

Multivariable association discovery in population-scale

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Effects of <i>Limosilactobacillus reuteri</i> LR-99 Supplementation on Body Mass Index, Social Communication, Fine Motor Function, and Gut Microbiome Composition in Individuals with Prader-Willi Syndrome: a Randomized Double-Blinded Placebo-Controlled Trial. <i>Probiotics and Antimicrobial Proteins</i> , 2021, 13, 1508-1520.	1.9	9
2	Altered oral and gut microbiota and its association with SARS-CoV-2 viral load in COVID-19 patients during hospitalization. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 61.	2.9	121
3	Differential Analysis of Longitudinal Methicillin-Resistant <i>Staphylococcus aureus</i> Colonization in Relation to Microbial Shifts in the Nasal Microbiome of Neonatal Piglets. <i>MSystems</i> , 2021, 6, e0015221.	1.7	4
5	Non-diphtheriae <i>Corynebacterium</i> species are associated with decreased risk of pneumococcal colonization during infancy. <i>ISME Journal</i> , 2022, 16, 655-665.	4.4	14
6	Characterization of the blood microbiota in children with Celiac disease. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100069.	1.4	0
7	Alterations in Gut Microbiome Composition and Function in Irritable Bowel Syndrome and Increased Probiotic Abundance with Daily Supplementation. <i>MSystems</i> , 2021, 6, e0121521.	1.7	12
8	The Gut Microbiome Modifies the Association Between a Mediterranean Diet and Diabetes in USA Hispanic/ Latino Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e924-e934.	1.8	9
9	Human Milk-Based or Bovine Milk-Based Fortifiers Differentially Impact the Development of the Gut Microbiota of Preterm Infants. <i>Frontiers in Pediatrics</i> , 2021, 9, 719096.	0.9	8
10	Aryl Hydrocarbon Receptor (AhR) Activation by 2,3,7,8-Tetrachlorodibenzo-p-Dioxin (TCDD) Dose-Dependently Shifts the Gut Microbiome Consistent with the Progression of Non-Alcoholic Fatty Liver Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12431.	1.8	5
11	scCODA is a Bayesian model for compositional single-cell data analysis. <i>Nature Communications</i> , 2021, 12, 6876.	5.8	98
12	Altered Fecal Microbiota Correlated With Systemic Inflammation in Male Subjects With Methamphetamine Use Disorder. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 783917.	1.8	11
13	Assessing saliva microbiome collection and processing methods. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 81.	2.9	8
14	Size-Resolved Community Structure of Bacteria and Fungi Transported by Dust in the Middle East. <i>Frontiers in Microbiology</i> , 2021, 12, 744117.	1.5	12
15	Two microbiota subtypes identified in irritable bowel syndrome with distinct responses to the low FODMAP diet. <i>Gut</i> , 2022, 71, 1821-1830.	6.1	63
16	Weaning Age and Its Effect on the Development of the Swine Gut Microbiome and Resistome. <i>MSystems</i> , 2021, 6, e0068221.	1.7	26
17	Randomized quantile residuals for diagnosing zero-inflated generalized linear mixed models with applications to microbiome count data. <i>BMC Bioinformatics</i> , 2021, 22, 564.	1.2	2
18	Microbiome differential abundance methods produce different results across 38 datasets. <i>Nature Communications</i> , 2022, 13, 342.	5.8	286
19	Early-life viral infections are associated with disadvantageous immune and microbiota profiles and recurrent respiratory infections. <i>Nature Microbiology</i> , 2022, 7, 224-237.	5.9	25

