

Poster No.	Name	Title	Country	Onsite/Online
1	Oliver Aasmets	Evaluation of accumulative drug effects in the gut microbiome using electronic health records data in the Estonian Microbiome Cohort	Estonia	Online
2	Oliver Aasmets	Similarity to the gut microbiome of non-westernized populations predicts health outcomes in the Estonian Microbiome Cohort	Estonia	Online
3	Samuel JK Abraham	Beneficial balancing of amino-acids through gut-microbiome modulation using two unique variants of beta glucans in Non-alcoholic steatohepatitis (NASH) animal model	Japan	Onsite
4	Samuel JK Abraham	Regulation of dysbiosis and increase in abundance of beneficial gut microbiota by biological response modifier glucan in a clinical study in Duchenne Muscular Dystrophy.	Japan	Onsite
5	Cheri Ackerman	Measuring microbial interactions at scale reveals the skin microbiome interactome and a microbial ensemble for atopic dermatitis	USA	Onsite
6	Herve Affagard	Alliance Promotion Microbiote, the voice of the French microbiome industry	France	Onsite
7	Tsubasa Aiyoshi	Microbial profile of peritoneal fluid in pediatric patients with acute appendicitis	Japan	Onsite
8	Baraa Altaha	Genetic and environmental circadian disruption induce metabolic impairment through changes in the gut microbiome	Germany	Onsite
9	Ryuta Amamoto	Yearly changes in the composition of gut microbiota in the elderly, and the effect of lactobacilli intake on these changes	Japan	Onsite
10	Sergio Andreu Sanchez	Genetic, environmental and intrinsic determinants of the human antibody epitope repertoire	Netherlands	Onsite
11	Reika Aoyama	Skin microbiome-based disease prediction and prevention in infantile atopic dermatitis and food allergy	Japan	Onsite
12	Daniel Arens	A Review of the Oral Mycobiome and its Relation to Health and Disease	USA	Onsite
13	Eric Armstrong	<i>L. crispatus</i> CTV-05 colonization following vaginal LACTIN-V administration: patterns and genital immune impact	Canada	Onsite
14	Jae woo Baek	Longitudinal analysis of human gut microbiota reveals the emerging pattern of multi-resistant bacteria and its characteristics	Korea	Onsite
15	Yuying Bai	Gut associated <i>Lactobacillus johnsonii</i> enhanced barrier function in colitis model mouse	Japan	Onsite
16	Naoko Goto	MetaPore-C: using chromatin conformation capture and long reads for metagenomic analysis	Japan	Onsite
17	John Beaulaurier	Using long native reads to reveal multiple types of DNA methylation in bacterial genomes	UK	Online
18	Vincent Thomas	Shedding Light on the Dark Matter of the Gut Microbiome: targeted enrichment and culture using flow cytometry under anaerobic conditions	France	Onsite
19	Lara Bereza-Malcolm	The gut and oral microbiome of rheumatoid- and psoriatic arthritis patients	Australia	Onsite
20	Cindy Bermudez	The effects of individual nut consumption on host large intestine microbiota	Australia	Onsite
21	Sandra Bermudez-Sanchez	Oral amoxicillin treatment affects the caecal microbiome, metabolome and pH in Han Wistar rats	Denmark	Onsite
22	Anna Bircher	First steps to unravel the mechanism behind the anti-tumor effect of commensal gut microbes in solid tumors	Switzerland	Onsite
23	Carlos Blazquez-Bondia	PROBIOTIC EFFECTS ON IMMUNITY AND MICROBIOME IN HIV-1 DISCORDANT PATIENTS	Spain	Onsite
24	Miquel Angel Bonachera-Sierra	Probiotic Effect on SARS-CoV2 Immunity Is Associated to Type-1 Interferons: A Post-Hoc Analysis of a Randomized, Placebo-Controlled Trial	Spain	Onsite
25	Miquel Angel Bonachera-Sierra	Heat-inactivated <i>Lactiplantibacillus plantraum</i> KABP-061 postbiotic exerts antipathogenic activity against causative agents of vulvovaginal candidiasis	Spain	Onsite
26	Tatiana Borodovich	Footprints in the sand: bacterial DNA in human gut viromes as a snapshot of particle-mediated horizontal gene transfer.	Ireland	Onsite
27	Mahesh Desai	Mucolytic bacteria mediate fiber deprivation-induced colitis in IL-10 deficient mice	Luxembourg	Onsite
28	Milla Brandao Gois	Characterization of the metabolome and microbiome landscape throughout pregnancy	Netherlands	Onsite
29	Francois Brillet	Skin microbiome: from observations to in vivo modulation with healthy human skin commensals.	Belgium	Onsite
30	Bernard Berger	Personalization of dietary fibre consumption based on CAZymes clusters of the human gut microbiome	Switzerland	Onsite
31	Siobhan Brushett	Gut feelings: Investigating the relations between depression, anxiety, psychotropic drugs and the gut microbiome	Netherlands	Onsite
32	Louise Campbell	Comparative assessment of 16S amplicon-based and metagenome-assembled units for monitoring population dynamics in a mouse model	Australia	Onsite
33	Long Long Chen	Gut microbiota in psychiatric disorders, a systematic review	Sweden	Onsite
34	Eun-Chae Choi	Clinical-based Human Microbiome Project in Republic of Korea	Korea	Onsite
35	Isin Comba	Physical Environment Contributes Greater Than Diet to The Industrialization of Immigrant Microbiome	USA	Onsite
36	Britta De Pessemer	The impact of the skin microbiome in Psoriasis capitis	Belgium	Onsite
37	Celia Diez Lopez	Effect of wearing, washing and drying on odour formation and the microbiome of textile clothing	Belgium	Onsite
38	Katherine Donald	Passive secretory IgA in milk protects against allergic disease through modulation of the gut microbiota	Canada	Onsite

Poster No.	Name	Title	Country	Onsite/Online
39	Aurore DUQUENY	Development of a manufacturing process preserving the entire dominant profile of complex microbiota for therapeutic purposes and process optimization through modelling tools	France	Onsite
40	Thilini N Jayasinghe	Identification of oral bacteria in the gut and foot ulcer of patients with diabetes mellitus ? A secondary analysis of whole-metagenome and meta-transcriptomic microbiome data	Australia	Onsite
41	Kristen A. Engevik	Mucin-degrading microbes alter the decoy capacity of mucus in rotavirus infection	USA	Online
42	Pande Putu Erawijantari	Gut microbiome signatures are robustly associated with incident type 2 diabetes over long-term follow-up in different age groups of the Finnish adults population	Finland	Online
