

Aasmets, Oliver		
<b>Systematic evaluation of long-term drug effects on the gut microbiome in the Estonian Microbiome Cohort</b>		48
Aasmets, Oliver	Presenter: Org, Elin	
<b>Similarity to the gut microbiome of non-westernized populations predicts health outcomes in the Estonian Microbiome Cohort</b>		49
Aguilar Ramos, Miguel		
<b>Development of irreversible covalent inhibitors of the colibactin activating protease</b>		50
Alvarez-Silva, Camila		
<b>Impact of acute alcohol consumption on circulating microbiome in asymptomatic alcohol-related liver disease</b>		51
Alvi, Tayyaba		
<b>Causal links between the gut microbiome and age associated functional and structural changes in the brain</b>		52
Andreu Sánchez, Sergio		
<b>From strain to host: unraveling the link between gut microbial genetic diversity and health</b>		53
Andrikopoulos, Petros		
<b>Evidence of a causal and modifiable relationship between kidney function and circulating trimethylamine N-oxide</b>		54
Avershina, Ekaterina		
<b>Phage-bacteria interactions and post colonoscopy shifts in gut microbiome through the lens of CRISPR-Cas system</b>		55
Awan, Ayesha		
<b>Intestinal microbiota consumes specific dietary proteins that evade host digestion</b>		56
Baev, Vesselin		
<b>Genome sequencing and analysis of <i>P. pentosaceus</i> strain SM2D17 with Nanopore technology - potential probiotic strain to complement the human microbiota</b>		57

Binkowska, Justyna	
<b>Right place, right time: consequences of preterm birth for the early-life airway microbiota and respiratory health</b>	58
Birkeland, Einar	
<b>Characterization of the gut virome in a large Norwegian cohort using colorectal cancer screening test kits</b>	59
Birkner, Till	
<b>MetadeconfoundR: Confounder-aware Biomarker Analysis</b>	60
Bloom, Seth	
<b>Microbiota effects of a <i>Lactobacillus crispatus</i> live biotherapeutic to prevent recurrent bacterial vaginosis: findings from a randomized, double-blind, placebo-controlled trial</b>	61
<i>Cancelled</i>	62
Boverhoff, David	
<b>Nation-wide study of the human faecal microbiome across ages in the Netherlands</b>	63
Brüggemann, Ann-Kathrin	Presenter: Kraiselburd, Ivana
<b>Towards reliable prediction of significant changes in microbial communities based on time series data</b>	64
Buijink, Jesse	
<b>An imaging based in vitro screening method to investigate effects of the intestinal microbiome on adipogenesis</b>	65
Capeding, Maria Rosario Z.	Presenter: Berger, Bernard
<b>Ecology of <i>Bifidobacterium longum</i> subspecies <i>infantis</i> strains in a randomized, double-blind, controlled supplementation trial in Filipino healthy term infants</b>	66
Cappio Barazzone, Elisa	
<b>Microbiota influence on urea cycle disorders and host's nitrogen metabolism</b>	67

Chakraborty, Ardhendu		
<b>Influence of metformin exposure on the gut microbial composition of diabetic Indians</b>		68
Charalambous, Eleftheria		
<b>Herpesviridae shape the oral microbiome, in a compositional and a functional level</b>		69
Chatzigiannidou, Ioanna		
<b>Environmental impact on quantitative resistome dynamics in the human gut during early life</b>		70
Chatzigiannidou, Ioanna	Presenter: Johansen, Pi Lærke	
<b>Microbiota-based skin phenotypes in children with atopic dermatitis reflect a distinctive host response</b>		71
Chen, Muxuan	Presenter: Qi, Cancan	
<b>Vaginal microbiome landscape of sexually transmitted infections in Chinese reproductive-age women: a multi-center cohort study</b>		72
Chen, Xiuqiang		
<b>Exploring the influence of gut and lung microbiomes in <i>Aspergillus fumigatus</i> infection: an integrated analysis of humans and mice</b>		73
Cole, Cody		
<b>Lantibiotic-producing gut commensal prolongs dysbiosis and increases susceptibility to <i>Clostridioides difficile</i> infection</b>		74
Daryoush, Tanine		
<b>Studying variation within human gut microbiota dysbiosis</b>		75
Dawkins, Jennifer		
<b>Predicting host status from gut metabolites and microbial abundances</b>		76
De Franco, H�el�ene		
<b>Individualized food response prediction according to baseline makers</b>		77