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20	Multi-omics investigation of Clostridioides difficile-colonized patients reveals pathogen and commensal correlates of C. difficile pathogenesis. <i>ELife</i> , 2022, 11, .	2.8	16
21	Associations of Childhood and Perinatal Blood Metals with Children's Gut Microbiomes in a Canadian Gestation Cohort. <i>Environmental Health Perspectives</i> , 2022, 130, 17007.	2.8	13
22	Early intestinal microbial features are associated with CD4 T-cell recovery after allogeneic hematopoietic transplant. <i>Blood</i> , 2022, 139, 2758-2769.	0.6	25
23	Vitamin D Supplementation in Exclusively Breastfed Infants Is Associated with Alterations in the Fecal Microbiome. <i>Nutrients</i> , 2022, 14, 202.	1.7	6
24	Revealing General Patterns of Microbiomes That Transcend Systems: Potential and Challenges of Deep Transfer Learning. <i>MSystems</i> , 2022, 7, e0105821.	1.7	3
25	Consistent changes in the intestinal microbiota of Atlantic salmon fed insect meal diets. <i>Animal Microbiome</i> , 2022, 4, 8.	1.5	9
27	Multi-kingdom microbiota analyses identify bacterial-fungal interactions and biomarkers of colorectal cancer across cohorts. <i>Nature Microbiology</i> , 2022, 7, 238-250.	5.9	99
28	Axillary Microbiota Is Associated with Cognitive Impairment in Parkinson's Disease Patients. <i>Microbiology Spectrum</i> , 2022, 10, e0235821.	1.2	3
29	Stratification of the Gut Microbiota Composition Landscape across the Alzheimer's Disease Continuum in a Turkish Cohort. <i>MSystems</i> , 2022, 7, e0000422.	1.7	20
30	Influence of Geographical Location on Maternal-Infant Microbiota: Study in Two Populations From Asia and Europe. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663513.	1.8	6
31	A catalogue of 1,167 genomes from the human gut archaeome. <i>Nature Microbiology</i> , 2022, 7, 48-61.	5.9	72
32	Human gut metatranscriptome changes induced by a fermented milk product are associated with improved tolerance to a flatulogenic diet. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1632-1641.	1.9	0
33	The effect of a hydrolyzed protein diet on the fecal microbiota in cats with chronic enteropathy. <i>Scientific Reports</i> , 2022, 12, 2746.	1.6	3
34	Habitual Dietary Fiber Intake, Fecal Microbiota, and Hemoglobin A1c Level in Chinese Patients with Type 2 Diabetes. <i>Nutrients</i> , 2022, 14, 1003.	1.7	10
35	Short- and long-read metagenomics of urban and rural South African gut microbiomes reveal a transitional composition and undescribed taxa. <i>Nature Communications</i> , 2022, 13, 926.	5.8	26
36	Gut Microbiome Characteristics in feral and domesticated horses from different geographic locations. <i>Communications Biology</i> , 2022, 5, 172.	2.0	20
37	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	15.2	158
38	Gut Health and Microbiota in Out-of-Season Atlantic Salmon (<i>Salmo salar</i> L.) Smolts Before and After Seawater Transfer Under Commercial Arctic Conditions: Modulation by Functional Feed Ingredients. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	4

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39	Analysis of the Ability of Capsaicin to Modulate the Human Gut Microbiota In Vitro. <i>Nutrients</i> , 2022, 14, 1283.	1.7	11
40	Metagenomic Insights Into the Changes of Antibiotic Resistance and Pathogenicity Factor Pools Upon Thermophilic Composting of Human Excreta. <i>Frontiers in Microbiology</i> , 2022, 13, 826071.	1.5	6
41	The effects of the Green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. <i>Genome Medicine</i> , 2022, 14, 29.	3.6	46
42	Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. <i>Microbial Genomics</i> , 2022, 8, .	1.0	15
43	Omitting Ciprofloxacin Prophylaxis in Patients Undergoing Allogeneic Hematopoietic Stem Cell Transplantation and Its Impact on Clinical Outcomes and Microbiome Structure. <i>Transplantation and Cellular Therapy</i> , 2022, 28, 168.e1-168.e8.	0.6	3
44	Insights from shotgun metagenomics into bacterial species and metabolic pathways associated with NAFLD in obese youth. <i>Hepatology Communications</i> , 2022, 6, 1962-1974.	2.0	20
45	Experimental manipulation of microbiota reduces host thermal tolerance and fitness under heat stress in a vertebrate ectotherm. <i>Nature Ecology and Evolution</i> , 2022, 6, 405-417.	3.4	27
46	Human gut bacteria produce Ï—17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	13.7	210
47	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
48	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant Enterobacteriaceae. <i>Microbiome</i> , 2022, 10, 43.	4.9	8
49	Daily Exposure to a Cranberry Polyphenol Oral Rinse Alters the Oral Microbiome but Not Taste Perception in PROP Taster Status Classified Individuals. <i>Nutrients</i> , 2022, 14, 1492.	1.7	4
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54	Increasing transparency and reproducibility in stroke-microbiota research: A toolbox for microbiota analysis. <i>iScience</i> , 2022, 25, 103998.	1.9	3
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56	Characterization of microbial intolerances and ruminal dysbiosis towards different dietary carbohydrate sources using an in vitro model. <i>Journal of Applied Microbiology</i> , 2022, 133, 458-476.	1.4	4