43	Mi Kyung Kim	Taxonomic and functional differences in oral microbiome associated with several cancers (oral, head and neck, pancreatic and gastric cancer) identified through machine learning	Korea	Onsite
44	Bouchra Ezzamouri	Metabolic modelling of the human gut microbiome in type 2 diabetes patients in response to metformin treatment	UK	Onsite
45	Pamela Ferretti	C. difficile is overdiagnosed in adults and a commensal in infants	Germany	Onsite
46	Kristina Franz	Sex-hormone dependent interactions between host and gut microbiome in cardiovascular risk (XCVD study) - Study protocol of a longitudinal cohort approach	Germany	Onsite
47	Taro Fuchigami	Limosilactobacillus coleohominis DL81 isolated from the vagina of healthy pregnant promotes the immune response in macrophages.	Japan	Onsite
48	Hideaki Fujihara	Altered composition of gut microbiome associated with cognitive function in preschool children	Japan	Onsite
49	Sadayuki Fujishiro	Dysbiosis in Gut Microbiota in Children Born Preterm who developed Autism Spectrum Disorder: A Pilot Study	Japan	Onsite
50	Shinji Fukuda	High body temperature increases gut microbiota-dependent host resistance to influenza A virus and SARS-CoV-2 infection	Japan	Onsite
51	Hironori Fukuoka	Analysis of tumor-associated microbiota from surgical resection specimens of colorectal cancer without bowel preparation	Japan	Onsite
52	Toshikazu Fukushima	Development of statistical method for identification of important species from complex microbial community	Japan	Onsite
53	Herve Affagard	Pooling of faecal material results in standardized and high-richness microbiotherapy products MaaT013 and MaaT033	France	Onsite
54	Anupam Gautam	Faster assignment of metagenomic reads, using AnnoTree, UniRef or clustered NCBI-nr	Germany	Onsite
55	Nicholas Gauthier	Alterations in the Nasopharyngeal Microbiome Associated with SARS-CoV-2 Disease Status and Infection Severity	Canada	Onsite
56	Mallia Geiger	Faecal microbial transplantation to reduce radiation-induced colonic epithelial damages: application to Pelvic Radiation disease	France	Onsite
57	Daniel Globisch	Exploring Gut Microbiota Metabolism ? New Chemical Biology Tools for Metabolomics Analysis	Sweden	Onsite
58	Erica T Grant	Low dietary fiber intake fuels gut bacterial mucolytic activity in healthy humans	Luxembourg	Onsite
59	Friederike Gutmann	Gut microbiome alterations in atrial fibrillation	Germany	Onsite
60	Fumiaki Hamazato	Multiple nutritional and gut microbial factors associated with allergic rhinitis: the Hitachi Health Study	Japan	Onsite
61	Song-yi Han	Anti-Diabetic Effects of Galgeun-tang in High-Fat-Diet-Induced metabolic dysfunction Mice via Regulation of Gene Expression and Alteration of the Microbiome Composition	Korea	Onsite
62	Yaeko Hashimoto	A role of gut-lung axis in LPS-induced acute lung injury	Japan	Onsite
63	Yuichiro Hayashi	Comprehensive viral analysis using next-generation sequencing	Japan	Onsite
64	Vitor Heidrich	Longitudinal analysis at three oral sites links oral microbiota to clinical outcomes in allogeneic hematopoietic stem-cell transplant	Brazil	Onsite
65	Koichi Higashi	PZLAST: an ultra-fast amino acid sequence similarity search server against public metagenomes	Japan	Onsite
66	Evette Hillman	Can Manipulating the Microbiome be used to Treat Primary Bile Acid Diarrhoea	UK	Onsite
67	Daisuke Hisamatsu	Precision diagnosis of neurodegenerative diseases based on salivary microbiome profiles	Japan	Onsite
68	Emily Hoedt	16S amplicon and metagenomic shotgun sequencing of the mucosal associated microbiota reveals differential profiles preceding incidences of anastomotic leaks	Australia	Onsite
69	Emily Hoedt	Functional Dyspepsia Mucosal Associated Microbiota of the Upper Gastrointestinal Tract	Australia	Onsite
70	Mi Young Lim	Microbe?microbe interactions in Korean gut microbial ecosystems	Korea	Onsite
71	Ayako Horigome	The impact of indigenous gut microbiota on the prebiotic effects of 2'-fucosyllactose in adults	Japan	Onsite
72	Thomas Horvath	Developing Multi-Omic Visualization Tools to Aid in Bacterial Metabolite Screening	USA	Onsite
73	Masahito Hosokawa	Exploring strain diversity in human microbiome using single-cell genome sequencing	Japan	Onsite
74	Koji Hosomi	Unique carbohydrate and amino acid metabolisms of Blautia wexlerae ameliorate obesity and type 2 diabetes	Japan	Onsite
75	Ji-Won Huh	Enterotypical Prevotella and three novel bacterial species predict clinical outcomes of colorectal cancer	Korea	Onsite
76	Seung-Ju Hwang	Bacillus subtilis-fermented Amonum xanthioides Mitigates Overnutrition-induced Nonalcoholic Fatty Liver in Mice	Korea	Onsite

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77	Koji Ishikawa	Improvement in depressive symptoms after probiotic treatment associates with gut microbiota composition in patients with depression	Japan	Onsite
78	Shiori Ishizawa	Illuminating the relationship between traditional Japanese Kampo medicine and the gut microbiome in non-alcoholic fatty liver disease	Japan	Onsite
79	Issei Ishida	Immunomodulatory effects of Lactobacillus biogenics administration in dogs	Japan	Onsite
80	Saori Iwase	Longitudinal gut microbiota composition of South African and Nigerian infants in relation to tetanus vaccine responses	South Africa	Onsite
81	Jacob Dehinsilu	The role of the microbiome and IgA in checkpoint inhibitor therapy induced colitis	UK	Onsite
82	Lae-Guen Jang	Constructing a culture collection for Bacteroidales isolated from the human or mouse gut microbiota	Korea	Onsite
83	Daan Jansen	Community typing as a way to explore virome compositional changes in IBD patients	Belgium	Onsite
84	Robert Jenq	Mucus-degrading commensal bacteria contribute to toxicities of hematopoietic cell transplantation	USA	Onsite
85	Ryutaro Jo	Comparison of oral microbiome profiles in 18-month-old infants and their parents	Japan	Onsite
86	Harshitha Jois	Impact of Human milk oligosaccharides on microbiota restoration post amoxicillin treatment.	Denmark	Onsite