de Nies, Laura	
<b>Understanding antibiotic-induced blooms of resistant E. coli in gut microbial communities</b>	78
Degraeve, Alexandra L.	
<b>Gut microbiome modulates tacrolimus pharmacokinetics through the transcriptional regulation of ABCB1</b>	79
Degraeve, Alexandra L.	
<b>Tacrolimus pharmacokinetics is associated with gut microbiota diversity in kidney transplant patients: results from a cross-sectional study</b>	80
Del Castillo Izquierdo, Ángela	
<b>Predicted drug metabolism of human gut microbes</b>	81
Delannoy-Bruno, Omar	Presenter: Berger, Bernard
<b>Precision nutrition for dietary fiber consumption based on the CAZymes clusters of the human gut microbiome</b>	82
Dötsch, Andreas	
<b>Variation in human intestinal microbiome studies: the effects of time and space</b>	83
Ducarmon, Quinten	
<b>Cayman: a novel bioinformatics tool for profiling carbohydrate-active enzymes (CAZymes) in microbiomes and its application in population cohorts</b>	84
Edfeldt, Gabriella	
<b>Understanding the microbial diversity in the healthy vagina</b>	85
Elhag, Duaa	
<b>Dynamics of the vaginal microbiome and cytokines levels in women with gestational diabetes</b>	86
Elnour, Reem	
<b>The role of macronutrient distribution and diet-microbiome interactions in the development of Colorectal Cancer</b>	87

Erawijantari, Pande Putu	
<b>The FINRISK DREAM challenge: predicting incident heart failure from the microbiome</b>	88
Erez, Amir	
<b>Systematic analysis of over-expressed genes in the human gut microbiome</b>	89
Eriksen, Carsten	
<b>Specific gut pathobionts escape antibody coating and are enriched during flares in patients with severe Crohn's disease</b>	90
Fackelmann, Gloria	
<b>Dietary patterns shape gut metagenomic composition in the ZOE PREDICT, large-scale, cross-cohort study of over 22 000 individuals</b>	91
Ferretti, Pamela	
<b>Composition, function and strain-sharing between maternal breast milk and the infant gut microbiome</b>	92
Forrest, Leysa	
<b>Microbial biomarkers in preeclampsia: a pilot study</b>	93
Fu, Jingyuan	
<b>Tackling the gut-liver axis in human metabolism: from cohort-based association to iPSC-based organ-on-a-chip</b>	94
Gacesa, Ranko	
<b>High resolution microbiome timeseries in patients with Inflammatory Bowel Diseases: pilot data of the IBD Tracker study</b>	95
Gao, Yuan	
<b>Gut microbiota maturity in infancy and atopic wheeze in childhood</b>	96
Garcia, Yuselys	
<b>Is gut microbiota dysbiosis linked to hydrogen sulfide and lanthionine alterations in chronic kidney disease?</b>	97

Ghozlane, Amine	
<b>SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis</b>	98
Giordano, Laura	
<b>Microbial-derived short chain fatty acids stimulate kidney tubular transport</b>	99
Gitton-Quent, Oscar	
<b>Gut microbiota and rheumatoid arthritis: from in silico exploration to in vitro validation</b>	100
Gois, Milla	
<b>Impact of occupational pesticide exposure on the human gut microbiome</b>	101
Grant, Erica	
<b>Diet-dependent availability of microbial B vitamins shapes host immunity</b>	102
Grant, Erica	
<b>Low dietary fiber intake fuels gut bacterial mucolytic activity in healthy humans</b>	103
Grant, Erica	Presenter: Monzel, Elena
<b>Maternal diet and gut microbiome composition regulate early-life immune maturation</b>	104
Gutmann, Friederike	
<b>A ketogenic diet leads to a shift in tryptophan metabolism associated with positive clinical outcomes in multiple sclerosis patients</b>	105
Haag, Mathias	
<b>Interactions of the breast cancer drug tamoxifen and its liver-derived metabolites with the human gut microbiota</b>	106
Hagi, Tatsuro	
<b>Bile resistance systems in Akkermansia muciniphila</b>	107

