Aasmets, Oliver
Systematic evaluation of long-term drug effects on the gut microbiome in the Estonian Microbiome Cohort 48

Aasmets, Oliver
Similarity to the gut microbiome of non-westernized populations predicts health outcomes in the Estonian Microbiome Cohort 49

Aguilar Ramos, Miguel
Development of irreversible covalent inhibitors of the colibactin activating protease 50

Alvarez-Silva, Camila
Impact of acute alcohol consumption on circulating microbiome in asymptomatic alcohol-related liver disease 51

Alvi, Tayyaba
Causal links between the gut microbiome and age associated functional and structural changes in the brain 52

Andreu Sánchez, Sergio
From strain to host: unraveling the link between gut microbial genetic diversity and health 53

Andrikopoulos, Petros
Evidence of a causal and modifiable relationship between kidney function and circulating trimethylamine N-oxide 54

Avershina, Ekaterina
Phage-bacteria interactions and post colonoscopy shifts in gut microbiome through the lens of CRISPR-Cas system 55

Awan, Ayesha
Intestinal microbiota consumes specific dietary proteins that evade host digestion 56

Baev, Vesselin
Genome sequencing and analysis of P. pentosaceus strain SM2D17 with Nanopore technology - potential probiotic strain to complement the human microbiota 57
Binkowska, Justyna
**Right place, right time: consequences of preterm birth for the early-life airway microbiota and respiratory health**

Birkeland, Einar
**Characterization of the gut virome in a large Norwegian cohort using colorectal cancer screening test kits**

Birkner, Till
**MetadeconfoundR: Confounder-aware Biomarker Analysis**

Bloom, Seth
**Microbiota effects of a Lactobacillus crispatus live biotherapeutic to prevent recurrent bacterial vaginosis: findings from a randomized, double-blind, placebo-controlled trial**

---

Cancelled

---

Boverhoff, David
**Nation-wide study of the human faecal microbiome across ages in the Netherlands**

Brüggemann, Ann-Kathrin
**Towards reliable prediction of significant changes in microbial communities based on time series data**

Buijink, Jesse
**An imaging based in vitro screening method to investigate effects of the intestinal microbiome on adipogenesis**

Capeding, Maria Rosario Z.
**Ecology of Bifidobacterium longum subspecies infantis strains in a randomized, double-blind, controlled supplementation trial in Filipino healthy term infants**

Cappio Barazzone, Elisa
**Microbiota influence on urea cycle disorders and host’s nitrogen metabolism**
<table>
<thead>
<tr>
<th>Name</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chakrabortty, Ardhendu</td>
<td>Influence of metformin exposure on the gut microbial composition of diabetic Indians</td>
<td>68</td>
</tr>
<tr>
<td>Charalambous, Eleftheria</td>
<td>Herpesviridae shape the oral microbiome, in a compositional and a functional level</td>
<td>69</td>
</tr>
<tr>
<td>Chatzigiannidou, Ioanna</td>
<td>Environmental impact on quantitative resistome dynamics in the human gut during early life</td>
<td>70</td>
</tr>
<tr>
<td>Chatzigiannidou, Ioanna</td>
<td>Microbiota-based skin phenotypes in children with atopic dermatitis reflect a distinctive host response</td>
<td>71</td>
</tr>
<tr>
<td>Chen, Muxuan</td>
<td>Vaginal microbiome landscape of sexually transmitted infections in Chinese reproductive-age women: a multi-center cohort study</td>
<td>72</td>
</tr>
<tr>
<td>Chen, Xiuqiang</td>
<td>Exploring the influence of gut and lung microbiomes in Aspergillus fumigatus infection: an integrated analysis of humans and mice</td>
<td>73</td>
</tr>
<tr>
<td>Cole, Cody</td>
<td>Lantibiotic-producing gut commensal prolongs dysbiosis and increases susceptibility to Clostridioides difficile infection</td>
<td>74</td>
</tr>
<tr>
<td>Daryoush, Tanine</td>
<td>Studying variation within human gut microbiota dysbiosis</td>
<td>75</td>
</tr>
<tr>
<td>Dawkins, Jennifer</td>
<td>Predicting host status from gut metabolites and microbial abundances</td>
<td>76</td>
</tr>
<tr>
<td>De Franco, Hélène</td>
<td>Individualized food response prediction according to baseline makers</td>
<td>77</td>
</tr>
</tbody>
</table>
de Nies, Laura
Understanding antibiotic-induced blooms of resistant E. coli in gut microbial communities 78

