

Poster Board Number	Title	Presenting author	Affiliation	Country
PS3.19.178	<i>A metataxonomic and metabolomic approach reveals the impact of maternal microbial succession on infant microbiome development</i>	Mitali Inamdar	National Center Cell Science	India
PS3.19.179	<i>Antibiotics that promote carbapenem-resistant <i>Pseudomonas aeruginosa</i> intestinal colonisation reduce nutrient competition and inhibitory metabolite production by the gut microbiome</i>	Lauren C. Mason		United Kingdom
PS3.19.180	<i>A population-scale analysis of gut microbiome across lifestyles and diseases revealed missing microbes and functional traits</i>	Nuria Alegre Hospitaler		Austria
PS3.19.181	<i>A specific <i>Weissella</i> strain from Kimchi protects against colitis by modulating host immune signaling via bioactive metabolites</i>	Juhye Baek	Chung-Ang university	Korea, Republic of
PS3.19.182	<i>A Unified Whole-Metagenome Framework for Multi-Kingdom Taxonomy and Functional Reconstruction of the Human Gut Microbiome</i>	Joon-Young Park		Korea, Republic of
PS3.19.183	<i>Australian Human Microbiome Biobank: A high-throughput isolation platform for expanding cultured diversity across the human microbiome</i>	James Volmer	Queensland University of Technology	Australia
PS3.19.184	<i>Baseline gut microbiota shapes antibiotic-induced pathogen overgrowth</i>	Michelle Fan		United Kingdom
PS3.19.185	<i>Beyond taxonomy: conserved microbial metabolic programs associate with melanoma immunotherapy response</i>	Kshitij Tandon	University of Melbourne	Australia
PS3.19.186	<i>Characterizing phage-bacteria interactions shaping gut microbial development in childhood stunting</i>	Tommy Boutin	McGill University	Canada
PS3.19.187	<i>Characterizing the gut-lung axis: gut microbiome shifts in asthmatic mice following pulmonary cyanotoxin exposure</i>	Jayun Kim		United States of America
PS3.19.188	<i>Comparative analysis of gut microbiome composition and function in elite endurance and sprint cyclists</i>	Nadija Palinich	The University of Auckland	New Zealand
PS3.19.189	<i>Complex periodontal biofilms comprising <i>Fusobacterium nucleatum</i>, <i>Porphyromonas gingivalis</i>, <i>Tannerella forsythia</i> and <i>Prevotella intermedia</i>, and their disruption by the <i>Fusobacterium bacteriophage FNU1</i></i>	Siti Saleha Binte Mohamed Yakob Adil	La Trobe University	Australia
PS3.19.190	<i>Conventional diagnostics misrepresent the small intestinal microbiome: evidence from 16S rRNA profiling</i>	Michał Stanowski	University of Warsaw	Poland
PS3.19.191	<i>Cross-cohort analysis reveals conserved gut virome signatures and phage-encoded auxiliary functions in ulcerative colitis</i>	Hongjae Park	Inha University	Korea, Republic of

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PS3.19.192	<i>Culturomics-based exploration and comparative genomic analysis of commensal bacteria isolated from healthy human skin to characterize functional potential</i>	Hye Rim Do	Chung-Ang University	Korea, Republic of
PS3.19.193	<i>Discovery of putative active and cryptic viral infections in prevalent gut fungi</i>	Andrea Silverj	University of Calgary	Canada
PS3.19.194	<i>Disease-associated dysbiosis reshapes diet-microbiome interactions in Parkinson's disease and prodromal REM sleep behaviour disorder</i>	Sungyang Jo	Asan Medical Center, University of Ulsan College of Medicine, Seoul, 05505	Korea, Republic of
PS3.19.195	<i>Distinct Gut Microbiome Dynamics in Parkinson's Disease According to Premotor REM Sleep Behaviour Disorder Status</i>	Hyuna Im	Asan Medical Center	Korea, Republic of
PS3.19.196	<i>Ecological sensitivity of the human microbiome</i>	Jie Deng	University of Oxford	United Kingdom
PS3.19.197	<i>Ecological Trajectories of Gut Bacterial and Phage Communities across the Human Lifespan in a Korean Cohort</i>	Hyo-Eun Kim		Korea, Republic of
PS3.19.198	<i>Effects of stress hormones on microbial growth physiology, community structure and function</i>	Michael Daniels		Austria
PS3.19.199	<i>Environmental Factors Affecting Early Gut Microbiome Development in a Rural Setting</i>	Mona Parizadeh	University of Calgary	Canada
PS3.19.200	<i>Exploring the Influence of Medications on the Gut Microbiome in Parkinson's disease: Disentangling Disease- and Medication-Associated Taxonomic and Functional Features</i>	Jae-Yun Lee	KAIST	Korea, Republic of
PS3.19.201	<i>From Diet to Circulation: Gut Microbial Pathways Shape Human Responses to Blueberries</i>	Jared Ellenbogen	Colorado State University	United States of America
PS3.19.202	<i>Functional heterogeneity of vaginal community state types and their ecological connectivity across female urogenital niches</i>	Da-Ryung Jung		Korea, Republic of
PS3.19.203	<i>GLP-1 RA-Exacerbated Gut Microbiome Dysbiosis in Obesity Mediates Post-Cessation Weight Regain</i>	Chenhong Zhang		China
PS3.19.204	<i>Gut microbial BCAA biosynthesis is a key contributor to insulin resistance pathogenesis</i>	Mingwei CAI	Shenzhen Bay Laboratory	China
PS3.19.205	<i>Gut microbiota contributes to the therapeutic effect of acupuncture in atopic dermatitis</i>	Yerin Seo	Gyeongsang National University	Korea, Republic of