Hajra, Dipasree		
<b>Salmonella-induced SIRT1 and SIRT3 are crucial for maintaining the metabolic switch in bacteria and host for successful pathogenesis</b>		108
Han, Song-Yi		
<b>DSHT, an herbal formula, attenuates insulin resistance and improves glucose metabolism in prediabetic diet-induced obese mice by regulating the gut microbiota</b>		109
Hasson, Alexander	Presenter: Dogra, Shaillay Kumar	
<b>A machine-learning approach identified key lifestyle factors as predictive of low gut microbiota diversity status in two large population cohorts</b>		110
He, Zhen		
<b>Microbiota-induced alteration of kynurenine metabolism in macrophages mediate the reconstruction of mesenteric adipose in Crohn's disease</b>		111
He, Zhen		
<b>Gut microbe alleviates stress-related cancer metastasis by oleic acid degradation</b>		112
Heinken, Almut		
<b>Personalized genome-scale metabolic modeling of the infant gut microbiome</b>		113
Hela, Anupama	Presenter: Arunasri, Kotakonda	
<b>Tear film bacterial microbiome changes in Dry eye disease</b>		114
Herz, Michaela		
<b>Visualization of the mycobiome</b>		115
Hickman, Brandon		
<b>Gut microbiota wellbeing index predicts overall health in a cohort of 1000 infants</b>		116
Hjoerne, Anna Pii		
<b>Intestinal transit time and the gut microbiota: causality and implications?</b>		117

Hübner, Alexander <b>The impact of dairy-based diets on the human gut microbiome in Mongolia</b>	118
Hülsmann, Matthias <b>The redox environment dictates butyrate production during in vitro dietary fibre fermentations</b>	119
Ioannou, Athanasia <b>Disentangling the formation of infant gut microbiota communities</b>	120
Istvan, Paula <b>VirMake: a comprehensive Snakemake pipeline for viral metagenomic data analysis</b>	121
Jaagura, Madis <b>Identification of microbiota-related metabolic risk factors for chronic disease</b>	122
<i>Cancelled</i>	123
Jansma, Jack <b>Dynamic effects of probiotic formula Ecologic®825 on human small intestinal ileostoma microbiota: a network theory approach</b>	124
Jimenez Rus, Maria <b>Host-microbial homeostasis associated with fertility</b>	125
Jin, Shen <b>Bacterial oral-gut translocation in chronic liver disease is associated with gut barrier dysfunction</b>	126
Jokela, Roosa <b>Sources of gut microbiota variation in a large longitudinal infant cohort</b>	127
Presenter: Salonen, Anne	



Jovanovic, Nina	
<b>Baseline associations of gut microbiome to deep-phenotyping clinical parameters in patients at high risk of or presenting with acute cardiovascular disease (CVD)</b>	128
Kadam, Snehal	
<b>To deplete or not to deplete: the effect of host-DNA depletion on wound microbiome and its implications for microbiome research</b>	129
Kang, Youn-Goo	
<b>Inducing synergistic effects on obesity by increasing the bioavailability of rutin, a flavonoid with <i>Lactobacillus plantarum</i></b>	130
Kartal, Ece	
<b>Decoding microbial signatures in lung cancer</b>	131
Katz, Zohar	
<b>The cooperation inside us: investigating bacterial cooperation in the human gut</b>	132
Kehrmann, Jan	
<b>The lesional skin microbiome of actinic keratosis patients is altered after field-directed therapies and linked to treatment response</b>	133
Keller, Marisa Isabell	
<b>A global human gut microbiome analysis across enterotypes and dysbiosis</b>	134
Kha, My-Lan	
<b>Impact of <i>Fusobacterium nucleatum</i> and <i>Parvimonas micra</i> on inflammatory carcinogenesis in colorectal cancer</b>	135
Khachatryan, Lusine	
<b>A multi-omics approach for inflammatory bowel disease biomarkers detection</b>	136
Kiguchi, Yuya	
<b>Dysbiosis of the bacteriophage-bacteria interactions exacerbate the pathology of multiple sclerosis</b>	137