Degraeve, Alexandra L.
Gut microbiome modulates tacrolimus pharmacokinetics through the transcriptional regulation of ABCB1 79

Degraeve, Alexandra L.
Tacrolimus pharmacokinetics is associated with gut microbiota diversity in kidney transplant patients: results from a cross-sectional study 80

Del Castillo Izquierdo, Ángela
Predicted drug metabolism of human gut microbes 81

Delannoy-Bruno, Omar
Presenter: Berger, Bernard
Precision nutrition for dietary fiber consumption based on the CAZymes clusters of the human gut microbiome 82

Dötsch, Andreas
Variation in human intestinal microbiome studies: the effects of time and space 83

Ducarmon, Quinten
Cayman: a novel bioinformatics tool for profiling carbohydrate-active enzymes (CAZymes) in microbiomes and its application in population cohorts 84

Edfeldt, Gabriella
Understanding the microbial diversity in the healthy vagina 85

Elhag, Duaa
Dynamics of the vaginal microbiome and cytokines levels in women with gestational diabetes 86

Elnour, Reem
The role of macronutrient distribution and diet-microbiome interactions in the development of Colorectal Cancer 87
Erawijantari, Pande Putu
The FINRISK DREAM challenge: predicting incident heart failure from the microbiome

Erez, Amir
Systematic analysis of over-expressed genes in the human gut microbiome

Eriksen, Carsten
Specific gut pathobionts escape antibody coating and are enriched during flares in patients with severe Crohn's disease

Fackelmann, Gloria
Dietary patterns shape gut metagenomic composition in the ZOE PREDICT, large-scale, cross-cohort study of over 22 000 individuals

Ferretti, Pamela
Composition, function and strain-sharing between maternal breast milk and the infant gut microbiome

Forrest, Leysa
Microbial biomarkers in preeclampsia: a pilot study

Fu, Jingyuan
Tackling the gut-liver axis in human metabolism: from cohort-based association to iPSC-based organ-on-a-chip

Gacesa, Ranko
High resolution microbiome timeseries in patients with Inflammatory Bowel Diseases: pilot data of the IBD Tracker study

Gao, Yuan
Gut microbiota maturity in infancy and atopic wheeze in childhood

Garcia, Yuselys
Is gut microbiota dysbiosis linked to hydrogen sulfide and lanthionine alterations in chronic kidney disease?
Ghozlane, Amine
SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis

Giordano, Laura
Microbial-derived short chain fatty acids stimulate kidney tubular transport

Gitton-Quent, Oscar
Gut microbiota and rheumatoid arthritis: from in silico exploration to in vitro validation

Gois, Milla
Impact of occupational pesticide exposure on the human gut microbiome

Grant, Erica
Diet-dependent availability of microbial B vitamins shapes host immunity

Grant, Erica
Low dietary fiber intake fuels gut bacterial mucolytic activity in healthy humans

Grant, Erica
Maternal diet and gut microbiome composition regulate early-life immune maturation

Gutmann, Friederike
A ketogenic diet leads to a shift in tryptophan metabolism associated with positive clinical outcomes in multiple sclerosis patients

Haag, Mathias
Interactions of the breast cancer drug tamoxifen and its liver-derived metabolites with the human gut microbiota

Hagi, Tatsuro
Bile resistance systems in Akkermansia muciniphila
Hajra, Dipasree
Salmonella-induced SIRT1 and SIRT3 are crucial for maintaining the metabolic switch in bacteria and host for successful pathogenesis

Han, Song-Yi
DSHT, an herbal formula, attenuates insulin resistance and improves glucose metabolism in prediabetic diet-induced obese mice by regulating the gut microbiota

Hasson, Alexander
A machine-learning approach identified key lifestyle factors as predictive of low gut microbiota diversity status in two large population cohorts