87	Shinya Kageyama	Breastfeeding delays maturation of oral microbiota in infancy	Japan	Onsite
88	Shotaro Kai	Effects of prenatal antibiotic exposure on autism spectrum disorder-like behavior in mouse	Japan	Onsite
89	Tomo Kakhara	Microbial analysis of appendicolith from pediatric appendicitis patients	Japan	Onsite
90	Jonathan Teo	Long-term ecological and evolutionary dynamics in the gut microbiomes of carbapenemase-producing Enterobacteriaceae colonized subjects	Singapore	Onsite
91	Ece Kartal	Predicting Incident Heart Failure from the Microbiome: The DREAM FINRISK challenge	Germany	Onsite
92	Kazuyuki Kasahara	Exploring the Impact of Gut Microbial Modulation of Purines on Cardiovascular Disease	Singapore	Onsite
93	Yuka Katayama	Comprehensive genomic analysis uncovered CO-utilizing pathways in human gut microbiome	Japan	Onsite
94	Egle Katkeviciute	Recolony ? bacteria-based cancer therapy	Switzerland	Onsite
95	Nobuhiro Kawachi	Sustainable onshore aquaculture techniques with overgrowing seagrass: modulation of the symbiotic microbial structure of seagrass sediment by thermophilic Bacillaceae-fermented compost as a feed additive	Japan	Onsite
96	Yuya Kiguchi	Dysbiosis of the human gut bacteria-phage interactions associated with propionate reduction in multiple sclerosis	Japan	Onsite
97	Seolah Kim	Characterization of commensal streptococci that show potent antagonistic activities against the pathobiont Fusobacterium nucleatum	Korea	Onsite
98	Natasha Kitchin	Gut microbial alterations in Foetal Alcohol Spectrum Disorders (FASD)	South Africa	Onsite
99	Rebecca Knoll	Elexacaftor/tezacaftor/ivacaftor shows specific impact on lung microbiome in people with cystic fibrosis.	Germany	Onsite
100	Seiga Komiyama	$\gamma\delta T17$ cells in Peyer's patches acquire the encephalitogenic phenotype through the activation by commensals	Japan	Onsite
101	Prokopis Konstanti	Production of γ -aminobutyric acid by Akkermansia muciniphila and characterization of its glutamate decarboxylase	Netherlands	Onsite
102	Lutz Krause	Improving Human Health with Precision Microbiome Science: Development of MAP 315 as a Live Biotherapeutic Product for the treatment of Ulcerative Colitis	Australia	Onsite
103	Naveen Kumar	Analyzing horizontal gene transfer events in the long-read metagenomics of Japanese gut microbiomes	Japan	Onsite
104	Mao Kunimitsu	Relationship between healing status and microbial dissimilarity in wound and peri-wound skin in pressure injuries	Japan	Onsite
105	Masaomi Kurokawa	Metagenomic Thermometer	Japan	Onsite
106	Rina Kurokawa	Agar-containing solution enhances recovery of microbial DNA from extremely low biomass specimens including skin.	Japan	Onsite
107	Gavin Kuziel	Functional diversification of plant small molecules by the gut microbiome tunes intestinal homeostasis	USA	Onsite
108	Soon-Kyeong Kwon	Gastric microbiota of patients with different disease states and transplantation to germ-free mice	Korea	Onsite
109	Heeun Kwon	Metagenome analysis of the gut microbiome of drug-naive type 2 diabetes patients	Korea	Onsite
110	Manolo Laiola	Toxic microbiome and chronic kidney disease: insights from the CKD-REIN cohort study	France	Onsite
111	Manolo Laiola	Longitudinal salivary metagenomics in acute-on-chronic liver failure patients	France	Onsite
112	Arun Prasath Lakshmanan	Gut Microbiome and Lipidome Profiling in a Pilot Study on the Obese Qatari Female Population	Qatar	Onsite
113	Arun Prasath Lakshmanan	The Potential impact of Haemophilus in Obese Population with acute graft-versus-host disease (aGvHD)	Qatar	Onsite
114	Arun Prasath Lakshmanan	Gut microbiota in children and adults with morbid obesity- A pilot study	Qatar	Onsite

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115	Anna Lambert	Exploring and predicting host-microbiota interactions in the small intestine through metabolic modeling.	France	Onsite
116	Martin Laursen	Key bacterial taxa producing aromatic amino acid catabolites in the gut during early infancy	Denmark	Onsite
117	Christophe Lay	A synbiotic intervention prevents the establishment of a compromised microbiome in elective caesarean born infants	Singapore	Onsite
118	Sungho Lee	Systematic comparison of data preprocessing and algorithms for disease classifiers based on whole metagenome sequencing	Korea	Onsite
119	Soo-Jeong Lee	Therapeutic potential of flavonoids in inflammatory bowel disease mouse model and regulation of disrupted gut microbiota	Korea	Onsite
120	Hyeongwon Lee	A comprehensive repertoire of Fusobacterium genome dataset reveals pedigree-dependent and -independent ecological differentiation	Korea	Onsite
121	Ting Fan Leung	Interactions between perinatal factors and airway microbiota modulate the risk for pre-school wheeze	Hong Kong	Onsite
122	Ting Fan Leung	Relationship between eczema phenotypes and evolution of early-life skin microbiome in Chinese children	Hong Kong	Onsite
123	Suisha Liang	Multi-cohort analysis of depression-associated gut microbiota sheds insight on bacterial biomarkers across populations	Hong Kong	Onsite
124	Yi-Ting Lin	Specific gut microbiota species are associated with 24-hour blood pressure measurements in 4,359 individuals from the SCAPIS cohort	Sweden	Onsite
125	Lei Liu	Anaerostipes hadrus ability to degrade inositol relates to human health: implications for possible PCOS treatment	Netherlands	Onsite
126	Lin Zhang	Food additive affects maternal health and virulence factors of gut microbiome: data from prospective MOMmy cohort	Hong Kong	Onsite
127	Veronica Llorens-Rico	Microbial detection in host-derived single-cell RNA-seq data reveals specific host-microbe interactions in COVID-19 patients	Belgium	Onsite
128	Amy Loughman	Introducing the Australasian Human Microbiome Research Network	Australia	Onsite
129	Yoram Louzoun	MIPMLP ? Microbiome Preprocessing Machine Learning Pipeline	Israel	Onsite
130	Yoram Louzoun	Projection of Gut Microbiome Pre- and Post-Bariatric Surgery To Predict Surgery Outcome	Israel	Onsite