Kim, Na hyun	Presenters: Park, Suk Young; Kim, Na hyun	
<b>Short-chain fatty acids can attenuate antibiotics induced emphysema aggravation</b>		138
Klier, Kristin	Presenter: Fässler, Daniel	
<b>Combined evidence from general population cohorts and constraint-based community modelling reveal urinary methanol as a marker of high fiber intake</b>		139
Knoll, Rebecca		
<b>Probiotic Bifidobacterium infantis fosters eubiosis in preterm infants' gut microbiome and is environmentally taken up during a randomized controlled trial</b>		140
Koo, Bon Sang		
<b>Comprehensive effects of fecal microbiota transplantation and probiotic therapy on host response and gut microbiome in cynomolgus macaques</b>		141
Kool, Jolanda		
<b>Reducing bias in microbiome research: Comparing methods from sample collection to sequencing</b>		142
Krasenbrink, Julia		
<b>Role of the green-diet-derived, exclusive nutrient sulfoquinovose in gut microbiome-mammalian host interactions</b>		143
Krause, Jannike		
<b>Impact of sample logistics on structural and functional profiles of faecal microbiota</b>		144
Krigul, Kertu Liis		
<b>Fecal microbiota transplant from EstMB participants repeatedly using antibiotics results in gut barrier malfunction in mice</b>		145
Kullberg, Robert		
<b>Impact of butyrate-producing gut microbiota on the risk of infectious disease hospitalisation: results from two large population-based cohorts</b>		146

Lahtinen, Emilia		
<b>Bacterial vaginosis: understanding the effect of antibiotic-free treatment on the vaginal microbiome</b>		147
Larsson, Anna		
<b>Connections between common drugs and the gut microbiota indicate substance-specific and drug class associations and impact of polypharmacy</b>		148
Lee, Seungbaek		
<b>Gut bacteriome and vulnerability to mood disorders in women with polycystic ovary syndrome</b>		149
Leier, André		
<b>The role of human milk oligosaccharides in viral transmission from mothers to infants</b>		150
Leviatan, Sigal	Presenter: Shoer, Saar	
<b>An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species</b>		151
Li, Ruolin		
<b>Gut microbiome is correlated with appendicular lean mass in early adolescents population: the Generation R study</b>		152
Lin, Weifeng	Presenter: Globisch, Daniel	
<b>Exploring gut microbiome metabolism - novel tools for the discovery and investigation of unknown microbiome metabolites</b>		153
Liu, Bin		
<b>Starvation responses impact interaction dynamics of human gut bacteria Bacteroides thetaiotaomicron and Roseburia intestinalis</b>		154
Lohia, Sonnal		
<b>Fecal proteomics in investigation of the gut-kidney axis in patients with chronic kidney disease</b>		155
Lombardo, Isabella		
<b>Implementing standard operative procedures for respiratory tract microbiome assessment as a tool for clinical research in internal medicine wards: a pilot study</b>		156

Lopez Sandoval, Ruben	
<b>Studying host-microbe interactions in engineered human gut tissues</b>	157
Maier, George	
<b>The contribution of microbes in the origin of human serrated sessile lesions</b>	158
Malwe, Aditya	
<b>GutBug: machine learning-based tool for prediction of human gut bacteria mediated biotransformation of biotic and xenobiotic molecules</b>	159
Manghi, Paolo	
<b>curatedMetagenomiData 3 enables large-scale integrative analyses on the human microbiome in relation to health-related outcomes and phenotypes</b>	160
Marquez-Lago, Tatiana T	
<b>Algorithms for sample selection and sensitivity analysis: minimizing bias and confounding variables in microbiome research</b>	161
Marquez-Lago, Tatiana T	
<b>Models of CMV transmission involving the human microbiome and metabolome</b>	162
Martinez Medina, Jennifer Nazat	
<b>Mucosal washes representing the gut mucus-associated microbiota with less host DNA contamination</b>	163
Mattock, Jennifer	Presenter: Watson, Mick
<b>Better bioinformatics workflows for the precision analysis of human and animal microbiomes</b>	164
Mehrjerd, Ameneh	
<b>Generating digital twins via integrating population statistics with constraint-based modelling for characterizing the gut-brain-axis in large general population cohorts</b>	165