He, Zhen
Microbiota-induced alteration of kynurenine metabolism in macrophages mediate the reconstruction of mesenteric adipose in Crohn's disease

He, Zhen
Gut microbe alleviates stress-related cancer metastasis by oleic acid degradation

Heinken, Almut
Personalized genome-scale metabolic modeling of the infant gut microbiome

Hela, Anupama
Presenter: Arunasri, Kotakonda
Tear film bacterial microbiome changes in Dry eye disease

Herz, Michaela
Visualization of the mycobiome

Hickman, Brandon
Gut microbiota wellbeing index predicts overall health in a cohort of 1000 infants

Hjoerne, Anna Pii
Intestinal transit time and the gut microbiota: causality and implications?
<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hübner, Alexander&lt;br&gt;The impact of dairy-based diets on the human gut microbiome in Mongolia</td>
<td>118</td>
</tr>
<tr>
<td>Hülsmann, Matthias&lt;br&gt;The redox environment dictates butyrate production during in vitro dietary fibre fermentations</td>
<td>119</td>
</tr>
<tr>
<td>Ioannou, Athanasia&lt;br&gt;Disentangling the formation of infant gut microbiota communities</td>
<td>120</td>
</tr>
<tr>
<td>Istvan, Paula&lt;br&gt;VirMake: a comprehensive Snakemake pipeline for viral metagenomic data analysis</td>
<td>121</td>
</tr>
<tr>
<td>Jaagura, Madis&lt;br&gt;Identification of microbiota-related metabolic risk factors for chronic disease</td>
<td>122</td>
</tr>
<tr>
<td>Cancelled</td>
<td>123</td>
</tr>
<tr>
<td>Jansma, Jack&lt;br&gt;Dynamic effects of probiotic formula Ecologic®825 on human small intestinal ileostoma microbiota: a network theory approach</td>
<td>124</td>
</tr>
<tr>
<td>Jimenez Rus, Maria&lt;br&gt;Host-microbial homeostasis associated with fertility</td>
<td>125</td>
</tr>
<tr>
<td>Jin, Shen&lt;br&gt;Bacterial oral-gut translocation in chronic liver disease is associated with gut barrier dysfunction</td>
<td>126</td>
</tr>
<tr>
<td>Jokela, Roosa&lt;br&gt;Presenter: Salonen, Anne&lt;br&gt;Sources of gut microbiota variation in a large longitudinal infant cohort</td>
<td>127</td>
</tr>
</tbody>
</table>
Jovanovic, Nina
Baseline associations of gut microbiome to deep-phenotyping clinical parameters in patients at high risk of or presenting with acute cardiovascular disease (CVD) 128

Kadam, Snehal
To deplete or not to deplete: the effect of host-DNA depletion on wound microbiome and its implications for microbiome research 129

Kang, Youn-Goo
Inducing synergistic effects on obesity by increasing the bioavailability of rutin, a flavonoid with Lactobacillus plantarum 130

Kartal, Ece
Decoding microbial signatures in lung cancer 131

Katz, Zohar
The cooperation inside us: investigating bacterial cooperation in the human gut 132

Kehrmann, Jan
The lesional skin microbiome of actinic keratosis patients is altered after field-directed therapies and linked to treatment response 133

Keller, Marisa Isabell
A global human gut microbiome analysis across enterotypes and dysbiosis 134

Kha, My-Lan
Impact of Fusobacterium nucleatum and Parvimonas micra on inflammatory carcinogenesis in colorectal cancer 135

Khachatryan, Lusine
A multi-omics approach for inflammatory bowel disease biomarkers detection 136

Kiguchi, Yuya
Dysbiosis of the bacteriophage-bacteria interactions exacerbate the pathology of multiple sclerosis 137
EMBO | EMBL Symposium: The human microbiome

Kim, Na hyun Presenters: Park, Suk Young; Kim, Na hyun

Short-chain fatty acids can attenuate antibiotics induced emphysema aggravation 138

Klier, Kristin Presenter: Fässler, Daniel

Combined evidence from general population cohorts and constraint-based community modelling reveal urinary methanol as a marker of high fiber intake 139

Knoll, Rebecca

Probiotic Bifidobacterium infantis fosters eubiosis in preterm infants’ gut microbiome and is environmentally taken up during a randomized controlled trial 140

