>	Robin Starke		Germany
PS2.26.346	<i>Small watersheds, big threat: Plasmid-mediated horizontal gene transfer amplified the role of raw sewage influenced coastal streams to shape the seascape resistome</i>	Bowei Li		China
PS2.26.347	<i>Successive and transient states with unique microbial and host signatures underlie gut microbiome recovery and CPE decolonization</i>	Jean-Sebastien Gounot	Genome Institute of Singapore A*STAR	Singapore
PS2.26.348	<i>Surveillance design and antimicrobial resistance signals in wastewater: spatial sampling, pre-analytical processing, and risk-based interpretation</i>	Andrea Naziri	University of Cyprus	Cyprus
PS2.26.349	<i>Survey of Antimicrobial Resistant Bacteria in Urban Auckland Stormwater Systems</i>	Hannah Purdie	Auckland University of Technology	New Zealand
PS2.26.350	<i>Systematic Characterization of the Aeromonas Mobile Resistome Uncovers Its Role in Global Antibiotic Resistance Gene Dissemination</i>	Sang-Gyu Kim	Jeonbuk National University	Korea, Republic of
PS2.26.351	<i>Systematic review of wild birds as reservoirs of antimicrobial resistance: Implications for roof-harvested rainwater safety</i>	Mira Cooper-Beknazarova	Adelaide University	Australia
PS2.26.352	<i>Tackling antimicrobial resistance with a next-generation quaternary ammonium compound</i>	Raquel Ortega	The University of Auckland	New Zealand
PS2.26.353	<i>Wastewater antimicrobial resistance in transient community and hospital catchments reveals signals obscured in aggregated municipal influent</i>	Stavri Karasiali	University of Cyprus	Cyprus
PS2.26.354	<i>When anthropogenic and river microbiomes collide: who wins, who lose, what drives the spread of antimicrobial resistance?</i>	Christophe Merlin		France