Meiners, Franziska	
<b>A high-polyphenol strawberry-based dietary intervention increases SCFA-producing bacteria and induces a shift in gut microbial communities in healthy elderly people</b>	166
Mende, Daniel	
<b>Metapangenomics reveal novel interactions in the infant oral microbiome</b>	167
Meric, Guillaume	
<b>Exploring links between the gut microbiome and health using large multi-omics population cohort datasets</b>	168
Miari, Mariam	
<b>The gut microbiota and obesity in a population of 12 028 individuals</b>	169
Mikhaleva, Sofya	
<b>Gut organoids-based model for high resolution host-microbiome interaction studies</b>	170
Mollova, Daniela	
<b>Unlocking the genomic secrets of Lactiplantibacillus plantarum PU3: a promising probiotic strain with antibiotic resistance found in breast milk</b>	171
Morillo Sanz Dias, Felipe	
<b>Can shallow shotgun-based profiling of the gut microbiome improve the detection of host genetic effects?</b>	172
Mueller, Katherine	
<b>Potential speciation in the gastrointestinal microbe Akkermansia muciniphila and the resulting effects on human health</b>	173
NabiNejad, Amir	
<b>Identification of novel gut microbiota features in healthy aging</b>	174
Napoli, Stefania	
<b>The long-term effects of COVID-19 vaccination on the gut microbiome composition</b>	175

Narayan, Rohan	
<b>Gut microbial metabolism of the Parkinson's disease medication levodopa</b>	176
Nguyen, Khoi Nguyen	
<b>Microgenderome and the associations between weight gain, integrase inhibitors antiretroviral agents, and gut microbiome in HIV patients: a cross-sectional study</b>	177
Nguyen, Khoi Nguyen	
<b>Individualized differences in weight loss success during a one-year lifestyle program is associated with gut microbiome signatures and targeted serum metabolites</b>	178
Nishijima, Suguru	
<b>Machine learning-guided quantitative gut microbiome profiling enables accurate biomarker discovery</b>	179
Nooij, Sam	
<b>Global survey of the disease-associated gut bacterium Ruminococcus gnavus reveals genomic links to geography and disease</b>	180
Oestergaard, Stine	
<b>Unraveling the significance of epithelial-associated bacteria in gastrointestinal diseases: importance of choosing an optimal DNA extraction method</b>	181
Ozkan, Jerome	
<b>Ocular microbiome changes in meibomian gland dysfunction/dry eye disease</b>	182
Pagan, Lisa	Presenter: Henderickx, Jannie
<b>The vulvar microbiome in lichen sclerosus and high-grade intraepithelial lesions</b>	183
Pantiukh, Kateryna	
<b>EstMB MAGs database: unveiling the metagenomic landscape of the Estonian population through metagenome-assembled genomes</b>	184

Park, Ho-Young		
<b>Food additive low-acyl gellan gum regulated gut microbiota and metabolite production</b>		185
Park, Suk Young	Presenters: Kim, Na hyun; Park, Suk Young	
<b>Oral feeding with probiotic decreased Th1/IFN-<math>\gamma</math> cells and lung damage in smoking-induced COPD mouse model</b>		186
Patangia, Dhrati		
<b>Early life exposure of infants to benzylpenicillin and gentamicin is associated with a persistent amplification of the gut resistome</b>		187
Peh, Alex		
<b>Modulation of the gut microbiome to reverse poor post-stroke outcomes in mice</b>		188
Peng, Haoran		
<b>The role of horizontal gene transfer in microbial interactions and host exposures</b>		189
Pina-Beltran, Blanca		
<b>Influence of TDUT in drug metabolization and inflammation in a 5/6 nephrectomy mouse model</b>		190
Piperni, Elisa		
<b>Worldwide presence of Blastocystis in the human gut microbiome is linked to healthier diets and lower BMI</b>		191
Pita, Sara		
<b>The CM human microbiome profiler: beyond the gut</b>		192
Piticchio, Serena		
<b>Is the keto diet good for skin microbiome?</b>		193
Plavec, Tina Vida		
<b>Engineering of Lactococcus lactis for the expression of targeting- and cytokine-binding proteins</b>		194