Koo, Bon Sang

Comprehensive effects of fecal microbiota transplantation and probiotic therapy on host response and gut microbiome in cynomolgus macaques 141

Kool, Jolanda

Reducing bias in microbiome research: Comparing methods from sample collection to sequencing 142

Krasenbrink, Julia

Role of the green-diet-derived, exclusive nutrient sulfoquinovose in gut microbiome-mammalian host interactions 143

Krause, Jannike

Impact of sample logistics on structural and functional profiles of faecal microbiota 144

Krigul, Kertu Liis

Fecal microbiota transplant from EstMB participants repeatedly using antibiotics results in gut barrier malfunction in mice 145

Kullberg, Robert

Impact of butyrate-producing gut microbiota on the risk of infectious disease hospitalisation: results from two large population-based cohorts 146
Lahtinen, Emilia
Bacterial vaginosis: understanding the effect of antibiotic-free treatment on the vaginal microbiome 147

Larsson, Anna
Connections between common drugs and the gut microbiota indicate substance-specific and drug class associations and impact of polypharmacy 148

Lee, Seungbaek
Gut bacteriome and vulnerability to mood disorders in women with polycystic ovary syndrome 149

Leier, André
The role of human milk oligosaccharides in viral transmission from mothers to infants 150

Leviatan, Sigal
An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species 151

Li, Ruolin
Gut microbiome is correlated with appendicular lean mass in early adolescents population: the Generation R study 152

Lin, Weifeng
Exploring gut microbiome metabolism - novel tools for the discovery and investigation of unknown microbiome metabolites 153

Liu, Bin
Starvation responses impact interaction dynamics of human gut bacteria Bacteroides thetaiotaomicron and Roseburia intestinalis 154

Lohia, Sonna
Fecal proteomics in investigation of the gut-kidney axis in patients with chronic kidney disease 155

Lombardo, Isabella
Implementing standard operative procedures for respiratory tract microbiome assessment as a tool for clinical research in internal medicine wards: a pilot study 156
Lopez Sandoval, Ruben

**Studying host-microbe interactions in engineered human gut tissues** 157

Maier, George

**The contribution of microbes in the origin of human serrated sessile lesions** 158

Malwe, Aditya

**GutBug: machine learning-based tool for prediction of human gut bacteria mediated biotransformation of biotic and xenobiotic molecules** 159

Manghi, Paolo

**curatedMetagenomiData 3 enables large-scale integrative analyses on the human microbiome in relation to health-related outcomes and phenotypes** 160

Marquez-Lago, Tatiana T

**Algorithms for sample selection and sensitivity analysis: minimizing bias and confounding variables in microbiome research** 161

Marquez-Lago, Tatiana T

**Models of CMV transmission involving the human microbiome and metabolome** 162

Martinez Medina, Jennifer Nazat

**Mucosal washes representing the gut mucus-associated microbiota with less host DNA contamination** 163

Mattock, Jennifer

**Better bioinformatics workflows for the precision analysis of human and animal microbiomes** 164

Mehrjerd, Ameneh

**Generating digital twins via integrating population statistics with constraint-based modelling for characterizing the gut-brain-axis in large general population cohorts** 165
Meiners, Franziska
*A high-polyphenol strawberry-based dietary intervention increases SCFA-producing bacteria and induces a shift in gut microbial communities in healthy elderly people*

Mende, Daniel
*Metapangenomics reveal novel interactions in the infant oral microbiome*

Meric, Guillaume
*Exploring links between the gut microbiome and health using large multi-omics population cohort datasets*

Miari, Mariam
*The gut microbiota and obesity in a population of 12 028 individuals*

Mikhaleva, Sofya
*Gut organoids-based model for high resolution host-microbiome interaction studies*

Mollova, Daniela
*Unlocking the genomic secrets of Lactiplantibacillus plantarum PU3: a promising probiotic strain with antibiotic resistance found in breast milk*

Morillo Sanz Dias, Felipe
*Can shallow shotgun-based profiling of the gut microbiome improve the detection of host genetic effects?*

Mueller, Katherine
*Potential speciation in the gastrointestinal microbe Akkermansia muciniphila and the resulting effects on human health*