131	Claus Lykkebo	Impact of dietary fiber intake on uptake and excretion of Perfluorooctane sulfonic acid (PFOS) in male Sprague-Dawley rats	Denmark	Onsite
132	Junyeong Ma	Assembly of complete prokaryotic genomes for human gut microbiome using HiFi sequencing	Korea	Onsite
133	Angeli Dominique Macandog	More stable gut microbiota during anti-PD1 immunotherapy distinguishes complete responders among melanoma patients	Italy	Onsite
134	Léa Siegwald	A nutritional intervention to improve the resilience of the gut microbiome and mitigate the effect of dietary challenge on host health	Switzerland	Onsite
135	Herve Affagard	Pooled allogenic fecal microbiotherapy MaaT013 for the treatment of steroid-refractory gastrointestinal acute graft-versus-host disease: results from the phase IIa HERACLES study and expanded access program	France	Onsite
136	Lauren Schooth	Sodium stearoyl lactate inhibits growth of the duodenal mucosa-associated microbiota from subjects with and without functional upper gastrointestinal symptoms	Australia	Onsite
137	Daniel Martinez	A microbial metabolite controls cancer progression and chemotherapy	UK	Onsite
138	Rie Maskawa	Antibiotic perturbations to the mouse gut microbiome described by the intestinal transit model	Japan	Onsite
139	Reika Masuda	Multi-omic approach for the exploration of the gut microbiota function and functional redundancy through substrate utilisation	Australia	Onsite
140	Hiroaki Masuoka	Gut microbiome of Papua New Guinea highlanders can contribute to adaptability to protein deficiency	Japan	Onsite
141	Hirota Kawanabe-Matsuda	Dietary probiotic Lactobacillus delbrueckii subsp. bulgaricus OLL1073R-1-derived exopolysaccharide (EPS) enhances cancer immunotherapy	Japan	Onsite
142	Michiko Matsunaga	The Intestinal Microbiome, Dietary Habits, and Physical and Psychological Resilience in Postpartum Women	Japan	Onsite
143	Daniel McDonald	Greengenes2: Harmonizing amplicon and shotgun microbiome studies	USA	Onsite
144	Amelia McGuinness	Bowel preparation followed by colonoscopy induces persistent changes in gut microbiota composition	Australia	Onsite
145	Amelia McGuinness	Does the human appendix assist with reinoculation of the colon after bowel preparation and colonoscopy?	Australia	Onsite
146	Diana Mejia-Granados	Changes in gut microbiome in patients with different forms of epilepsy and autoimmune encephalitis	Spain	Onsite
147	Alessandra Mezzelani	Host-microbiome cross-talk: analysis of non-coding RNAs in stools of children with autism and dysbiosis	Italy	Onsite
148	Deirdre Mikkelsen	Both nut botanical origin and host origin of inoculum impact in vitro nut fermentability	Australia	Onsite
149	Astghik Pepoyan	Baseline gut microbiota composition and disease severity in Familial Mediterranean fever disease patients with COVID-19	Armenia	Onsite
150	Yuna Miyajima	Investigation of the relationship between gut microbiota and dyslipidemia in Japanese adults	Japan	Onsite
151	Hirokuni Miyamoto	Potential sustainable roles of thermophilic fermented compost in reducing antimicrobial use and greenhouse gas generation? Statistical structural causal inference of compost-plant-animal-symbiote ?	Japan	Onsite

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152	Hirokuni Miyamoto	Weizmannia coagulans SANK70258 with a protective role under heat stress - New aspects of traditional probiotics -	Japan	Onsite
153	Hirokuni Miyamoto	Design of viral surface antigen-HSP fusion protein to modulate nasal mucosal immunity	Japan	Onsite
154	Eiji Miyauchi	Prediction of pancreatic cancer with salivary and fecal metabolomic profiles	Japan	Onsite
155	Nanami Mizusawa	Effects of the intake of fish meat-derived peptides on the human gut microbiome	Japan	Onsite
156	Attayeb Mohsen	Optimizing and automating QIIME2 Microbiome data analysis using the Snakemake pipeline (Snaq)	Japan	Onsite
157	Norfilza Mohd Mokhtar	A Randomized Controlled Trial on the Use of Probiotics in Metabolic associated Fatty Liver Disease Patients: Focus on Clinical Outcomes and Gut Microenvironment.	Malaysia	Onsite
158	Hiroshi Mori	Microbiome Datahub: an integrated database of microbiome samples and MAG data	Japan	Onsite
159	Léa Siegwald	Benchmarking strain-level resolution of the upper respiratory microbiome through shotgun metagenomics	Switzerland	Onsite
160	Yumi Motoyama	The impact of natural environment to human skin microbiome~ In vitro evaluation of the impact with commensal microbiome on human skin ~	Japan	Onsite
161	Mercedeh Movassagh Movassagh	Role of microbial agents in development of neonatal sepsis in Sub Saharan Africa	USA	Onsite
162	Mercedeh Movassagh Movassagh	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever	USA	Onsite
163	Kisara Muroi	Dietary factors facilitate the differentiation of follicular helper T cells in Peyer's patches	Japan	Onsite
164	Selvasankar Murugesan	Saliva is a Source of biomarkers to predict diabetes at an early stage	Qatar	Onsite
165	Selvasankar Murugesan	Role of human microbiome and virome in the pathogenesis and disease course of idiopathic nephrotic syndrome in children	Qatar	Onsite
166	Selvasankar Murugesan	Analysis of the Salivary Microbiome in Qatari population with Hypertension	Qatar	Onsite
167	Yoshimi Muto	Identification and characterization of the gut microbial species responsible for hyperammonemia in hepatic encephalopathy from the analysis of patients administered rifaximin	Japan	Onsite
168	Taku Nakahara	Establishment of the Juntendo Microbiome Bank for Fecal Microbiota Transplantation	Japan	Onsite
169	Yoko Nakai	Dysbiosis of the gut microbiota in children with severe motor and intellectual disabilities receiving enteral nutrition	Japan	Onsite
170	Aruto Nakajima	Development of a simple method that increases the detection rate and abundance estimation accuracy of minority species in the microbiota: 16S Metagenome-DRIP (Deeper Resolution using an Inhibitory Primer)	Japan	Onsite
171	Nobuhiro Nakamoto	Gut microbiota determines the clinical course of primary sclerosing cholangitis regardless of the comorbidity of inflammatory bowel disease	Japan	Online