Prast-Nielsen, Stefanie	
<b>Profiling the intestinal microbiota, plasma bile acids and inflammation markers: their associations with inflammatory bowel disease</b>	195
Prast-Nielsen, Stefanie	
<b>Gut microbiota changes during ketogenic diet treatment of epilepsy are linked to lower inflammation and serum metabolites associated with seizure reduction</b>	196
Prins, Femke	
<b>The gut microbiome across the cardiovascular risk spectrum</b>	197
Pucci, Nicholas	
<b>Maternal influence and HMO metabolism shape early-life gut colonization dynamics of Bifidobacterium longum subspecies</b>	198
Puertolas Balint, Fabiola	
<b>Intestinal <math>\alpha</math>-Defensins play a minor role in modulating the small intestinal microbiota composition as compared to diet</b>	199
Rahman, Md Nannur	
<b>Probiotics in establishing alpha-diversity of the gut microbiota by eliminating pathogenic bacteria; systematic review and meta-analysis of clinical outcomes</b>	200
Richards-Corke, Khyle	
<b>A small molecule inhibitor of gut bacterial urease protects the host from liver injury</b>	201
Rocha, Nina	
<b>Exploring host-bacteria interactions in aged skin using long-read sequencing</b>	202
Rounge, Trine Ballestad	
<b>Gut microbiomes in three independent Norwegian studies reveal sex-specific implications of Phascolarctobacterium for developing colorectal cancer</b>	203



Rozenberga, Maija		
<b>Association between gut microbiome, intestinal permeability and inflammatory landscape in healthy individuals and irritable bowel syndrome patients</b>		204
Ruan, Xinwei		
<b>Dietary patterns and geographic origin determine the core composition and taxonomic diversity of bacteria in healthy adult saliva</b>		205
Ruiz-Moreno, Angel		
<b>MicrobeRX: a tool for enzymatic reaction-based metabolite prediction of xenobiotics in the gut microbiome</b>		206
Salim, Felix	Presenters: Salim, Felix; Yamada, Takuji	
<b>Enteropathway: the metabolic pathway database for the human gut microbiota</b>		207
Sandalli, Sofia	Presenters: Addington, Emily; Sandalli, Sofia	
<b>Repression of colibactin via amino acid supplementation</b>		208
Sanglekar, Deepa		
<b>Development of a multivariate predictive tool for gut dysbiosis in the general population</b>		209
Sanna, Serena		
<b>The Women4Health cohort: a multi-omics approach to understand the role of microbiome in women's metabolism.</b>		210
Sarathi, Arjun		
<b>Quantitative differences in synthetic gut microbial inoculums do not affect the final stabilized in vitro community compositions</b>		211
Sauco, Carlos		
<b>Hyposalivation without Sjögren's Syndrome: microbial dysbiosis in women</b>		212
Sayavedra, Lizbeth		
<b>Survival of the fittest: gut colonization by the sulphidogenic Bilophila wadsworthia under a high-fat diet</b>		213