NabiNejad, Amir
*Identification of novel gut microbiota features in healthy aging*

Napoli, Stefania
*The long-term effects of COVID-19 vaccination on the gut microbiome composition*
Narayan, Rohan
*Gut microbial metabolism of the Parkinson’s disease medication levodopa*

Nguyen, Khoi Nguyen
*Microgenderome and the associations between weight gain, integrase inhibitors antiretroviral agents, and gut microbiome in HIV patients: a cross-sectional study*

Nguyen, Khoi Nguyen
*Individualized differences in weight loss success during a one-year lifestyle program is associated with gut microbiome signatures and targeted serum metabolites*

Nishijima, Suguru
*Machine learning-guided quantitative gut microbiome profiling enables accurate biomarker discovery*

Nooij, Sam
*Global survey of the disease-associated gut bacterium Ruminococcus gnavus reveals genomic links to geography and disease*

Oestergaard, Stine
*Unraveling the significance of epithelial-associated bacteria in gastrointestinal diseases: importance of choosing an optimal DNA extraction method*

Ozkan, Jerome
*Ocular microbiome changes in meibomian gland dysfunction/dry eye disease*

Pagan, Lisa
*The vulvar microbiome in lichen sclerosus and high-grade intraepithelial lesions*

Presenter: Henderickx, Jannie

Pantiukh, Kateryna
*EstMB MAGs database: unveiling the metagenomic landscape of the Estonian population through metagenome-assembled genomes*
Park, Ho-Young
**Food additive low-acyl gellan gum regulated gut microbiota and metabolite production**

Park, Suk Young
Presenters: Kim, Na hyun; Park, Suk Young
**Oral feeding with probiotic decreased Th1/IFN-γ cells and lung damage in smoking-induced COPD mouse model**

Patangia, Dhrati
**Early life exposure of infants to benzylpenicillin and gentamicin is associated with a persistent amplification of the gut resistome**

Peh, Alex
**Modulation of the gut microbiome to reverse poor post-stroke outcomes in mice**

Peng, Haoran
**The role of horizontal gene transfer in microbial interactions and host exposures**

Pina-Beltran, Blanca
**Influence of TDUT in drug metabolism and inflammation in a 5/6 nephrectomy mouse model**

Piperni, Elisa
**Worldwide presence of Blastocystis in the human gut microbiome is linked to healthier diets and lower BMI**

Pita, Sara
**The CM human microbiome profiler: beyond the gut**

Piticchio, Serena
**Is the keto diet good for skin microbiome?**

Plavec, Tina Vida
**Engineering of Lactococcus lactis for the expression of targeting- and cytokine-binding proteins**
Prast-Nielsen, Stefanie  
**Profiling the intestinal microbiota, plasma bile acids and inflammation markers: their associations with inflammatory bowel disease**

Prast-Nielsen, Stefanie  
**Gut microbiota changes during ketogenic diet treatment of epilepsy are linked to lower inflammation and serum metabolites associated with seizure reduction**

Prins, Femke  
**The gut microbiome across the cardiovascular risk spectrum**

Pucci, Nicholas  
**Maternal influence and HMO metabolism shape early-life gut colonization dynamics of Bifidobacterium longum subspecies**

Puertolas Balint, Fabiola  
**Intestinal α-Defensins play a minor role in modulating the small intestinal microbiota composition as compared to diet**

Rahman, Md Nannur  
**Probiotics in establishing alpha-diversity of the gut microbiota by eliminating pathogenic bacteria; systematic review and meta-analysis of clinical outcomes**

Richards-Corke, Khyle  
**A small molecule inhibitor of gut bacterial urease protects the host from liver injury**

Rocha, Nina  
**Exploring host-bacteria interactions in aged skin using long-read sequencing**

Rounge, Trine Ballestad  
**Gut microbiomes in three independent Norwegian studies reveal sex-specific implications of Phascolarctobacterium for developing colorectal cancer**
Rozenberga, Maija
Association between gut microbiome, intestinal permeability and inflammatory landscape in healthy individuals and irritable bowel syndrome patients 204

Ruan, Xinwei
Dietary patterns and geographic origin determine the core composition and taxonomic diversity of bacteria in healthy adult saliva 205