172	Atsuo Nakamura	Effects of polyamines produced by intestinal bacteria on intestinal permeability	Japan	Onsite
173	Yumiko Nakanishi	Fecal microbiota and metabolite biomarkers involved in the onset of pediatric atopic dermatitis	Japan	Onsite
174	Koji Narita	Initiatives for acceleration of microbiome industrialization in the precompetitive collaboration by Japanese consortium	Japan	Onsite
175	Rhys Newell	Lorikeet: Strain resolved metagenome analysis using local reassembly	Australia	Onsite
176	H. Bjorn Nielsen	Using Cross-Cohort Microbiome Data for LBP Discovery	Denmark	Onsite
177	Suguru Nishijima	Multi-omics exploration of non-invasive biomarkers in alcohol-related liver disease	Germany	Onsite
178	Hiroshi Nishiwaki	Gut dysbiosis dysregulating short chain fatty acids and mucosal barrier in dementia with Lewy bodies	Japan	Onsite
179	Nathan Nuzum	How our gut may bug our brains: Assessing gut bacteria's role in cognition across healthy ageing	Australia	Onsite
180	Yusuke Ogata	Comparison and assessment of community DNA extraction methods based on enzymatic and mechanical lysis using human fecal samples	Japan	Onsite
181	Evgenii Olekhovich	Identification of reproducible stool metagenomic biomarkers linked to the melanoma immunotherapy outcome	Russia	Onsite
182	Dominic O'Neil	Optimized methods for wastewater-based viral and bacterial testing	Germany	Onsite
183	Dominic O'Neil	Optimized methods for antimicrobial resistance testing	Germany	Onsite
184	Kenji Oishi	Chronological analysis of bacterial composition in human small intestinal tract after an ingestion of fermented milk products	Japan	Onsite
185	Olivia Colberg Palmann	An in vitro model, simulating the infant colon, to study composition and activity of the infant gut microbiome	Denmark	Onsite
186	Maria Ioanna Papadaki	Investigating the gut microbiota dynamics in healthy Bangladeshi infants: An insight into the gut virome development in early life.	Belgium	Onsite
187	Jihye Yang	Cholesterol-lowering Activities of Lactococcus lactis JILC-140 and 167 and Their Influences on the Gut Microbiome in Mice: In Vitro and In Vivo Analysis	Korea	Onsite
188	Mahesh Desai	A mucin-degrading gut bacterium regulates food allergy sensitization in a diet-dependent manner	Luxembourg	Onsite

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189	Dhrati Patangia	IMPACT OF EARLY LIFE ANTIBIOTIC EXPOSURE AND DELIVERY MODE ON INFANT GUT MICROBIOME	Ireland	Onsite
190	Joseph Paulson	Paenibacillus infection with frequent viral coinfection contributes to post-infectious hydrocephalus in Ugandan infants	USA	Onsite
191	Virginia Pedicord	Functional mapping to translate between mouse and human microbiota research	UK	Onsite
192	Ye Peng	Maternal smoking during pregnancy increases the risk of gut microbiome-associated childhood overweight	Hong Kong	Onsite
193	Tyler Perdue	Targeted Virulence Reduction and Clearance of STEC using MAGICaST	USA	Onsite
194	Niels Plomp	Expansion of the human gut culturome - a rapid and user-friendly pipeline	Netherlands	Onsite
195	Jeremy E Wilkinson	Evaluation of taxonomic profiling methods for long-read shotgun metagenomic sequencing datasets	USA	Onsite
196	Niklas Probul	Privacy-Aware Microbiome Profiling for Colorectal Cancer Detection using Federated Learning	Germany	Onsite
197	Nicola Prochazkova	INTER-INDIVIDUAL DIFFERENCES IN SEGMENTAL GUT TRANSIT TIME AND PH ARE ASSOCIATED WITH DIFFERENCES IN GUT MICROBIAL METABOLISM	Denmark	Onsite
198	Nina Radisavljevic	Effects of Parkinson's disease medication on gut microbiota composition and non-motor symptoms in a transgenic mouse model of Parkinson's disease	Canada	Onsite
199	Deirdre Ricaurte	Deep transcriptional profiling reveals microbial responses to top pharmaceutical compounds	USA	Onsite
200	Marwa Saadaoui	Vaginal microbiome and inflammatory mediators in women with Gestational Diabetes Mellitus	Qatar	Onsite
201	Yuki Saito	Molecular mechanism of arabinoxylan-derived oligosaccharides utilization in Bifidobacterium pseudocatenulatum	Japan	Onsite
202	Rocio Sanchez Alvarez	Deletion of protein tyrosine phosphatase nonreceptor type 23 results in lethal microbiota-dependent disease	Switzerland	Onsite
203	Kengo Sasaki	An Ex Vivo Fermentation Screening Platform by Human Colonic and Oral Microbiota	Japan	Onsite
204	Naoko Satoh-Takayama	Bacterial isolation of family S24-7 and functional analysis	Japan	Onsite
205	Thomas Schmidt	Drivers and Determinants of Strain Dynamics Following Fecal Microbiota Transplantation	Germany	Onsite
206	Laurenz Holcik	GuaCAMOLE: fragment GC bias-aware abundance estimation from metagenomic data increases accuracy and comparability	Austria	Onsite
207	Catherine Sedrani	neuroHuMiX: a gut-on-a-chip model to study the gut microbiome-nervous system axis	Luxembourg	Onsite
208	Alexandra SEMONT	Action on the composition and diversity of the microbiota to decrease radiation-induced colonic epithelial damages: application to "Pelvic Radiation Disease".	France	Onsite
209	Akira Sen	Comprehensive analysis of metabolites produced by co-cultivation of B. breve MCC1274 with human iPS-derived intestinal epithelial cells	Japan	Onsite
210	Youngchang Seo	Metagenome-wide association studies with integrative multi-omics data in type 2 diabetes mellitus	Korea	Onsite
211	Chrysi Sergaki	Establishing the 1st WHO International Reference Reagents for microbiome analysis	UK	Onsite
212	Arunabh Sharma	Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families	Germany	Onsite
213	Nakako Shibagaki	Skin microbiome of sensitive facial skin among Japanese women	Japan	Onsite
214	Rajesh Shigdel	Association of the oral microbiome with snoring and nocturnal gastroesophageal reflux: RHINESSA study	Norway	Onsite
215	Tatsuichiro Shima	Characteristics of gut microbiome, organic acid profiles and viral antibody indexes of healthy Japanese with live Lactocaseibacillus detected in stool	Japan	Onsite
216	Yutaka Shimokawa	Subtype-level Composition Analysis of Cutibacterium acnes using Postally-Delivered Tape-Stripped Skin Material of Japanese Customers	Japan	Onsite