Schaefer-Ramadan, Stephanie	Presenter: Guan, Yue	
<b>Unveiling the <i>Helicobacter pylori</i> interactome through All-vs-All sequencing</b>		214
Schell, Kathleen		
<b>The potential of honey as a prebiotic food to re-engineer the gut microbiome toward a healthy state</b>		215
Schluter, Jonas		
<b>Gut microbiome ecosystem dynamics that result in bacteremia may be modulated by diet</b>		216
Schröder, Björn O.	Presenter: Holmberg, Sandra	
<b>Unraveling mechanisms of how a gut commensal modulates Western diet-induced colonic mucus defects</b>		217
Seelbinder, Bastian		
<b><i>Candida</i> expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions</b>		218
Sentausa, Erwin		
<b>A quality control pipeline for Nanopore sequencing data, applicable for metagenomics</b>		219
Seo, Yerin	Presenter: Kwon, Soon-Kyeong	
<b>Features of gut microbiome of responders to acupuncture treatment in patients with atopic dermatitis</b>		220
Shanahan, Erin		
<b>Longitudinal microbiome-immune dynamics during immune checkpoint inhibitor immunotherapy</b>		221
Sharma, Arunabh		
<b>Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families</b>		222
Shen, Zeyang		
<b>A multi-kingdom genome catalog of the infant skin microbiome indicates diversity, function, and transmission in early life</b>		223

Shigdel, Rajesh	
<b>Association between oral microbiota with nocturnal gastroesophageal reflux disease: RHINESSA study</b>	224
Shoer, Saar	
<b>Microbial strain-level genetic variations and their implications on the host</b>	225
Short, Nina	
<b>Bacterial proteins as drivers of host-microbiome interactions</b>	226
Simcock, Joshua	
<b>Evaluation of short and long-read sequencing approaches for taxonomic classification and profiling of in vitro gut microbiota communities</b>	227
Sinha, Trishla	
<b>CS baby biome: timing of maternal antibiotic prophylaxis during a cesarean section and the early infant gut microbiome</b>	228
So, Yunjeong	
<b>Utilisation of human milk oligosaccharides by the adult gut microbiota</b>	229
Solari, Sean	
<b>Leveraging genome-based phylogenies for deeply-resolved metagenomic analysis in inflammatory bowel disease</b>	230
Son, Sophie	
<b>Gut microbiota-derived secondary bile acids are essential for host protection against <i>Clostridioides difficile</i> infection</b>	231
Sridhar, Subasree	
<b>Constraint-based modelling of interaction between <i>Streptococcus pneumoniae</i> and lung epithelium to understand the metabolic changes during early stage pneumonia</b>	232
Steimle, Alex	
<b>Gut microbiome-based prediction of autoimmune neuroinflammation</b>	233

Su, Changxing	
<b>MicroCAT: deciphering host-microbiome interactions from single cell transcriptomic sequencing data</b>	234
Sun, Chuqing	
<b>Long-read sequencing reveals extensive DNA methylations contributing to phage viability in human gut</b>	235
Sunidhi, Sunidhi	
<b>Identification of tumor-relevant microbiome components from whole genome and transcriptome sequencing in breast cancer</b>	236
Swayambhu, Meghna	
<b>A roadmap towards integration of microbiome-based analyses in applied settings</b>	237
Szymanek, Agata	
<b>DynaMAP enables fast and sequencing-free microbiome analysis through optical mapping of fluorocoded DNA</b>	238
Taba, Nele	
<b>A novel framework for assessing causal effect of microbiome on health: long-term antibiotic usage as pseudo-randomizer</b>	239
Talukdar, Daizee	Presenter: Sarkar, Mousumi
<b>Co-existence of non-commensal bacteria in vaginal microbiome with differentially enriched inflammatory pathways are associated with preterm birth in Indian women</b>	240
Tamahane, Vaishali	
<b>Effect of probiotic supplementation on glycemic control and gut microbiome profile in Indian children with Type 1 Diabetes(T1DM): a pilot RCT</b>	241
Tamburini, Fiona	
<b>Gut microbial species and endotypes associate with remission in IBD patients treated with anti-TNF or anti-integrin therapy</b>	242
Tearle, Jacqueline	
<b>Profiling the mucosal interact-ome in diverse IBD pathologies</b>	243