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PS3.19.206	<i>In situ visualisation of the spatial and host dynamics of plasmids in the human gut</i>	Lara Carrington		Australia
PS3.19.207	<i>Investigating Multi-Omic Signatures of Ethnicity and Dysglycaemia in Asian Chinese and European Caucasian Adults: Cross-Sectional Analysis of the TOFI_Asia Study at 4-Year Follow-Up</i>	Saif Faraj		New Zealand
PS3.19.208	<i>Investigating Oxygen-Stable [FeFe]-Hydrogenases in Human Gut Bacteroides</i>	Warunika Karunasiri	Monash University	Australia
PS3.19.209	<i>Leveraging Microbial Competition to Fight Intestinal Multidrug-Resistant Infections</i>	Kankan Zhao	University of California, San Diego	United States of America
PS3.19.210	<i>Longitudinal eco-evolutionary dynamics of antibiotic survival in catheter-associated urobiomes</i>	Lieze Agten		Belgium
PS3.19.211	<i>Longitudinal Stool Multi-omics Indicates Temporal Remodeling of Gut Microbiome Function After Kidney Transplantation</i>	Boyun Choi		Korea, Republic of
PS3.19.212	<i>Long-read genomic profiling of a severe acne case reveals a novel F-lineage Cutibacterium acnes strain in the skin microbiome</i>	Hye Sun Cho	Chung-Ang University	Korea, Republic of
PS3.19.213	<i>Lysozymes as microbiome modulators: Molecular insights into Trichomonas vaginalis-bacteria interactions</i>	Bailey Dickson	University of Auckland	New Zealand
PS3.19.214	<i>Metabolic differences in the maternal gut microbiome precede the birth of large-for-gestational-age infants: A nested case-control study</i>	Anusha T Antony		Sweden
PS3.19.215	<i>Metabolic Profiling and Dietary Associations of Novel Gut Microbes Associated with Positive Mental Health</i>	Rebecca Kerstens	Queensland University of Technology	Australia
PS3.19.216	<i>Metagenomic analysis of early-life gut microbial ecology in children with febrile seizures</i>	Jun Kubota		Japan
PS3.19.217	<i>Microbiota analysis in colorectal cancer: mechanistic insights into microbial contribution to carcinogenesis</i>	Shu-Jung Lai	China Medical University, Taiwan	Taiwan, Province of China
PS3.19.218	<i>Niche-Specific Divergence of Cutibacterium and Staphylococcus Strains Isolated from Osteoarthritic Synovial Fluid Compared to Skin-Derived Isolates</i>	Hyeseon Jeong		Korea, Republic of
PS3.19.219	<i>Oxygen Modulates Microbe-Microbe Interactions Among Airway Commensals</i>	Sophie Pickelner	University of Michigan	United States of America

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PS3.19.220	<i>Oxygen-dependent gene expression by Lactobacillus crispatus correlates with vaginal community composition</i>	Michael France	University of Maryland	United States of America
PS3.19.221	<i>Protective effects of exopolysaccharide derived from Lacticaseibacillus rhamnosus IRO6 against UVB-induced photoaging in hairless mice</i>	Jin Hwan Kim		Korea, Republic of
PS3.19.222	<i>Rapid Respiratory Response in Rural and Remote Regions (RRR2) - an observational study of bronchiectasis using ground-breaking tools</i>	Jessica Carlson-Jones	Flinders University	Australia
PS3.19.223	<i>Rethinking TMA production: competing microbial pathways shape cardiometabolic risk</i>	Ayda Lewis	Colorado State University	United States of America
PS3.19.224	<i>Role of Fusobacterium nucleatum in proliferation and migration of oral squamous carcinoma cells</i>	Syeda Areeba Rehan	La Trobe University	Australia
PS3.19.225	<i>Shifts in bacterial and phage taxonomy and function associated with oral lyophilised faecal microbiota transplantation in Clostridioides difficile infection</i>	Isabelle Daly		Australia
PS3.19.226	<i>Site-specific Gene Catalogs to Enable Function-Centric Approaches in Human Microbiome Research</i>	Issac Chaudry		United States of America
PS3.19.227	<i>Strain-Level Genomic Diversification and Host-Integrated Functional Landscape of the Asian Skin Microbiome</i>	Hye Lim Keum	Chung-Ang University	Korea, Republic of
PS3.19.228	<i>Strain-level meta-analysis of metagenomics data in haematological cancer</i>	Ghjuvan Grimaud	Lund University	Sweden
PS3.19.229	<i>The adaptive potential of Staphylococcus aureus in chronic rhinosinusitis</i>	David Broderick		New Zealand
PS3.19.230	<i>Unravelling microbiota dynamics to inhibit carbapenem-resistant Enterobacteriaceae using an artificial gut chemostat model</i>	Alexander Y. G. Yip		United Kingdom