Ruiz-Moreno, Angel
MicrobeRX: a tool for enzymatic reaction-based metabolite prediction of xenobiotics in the gut microbiome 206

Salim, Felix Presenters: Salim, Felix; Yamada, Takuji
Enteropathway: the metabolic pathway database for the human gut microbiota 207

Sandalli, Sofia Presenters: Addington, Emily; Sandalli, Sofia
Repression of colibactin via amino acid supplementation 208

Sanglekar, Deepa
Development of a multivariate predictive tool for gut dysbiosis in the general population 209

Sanna, Serena
The Women4Health cohort: a multi-omics approach to understand the role of microbiome in women’s metabolism. 210

Sarathi, Arjun
Quantitative differences in synthetic gut microbial inoculums do not affect the final stabilized in vitro community compositions 211

Sauco, Carlos
Hyposalivation without Sjögren’s Syndrome: microbial dysbiosis in women 212

Sayavedra, Lizbeth
Survival of the fittest: gut colonization by the sulphidogenic Bilophila wadsworthia under a high-fat diet 213
Schaefer-Ramadan, Stephanie  
Presenter: Guan, Yue  
**Unveiling the Helicobacter pylori interactome through All-vs-All sequencing**  
214

Schell, Kathleen  
**The potential of honey as a prebiotic food to re-engineer the gut microbiome toward a healthy state**  
215

Schluter, Jonas  
**Gut microbiome ecosystem dynamics that result in bacteremia may be modulated by diet**  
216

Schröder, Björn O.  
Presenter: Holmberg, Sandra  
**Unraveling mechanisms of how a gut commensal modulates Western diet-induced colonic mucus defects**  
217

Seelbinder, Bastian  
**Candida expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions**  
218

Sentausa, Erwin  
**A quality control pipeline for Nanopore sequencing data, applicable for metagenomics**  
219

Seo, Yerin  
Presenter: Kwon, Soon-Kyeong  
**Features of gut microbiome of responders to acupuncture treatment in patients with atopic dermatitis**  
220

Shanahan, Erin  
**Longitudinal microbiome-immune dynamics during immune checkpoint inhibitor immunotherapy**  
221

Sharma, Arunabh  
**Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families**  
222

Shen, Zeyang  
**A multi-kingdom genome catalog of the infant skin microbiome indicates diversity, function, and transmission in early life**  
223
Shigdel, Rajesh
Association between oral microbiota with nocturnal gastroesophageal reflux disease: RHINESSA study 224

Shoer, Saar
Microbial strain-level genetic variations and their implications on the host 225

Short, Nina
Bacterial proteins as drivers of host-microbiome interactions 226

Simcock, Joshua
Evaluation of short and long-read sequencing approaches for taxonomic classification and profiling of in vitro gut microbiota communities 227

Sinha, Trishla
CS baby biome: timing of maternal antibiotic prophylaxis during a cesarean section and the early infant gut microbiome 228

So, Yunjeong
Utilisation of human milk oligosaccharides by the adult gut microbiota 229

Solari, Sean
Leveraging genome-based phylogenies for deeply-resolved metagenomic analysis in inflammatory bowel disease 230

Son, Sophie
Gut microbiota-derived secondary bile acids are essential for host protection against Clostridioides difficile infection 231

Sridhar, Subasree
Constraint-based modelling of interaction between Streptococcus pneumoniae and lung epithelium to understand the metabolic changes during early stage pneumonia 232

Steimle, Alex
Gut microbiome-based prediction of autoimmune neuroinflammation 233
Su, Changxing
MicroCAT: deciphering host-microbiome interactions from single cell transcriptomic sequencing data

Sun, Chuqing
Long-read sequencing reveals extensive DNA methylations contributing to phage viability in human gut

Sunidhi, Sunidhi
Identification of tumor-relevant microbiome components from whole genome and transcriptome sequencing in breast cancer

Swayambhu, Meghna
A roadmap towards integration of microbiome-based analyses in applied settings

Szymanek, Agata
DynaMAP enables fast and sequencing-free microbiome analysis through optical mapping of fluorocoded DNA