217	Hirotsugu Shiroma	Enteropathway: the metabolic pathway database for human gut microbiota	Japan	Onsite
218	Alicia Showering	Exploring role of the skin microbiome and host genetics in human attractiveness to Anopheles mosquitoes	UK	Onsite
219	Yoram Louzoun	Image and graph convolution networks improve microbiome based machine learning accuracy	Israel	Onsite
220	Jiyeon Si	Bacteroides vulgatus SNUG 40005 restores Akkermansia-depleted dysbiosis and reverses obese phenotypes by modulating the metabolite pool	Korea	Onsite
221	Rashmi Sinha	Quality control sample for future population-based microbiome studies	USA	Onsite
222	Anurag Sinha	Substrate availability and dietary fibers regulate production of aromatic amino acid catabolites by human gut bacteria	Denmark	Onsite
223	Trishla Sinha	Lifelines NEXT: temporal development of the gut microbiome in relation to health and environment in 713 mother-infant pairs	Netherlands	Onsite
224	Naoki Soga	The impact of natural environment to human skin microbiome ~ Variation of human skin microbiome through dairy life~	Japan	Onsite
225	Se Jin Song	Towards creating a standardized, rich, and diverse resource to better understand human microbiome variation	USA	Onsite
226	Tulika Srivastava	Associations of the Gut microbiota composition and functional dynamics with the host genes and dietary factors.	India	Onsite

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227	Wataru Suda	Discovery of numerous non-chromosomal genetic elements with high completeness by long-read metagenomics of Japanese gut microbiomes	Japan	Onsite
228	Takashi Sugihira	Host and microbiome multi-omics integration in acne vulgaris	Japan	Onsite
229	Satoshi Suyama	Investigating microbial modulation of irritable bowel syndrome in mouse models	UK	Onsite
230	Takashi Taida	The intestinal bacterial features associated with the development of non-alcoholic fatty liver disease in young adults.	Japan	Onsite
231	Masatoshi Takagaki	Metagenomic analysis of the gut microbiome in patients with subarachnoid hemorrhage	Japan	Onsite
232	Lena Takayasu	Evolution and dynamics in gut microbiome through the whole life in mice	Japan	Onsite
233	Daiki Takewaki	Progressive multiple sclerosis patients-derived gut bacterial strain accelerates neuronal inflammation via flagellin-Th17 axis	Japan	Onsite
234	Fumie Takewaki	Associations between gut microbiome and abdominal symptoms due to acarbose administration in patients with type 2 diabetes	Japan	Onsite
235	Taiga Tamiya	Potential for CRISPR-Cas9 Mediated Base Edited Live Biotherapeutic Products as a Potent Therapeutic Modality	Japan	Onsite
236	Tomoyo Taniguchi	Gut microbiota and malarial pathology in C57BL/6N mice with ameliorated experimental cerebral malaria	Japan	Onsite
237	Jing Jie Teh	Colonic mucosa-associated microbiota metagenomic sequencing reveals novel microbes, differences between geographical regions, and differences between health and Crohn's disease. The ENIGMA study.	Australia	Onsite
238	Yoshiki Teramoto	Gut microbiota as a susceptibility factor for Kawasaki disease	Japan	Onsite
239	Cyrille Thinnes	The Virtual Metabolic Human database for human-microbiome metabolic modelling	Ireland	Onsite
240	Melinda A. Engevik	Identifying microbial interactions in the setting of Clostridioides difficile infection	USA	Onsite
241	Takashi Ito	The propionate-GPR41 axis during lactation contributes to bronchial asthma protection	Japan	Onsite
242	Raul Tito Tadeo	Multi-domain intestinal microbiome study of Peruvian populations transitioning to a more industrialized lifestyle	Belgium	Onsite
243	Dieter Tourlousse	Developing Standards for Measuring Fecal Microbiota by Metagenomics to Support Human Microbiome Research and Development	Japan	Onsite
244	Dieter Tourlousse	Insights into the Gut Microbiome of Healthy Japanese and its Association with Host Factors	Japan	Onsite
245	Akinobu Toyoda	The impact of natural environment to human skin microbiome ~ Human skin microbiome transition by exposure of airborne microbiome derived from natural environment ~	Japan	Onsite
246	Shoji Tsuji	Characteristics of urobiome in patients with nocturnal enuresis with daytime urinary incontinence and its involvement in pathogenesis	Japan	Onsite
247	Kowa Tsuji	Targeted Lipidomics of Fatty Acid-derived Functional Metabolites Produced by Gut Microbiota using Liquid Chromatography Mass Spectrometry	Japan	Onsite
248	Naoki Tsukuda	Early-life gut ecosystem development and bacterial taxa contributing gut butyrate production	Japan	Onsite
249	Timur Tuganbaev	Diet Diurnally Regulates Small Intestinal Microbiome-Epithelial-Immune Homeostasis and Enteritis	Japan	Onsite
250	Jun Uchiyama	Gut microbiota reinforce host antioxidant capacity via the generation of reactive sulfur species.	Japan	Onsite
251	Eriko Ueda	The maturity of the gut microbiome is associated with temperament in preschool children	Japan	Onsite
252	Mia Fitria Utami	Development of fully automated laboratory for microbiome research	Japan	Onsite
253	Lore Van Espen	Human Gut Phage Diversity Is Increased in Patients with Acute-on-Chronic Liver Failure	Belgium	Onsite
254	Erik van Tilburg Bernarde	Antibiotic-induced Malassezia spp. expansion in infants elicits intestinal immune dysregulation and increases airway inflammation in mice	Canada	Onsite
255	Jorge Vazquez Castellanos	Long-term life history predicts current elderly gut microbiome	Belgium	Onsite
256	Giacomo Vitali	Major microbiome metaproteomics changes after bariatric surgery-induced metabolic improvement: burst of oral proteins and Proteobacteria	France	Onsite
257	Asa Walberg	Impact of Inta-tumor Microbiota on Metastasis of Colorectal Cancer	Switzerland	Onsite
258	Koen Dekkers	Prediction of atherosclerosis-associated streptococci species using plasma metabolites	Sweden	Onsite
259	Xiaoqian Wang	Analysis on vaginal micro-ecology of 32046 outpatients	China	Onsite
260	Daisuke Watai	An in vitro study of the effect of berberine chloride on periodontal pathogenic bacteria in the oral microbiome	Japan	Onsite