Thirion, Florence	
<b>Characterisation of gut microbiota from adult patients with autism spectrum disorder</b>	244
Tsamir-Rimon, Mor	
<b>A manifold-based framework for studying the dynamics of the vaginal microbiome</b>	245
Uppal, Gurdip	
<b>Probabilistic learning of microbiome spatial dynamics from high-throughput localization data</b>	246
Utkina, Irina	
<b>Developing effective prebiotics through community-based metabolic modelling</b>	247
Valkenburg, Sophie	
<b>Functional capacity of the intestinal microbiota to produce butyrate does not decrease with progressive stages of chronic kidney disease</b>	248
Vanhatalo, Sanja	
<b>The physical and microbial characteristics of appendicoliths in patients with CT differentiated complicated acute appendicitis</b>	249
Vázquez Castellanos, Jorge Francisco	
<b>Long-term life history predicts current elderly gut microbiome</b>	250
Velsko, Irina	
<b>Extensive genomic diversity of uncatalogued taxa in ancient and modern oral samples revealed through de novo genome assembly</b>	251
Wang, Daoming	
<b>Gut microbial genetic architecture of human health and environmental shaping revealed by metagenome-wide SNP association study</b>	252
Wang, Zhujun	
<b>Interspecies communication based on aromatic amino acid derivatives for the homeostatic microbiota</b>	253

Weber, Christian		
<b>The influence of the oral microbiome on the pathophysiology of Alzheimer's disease</b>		254
Wirbel, Jakob	Presenter: Essex, Morgan	
<b>A realistic benchmark for the identification of differentially abundant taxa in (confounded) human microbiome studies</b>		255
Wolter, Mathis	Presenter: Joja, Mihovil	
<b>Mucin-degrading gut bacteria promote anti-parasitic immunity</b>		256
Wolter, Mathis	Presenter: Rolof, Amrei	
<b>Akkermansia muciniphila expansion under dietary fiber deprivation enhances susceptibility to an attaching and effacing pathogen</b>		257
Wong, Jeremy		
<b>Fluid flow structures gut microbiota biofilm communities by distributing public goods</b>		258
Wortelboer, Koen	Presenter: Herrema, Hilde	
<b>Sterile faecal filtrate transplantation alters phage-microbe dynamics in individuals with metabolic syndrome</b>		259
Wortelboer, Koen		
<b>Lyophilized faecal microbiota capsules for clinical research</b>		260
Wu, Jiafei		
<b>Gut microbiome associations with human sleep behavior in a Dutch population</b>		261
Wu, Jiqiu		
<b>Gut microbiome associates renal function in a sex-dependent manner</b>		262
Wu, Liangliang		
<b>A promising probiotic, Bacteroides xylanivsolvens 4010B-1, prevents obesity and regulates metabolic disorders in mice fed a high-fat diet</b>		263

Yoon, Jaekyung		
<b>Identification of microbial biomarkers associated with the risk of gastric carcinogenesis</b>		264
Yoou, Myeonghyun		
<b>Comparative genomics analysis reveals distinct genetic and metabolomic characteristics in a gut microbiome species from elderly individuals</b>		265
You, Hyun Ju	Presenter: Si, Jiyeon	
<b>Bacteroides vulgatus SNUG 40005 restores Akkermansia-depleted dysbiosis and reverses obese phenotypes by modulating the metabolite pool</b>		266
<i>Cancelled</i>		267
Zafeiropoulou, Konstantina		
<b>Unravelling the beneficial role of Prevotella copri in the postoperative recovery of patients with colorectal cancer.</b>		268
Zahavi, Liron		
<b>Bacterial SNPs in the human gut microbiome associate with host BMI</b>		269
Zhang, Chenhong		
<b>Gut microbiota modulates distal symmetric polyneuropathy in diabetic patients</b>		270
Zhang, Shuyan		
<b>The gut microbiome in end-stage lung disease and lung transplantation</b>		271
Zhang, Yue		
<b>Gut microbial genetic ageing clock in human health</b>		272
Zhernakova, Daria		
<b>Host genetic regulation of human gut microbial structural variation</b>		273

Zhu, Jiaying

**Compared to histamine-2 receptor antagonist, proton pump inhibitor induces stronger oral-to-gut microbial transmission and gut microbiome alterations** 274

Zuzana, Karwowska

**Comparative analysis of transformations for microbiome dysbiosis classification: unraveling the impact of bacterial presence-absence in accurate disease discrimination** 275