Taba, Nele
A novel framework for assessing causal effect of microbiome on health: long-term antibiotic usage as pseudo-randomizer

Talukdar, Daizee
Co-existence of non-commensal bacteria in vaginal microbiome with differentially enriched inflammatory pathways are associated with preterm birth in Indian women

Tamahane, Vaishali
Effect of prebiotic supplementation on glycemic control and gut microbiome profile in Indian children with Type 1 Diabetes(T1DM): a pilot RCT

Tamburini, Fiona
Gut microbial species and endotypes associate with remission in IBD patients treated with anti-TNF or anti-integrin therapy

Tearle, Jacqueline
Profiling the mucosal interact-ome in diverse IBD pathologies
Thirion, Florence
Characterisation of gut microbiota from adult patients with autism spectrum disorder

Tsamir-Rimon, Mor
A manifold-based framework for studying the dynamics of the vaginal microbiome

Uppal, Gurdip
Probabilistic learning of microbiome spatial dynamics from high-throughput localization data

Utkina, Irina
Developing effective prebiotics through community-based metabolic modelling

Valkenburg, Sophie
Functional capacity of the intestinal microbiota to produce butyrate does not decrease with progressive stages of chronic kidney disease

Vanhatalo, Sanja
The physical and microbial characteristics of appendicoliths in patients with CT differentiated complicated acute appendicitis

Vázquez Castellanos, Jorge Francisco
Long-term life history predicts current elderly gut microbiome

Velsko, Irina
Extensive genomic diversity of uncatalogued taxa in ancient and modern oral samples revealed through de novo genome assembly

Wang, Daoming
Gut microbial genetic architecture of human health and environmental shaping revealed by metagenome-wide SNP association study

Wang, Zhujun
Interspecies communication based on aromatic amino acid derivatives for the homeostatic microbiota
Weber, Christian
The influence of the oral microbiome on the pathophysiology of Alzheimer’s disease

Wirbel, Jakob
Presenter: Essex, Morgan
A realistic benchmark for the identification of differentially abundant taxa in (confounded) human microbiome studies

Wolter, Mathis
Presenter: Joja, Mihovil
Mucin-degrading gut bacteria promote anti-parasitic immunity

Wolter, Mathis
Presenter: Rolof, Amrei
Akkermansia muciniphila expansion under dietary fiber deprivation enhances susceptibility to an attaching and effacing pathogen

Wong, Jeremy
Fluid flow structures gut microbiota biofilm communities by distributing public goods

Wortelboer, Koen
Presenter: Herrema, Hilde
Sterile faecal filtrate transplantation alters phage-microbe dynamics in individuals with metabolic syndrome

Wortelboer, Koen
Lyophilized faecal microbiota capsules for clinical research

Wu, Jiafei
Gut microbiome associations with human sleep behavior in a Dutch population

Wu, Jiqiu
Gut microbiome associates renal function in a sex-dependent manner

Wu, Liangliang
A promising probiotic, Bacteroides xylanivorans 4010B-1, prevents obesity and regulates metabolic disorders in mice fed a high-fat diet
Yoon, Jaekyung
Identification of microbial biomarkers associated with the risk of gastric carcinogenesis 264

Yoo, Myeonghyun
Comparative genomics analysis reveals distinct genetic and metabolomic characteristics in a gut microbiome species from elderly individuals 265

You, Hyun Ju
Bacteroides vulgatus SNUG 40005 restores Akkermansia-depleted dysbiosis and reverses obese phenotypes by modulating the metabolite pool 266

Cancelled 267

Zafeiropoulou, Konstantina
Unravelling the beneficial role of Prevotella copri in the postoperative recovery of patients with colorectal cancer. 268

Zahavi, Liron
Bacterial SNPs in the human gut microbiome associate with host BMI 269

Zhang, Chenhong
Gut microbiota modulates distal symmetric polyneuropathy in diabetic patients 270

Zhang, Shuyan
The gut microbiome in end-stage lung disease and lung transplantation 271

Zhang, Yue
Gut microbial genetic ageing clock in human health 272

Zhernakova, Daria
Host genetic regulation of human gut microbial structural variation 273
Zhu, Jiaying

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

Zuzana, Karwowska

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