261	Ayako Watanabe	Studies on biliary microbes in extrahepatic cholangiocarcinoma using 16S rRNA sequencing	Japan	Onsite
262	Yoshiyuki Watanabe	Isoxanthohumol improves obesity and insulin resistance through both pharmacological and gut microbial pathways	Japan	Onsite
263	Yohei Watanabe	Direct xylan utilization enhances adaptation of Bifidobacterium pseudocatenulatum to the human gastrointestinal tract	Japan	Onsite
264	Ran Wei	Effect of resistance starch on intestinal microbiome and immunity in mice	Japan	Onsite

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265	Patrick West	Widespread bacterial intragenic inversion revealed through long-read sequencing	USA	Onsite
266	Emma Whittle	"Answers in Hours" ? A prospective clinical study for rapid detection of pathogens and antibacterial resistance in bile aspirate using Oxford Nanopore Sequencing	USA	Onsite
267	Jeremy E Wilkinson	Maximizing MAGs from long-read metagenomic assemblies: a new post-assembly pipeline with circular-aware binning	USA	Onsite
268	Paul Wilmes	Integrated multi-omics identifies a gut archaeal compound as a driver of Parkinson's disease pathogenesis	Luxembourg	Onsite
269	Tong Wu	Evaluation of methods to model links between the gut microbiome and blood metabolome data	Germany	Onsite
270	Liangliang Wu	The Inhibitory Effect of Bacteroides spp. and its combinations isolated from human feces on the Adipogenesis of 3T3-L1 Cells	Korea	Onsite
271	Jia Xu	microMOM: A longitudinal survey of the maternal gut microbiome from preconception to postpartum and its link with metabolic health	Singapore	Onsite
272	Jia Xu	Early-life exposures, host genetics, and gut microbiome: insights from the Growing Up in Singapore Towards healthy Outcomes (GUSTO) birth cohort study	Singapore	Onsite
273	ChenDong Xu	The beneficial effects of Bifidobacterium longum subsp. infantis M-63 supplementation on healthy term infants	Japan	Onsite
274	Lin Zhang	Gut microbiome development and trajectory is altered in early life with eczema: Gut-skin axis	Hong Kong	Onsite
275	Sosuke Yagishita	The mechanisms of formation of social novelty by gut microbiota	Japan	Onsite
276	Kana Yahagi	Fucosylated HMO utilising bifidobacteria contribute formate and lactate production during breastfeeding period	Japan	Onsite
277	Kyosuke Yakabe	Dietary-protein sources modulate host susceptibility to Clostridioides difficile infection through the gut microbiota	Japan	Onsite
278	Kazuma Yama	Trends in detection of high prevalent oral bacteria during the first 60 months of life using a next-generation sequencer	Japan	Onsite
279	Kazuhiya Yamazaki	Oral microbiota shapes the gut microbiota, resulting in systemic effects	Japan	Online
280	Suh-Ching Yang	Effects of epidermal growth factor on gut microbiota composition and muscle loss in rats with alcoholic liver damage	Taiwan	Onsite
281	Yukiko Yano	The human oral microbiome and mortality in three prospective cohort studies	USA	Onsite
282	Takeshi Yasuda	Mucosa-associated microbiota associated with duodenal tumors	Japan	Onsite
283	Li-Fang Yeo	The tumour microbiota predicts immune enrichment in Malaysian breast cancer	Malaysia	Onsite
284	Takahide Yokoi	Evaluation of automated metagenomic DNA extraction systems using enzymatic method	Japan	Onsite
285	Jaekyung Yoon	Identification of microbial biomarkers associated with gastric carcinogenesis across East Asian populations through meta-analysis	Korea	Onsite
286	Frederikke Mortensen	Effect of cesarean section induced gut dysbiosis on the development of obesity	Denmark	Onsite
287	Lin Zhang	Microbiome signatures reflect COVID-19 mortality in population-based study	Hong Kong	Onsite
288	Chenhong ZHANG	Gut microbiota from healthy donors alleviates distal symmetric polyneuropathy in patients with diabetes mellitus	China	Onsite
289	Lin Zhang	Population-based microbiome signatures reflect COVID-19 mortality	Hong Kong	Onsite
290	Samuel Zimmerman	Quantifying shared and unique gene content across 17 microbial ecosystems	USA	Onsite
291	Moreno Zolfo	Stage-specific bacteriophages signatures in the Human Gut Virome of Colorectal Cancer Patients	Japan	Onsite
347	H. Bjorn Nielsen	An online atlas of human plasma metabolite signatures of gut microbiome composition	Denmark	Onsite
292	Afrouz Abbaspour	INTESTINAL MICROBIOME IN BINGE-TYPE EATING DISORDERS: THE BINGE EATING GENETICS INITIATIVE-SWEDEN (BEGIN-SE)	Sweden	Online
293	Christian Abnet	Correlates of the human oral microbial community in three large US cohort studies	USA	Online
294	Harithaa Anandakumar	Regional Diversity of the Gastrointestinal Microbiome and Immunome: A Comparison of Germ-Free and Colonized Mice	Germany	Online
295	David Barnett	microViz: an R package for microbiome data visualization and statistics	Netherlands	Online
296	Madhumita Bhattacharyya	AnnotIEM: A novel tool for microbiome species-level annotation of 16S gene based microbial sequencing	Germany	Online
297	Alessandra Borgognone	Vaccination with an HIV T-cell immunogen induces alterations in the mouse gut microbiota	Spain	Online
298	Ulrika Boulund	Gut microbiome associations with host genotype vary across ethnicities and potentially influence cardiometabolic traits	Netherlands	Online
299	Clara Bullich-Vilarrubias	Adaptive immunity is necessary for the glucoregulatory effects of Bacteroides uniformis CECT 7771 in diet-induced obese mice	Spain	Online

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300	Francesc Catala-Moll	Consensus-based robustness for differential abundance testing in microbiome data analysis	Spain	Online
301	Ebony Cave	Admixed peoples, admixed microbes: Within host evolution of Helicobacter pylori in Cabo Verde	UK	Online
302	Kwang Hyun Cha	A low dose of beryllium exposure influences gut microbiota and disrupts host metabolic homeostasis	Korea	Online
303	Carolyn Cooke	The effect of a prebiotic and probiotic protocol on the composition of the intestinal and semen microbiomes, as well as the sperm quality of stallions	Australia	Online
304	Pierre Dechelotte	THE PROBIOTIC STRAIN H. ALVEI HA4597R IMPROVES WEIGHT LOSS IN OVERWEIGHT SUBJECTS UNDER MODERATE HYPOCALORIC DIET: A MULTICENTER RANDOMIZED, PLACEBO-CONTROLLED STUDY	France	Online
305	Rene Erhardt	Assessment of the composition of the gut microbiota after supplementation with a prebiotic formulation for alleviating functional constipation	Australia	Online
306	Mathilde Flahaut	Distinctive features of the oropharyngeal microbiome in Inuit of Nunavik and its correlations with mild to moderate bronchial obstruction	Canada	Online
307	Sofia Forssten	Gastrointestinal models for probiotic-pathogen interactions	Finland	Online
308	Elena Franchitti	Gut microbiota indicators in MIS-C and COVID-19 onset: emerging differences and perspectives for early detection	Italy	Online
309	Jose Garcia-Guevara	The dynamics of the microbial biosynthetic gene cluster content in the gut microbiome of healthy individuals	Sweden	Online
310	Monami Hara	Gut microbiota of children with food allergy differs from that of healthy children	Japan	Online
311	Jiu-Yao Wang	Microbiome Change During and After Exacerbation in Asthmatic Children	Taiwan	Online
312	Midori Horiuchi	Dysbiosis in the gut microbiome accompanies skewed immunological and clinical parameters in patients with ME/CFS	Japan	Online
313	Claudia Huelguesch	Catching contaminants - Benchmarking the user-friendly microbiome decontamination tool MicroBIEM	Germany	Online
314	Cyrille Jarrin	Aging impact on skin microbiota across European and Asian women	Japan	Online
315	Tamotsu Kato	Examination of experimental conditions for mouse gut "Mycobiome" analysis and changes in microbiota due to differences in prebiotics.	Japan	Online
316	Jannike Krause	Sample logistics affect structural and functional profiles of faecal microbiota	Germany	Online
317	Abhijit Kulkarni	Microbiome composition of Indian tribal populations is structured by distinctive diets	India	Online
318	Amandine Lashermes	Deciphering the mechanisms of action underlying probiotic properties of Bacillus clausii by a functional genomics approach	France	Online
319	Rebeca Liebana-Garcia	Intestinal group 1 innate lymphoid cells cause gut barrier defects and microbiota imbalances preceding obesity and metabolic dysfunction	Spain	Online
320	Yijia Liow	Dietary fiber induces fat preference via the gut microbiota	Japan	Online
321	Victoria Meslier	In vitro modelling of oral microbial invasion in the human colon	France	Online
322	Matthew Miyasaka	Linking individual microbial and metabolite biomarkers of Colorectal Cancer using computational models of the gut microbiota metabolism	USA	Online
323	Makoto Miyoshi	Synbiotics with Bifidobacterium longum BB536 improves stool form via changes in the fecal microbiota and short-chain fatty acids in hemodialysis patients	Japan	Online
324	Efrat Muller	A multi-view perspective on predicting human diseases based on gut microbiome features	Israel	Online
325	Portia Murphy	Diarrhea-Predominant Irritable Bowel Syndrome (IBS-D) Patients Consecutively Treated with Vancomycin/Rifaximin Combination ? Retrospective Medical Record Review	Australia	Online
326	Marc Noguera-Julian	The gut microbiome and lifestyle, a multifactorial Mediterranean intervention study in the workplace	Spain	Online
327	Arjun OK	Identification of conserved genomic signatures specific to probiotic microbes colonising the human gut.	India	Online
328	Yangwenshan Ou	Gut microbiota and child behavior in early puberty: does child gender play a role?	Netherlands	Online
329	Natalia Palacios	The Gut Microbiome in Parkinson's Disease	USA	Online
330	Theo Portlock	Global Compositional and Functional State of the Human Gut Microbiome in Health and Disease	Sweden	Online
331	Zeba Praveen	The association of oral cancer and oral microbiome dysbiosis as a potential prognosis biomarker	Korea	Online
332	Justine Purina	The composition, stability, and origin of the human blood microbiome in healthy people and irritable bowel syndrome patients.	Latvia	Online
333	Luise Rauer	The power of mocks: A meta-analysis of positive controls and laboratory metainformation in microbiome data	Germany	Online
334	Chikako Shimokawa	Induction of Anisakis-specific IgE dependent on commensal bacteria in stomach during gastric Anisakis infection	Japan	Online
335	Daniella Susic	Microbiome in Maternity Study (MUMS) - Gut microbiome in pregnancy and its association with adverse pregnancy outcomes	Australia	Online
336	Daniella Susic	Microbiome in Maternity Study (MUMS) - Oral microbiome and its association with adverse pregnancy outcomes	Australia	Online
337	Daniella Susic	Microbiome in Maternity Study (MUMS) - Vaginal microbiome and its association with adverse pregnancy outcomes	Australia	Online

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338	Julien Tap	Global branches and local states of the human gut microbiome	France	Online
339	Dominik Ternes	THE GUT MICROBIAL METABOLITE FORMATE EXACERBATES COLORECTAL CANCER PROGRESSION	Luxembourg	Online
340	Viet Tran	Characterisation of synbiotics and their impact on human faecal microbiota during in vitro fermentation	Australia	Online
341	Emily Vogtmann	The human oral microbiome and risk of colorectal cancer from three prospective cohort studies in the United States	USA	Online
342	Xiayun Wan	Effects of (R)-ketamine on reduced bone mineral density in ovariectomized mice: A role of gut microbiota	Japan	Online
343	Shilan Wang	Host refined gut microbiome during pregnancy favor bacteria vertical transmission to offspring: the implication from MOMmy Cohort	Hong Kong	Online
344	Koji Yahara	Long-read metagenomics using PromethION uncovers oral bacteriophages and their interaction with host bacteria	Japan	Online
345	Yong Yang	A role of subdiaphragmatic vagus nerve in depressive-like phenotypes in Chrna7 knock-out mice	Japan	Online
346	Janine Ziemons	In vitro effects of the chemotherapeutic compound 5-Fluorouracil (5-FU) on gut microbiota composition and SCFA concentrations	Netherlands	Online