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58	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	1.8	48
59	3MCor: an integrative web server for metabolome-microbiome-metadata correlation analysis. <i>Bioinformatics</i> , 2022, 38, 1378-1384.	1.8	3
60	Population study of the gut microbiome: associations with diet, lifestyle, and cardiometabolic disease. <i>Genome Medicine</i> , 2021, 13, 188.	3.6	27
61	Multi-Strain Probiotic Supplementation with a Product Containing Human-Native <i>S. salivarius</i> K12 in Healthy Adults Increases Oral <i>S. salivarius</i> . <i>Nutrients</i> , 2021, 13, 4392.	1.7	1
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63	Butyrate producing microbiota are reduced in chronic kidney diseases. <i>Scientific Reports</i> , 2021, 11, 23530.	1.6	17
64	Gut microbiomes from Gambian infants reveal the development of a non-industrialized <i>Prevotella</i> -based trophic network. <i>Nature Microbiology</i> , 2022, 7, 132-144.	5.9	30
65	Investigation of the impact of commonly used medications on the oral microbiome of individuals living without major chronic conditions. <i>PLoS ONE</i> , 2021, 16, e0261032.	1.1	8
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67	Fecal DNA Virome Is Associated with the Development of Colorectal Neoplasia in a Murine Model of Colorectal Cancer. <i>Pathogens</i> , 2022, 11, 457.	1.2	7
68	LinDA: linear models for differential abundance analysis of microbiome compositional data. <i>Genome Biology</i> , 2022, 23, 95.	3.8	79
70	<i>Bifidobacterium infantis</i> treatment promotes weight gain in Bangladeshi infants with severe acute malnutrition. <i>Science Translational Medicine</i> , 2022, 14, eabk1107.	5.8	61
71	Acute and persistent effects of commonly used antibiotics on the gut microbiome and resistome in healthy adults. <i>Cell Reports</i> , 2022, 39, 110649.	2.9	64
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73	Alterations of mucosa-attached microbiome and epithelial cell numbers in the cystic fibrosis small intestine with implications for intestinal disease. <i>Scientific Reports</i> , 2022, 12, 6593.	1.6	10
74	Longitudinal analysis of the impact of oral contraceptive use on the gut microbiome. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	8
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76	Differences of the Nasal Microbiome and Mycobiome by Clinical Characteristics of COPD Patients. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla)</i> , 2022, , 309-324.	0.5	3
78	Fecal microbiota transplantation is safe and tolerable in patients with multiple sclerosis: A pilot randomized controlled trial. <i>Multiple Sclerosis Journal - Experimental, Translational and Clinical</i> , 2022, 8, 205521732210866.	0.5	16
79	Disordered development of gut microbiome interferes with the establishment of the gut ecosystem during early childhood with atopic dermatitis. <i>Gut Microbes</i> , 2022, 14, 2068366.	4.3	20
80	Associations between maternal obesity and offspring gut microbiome in the first year of life. <i>Pediatric Obesity</i> , 2022, 17, e12921.	1.4	15
81	A Low Glycemic Index Mediterranean Diet Combined with Aerobic Physical Activity Rearranges the Gut Microbiota Signature in NAFLD Patients. <i>Nutrients</i> , 2022, 14, 1773.	1.7	24
83	Supplementation with SCFAs Re-Establishes Microbiota Composition and Attenuates Hyperalgesia and Pain in a Mouse Model of NITG-Induced Migraine. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4847.	1.8	10
84	Altered Salivary Microbiota Following <i>Bifidobacterium animalis</i> Subsp. <i>Lactis</i> BL-11 Supplementation Are Associated with Anthropometric Growth and Social Behavior Severity in Individuals with Prader-Willi Syndrome. <i>Probiotics and Antimicrobial Proteins</i> , 2022, , 1.	1.9	0
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86	Microbiome "Inception" an Intestinal Cestode Shapes a Hierarchy of Microbial Communities Nested within the Host. <i>MBio</i> , 2022, 13, e0067922.	1.8	8
87	The healthy female microbiome across body sites: effect of hormonal contraceptives and the menstrual cycle. <i>Human Reproduction</i> , 2022, 37, 1525-1543.	0.4	41
88	Impacts of dietary exposure to pesticides on faecal microbiome metabolism in adult twins. <i>Environmental Health</i> , 2022, 21, 46.	1.7	14
89	Oral Microbiome of Crohn's Disease Patients With and Without Oral Manifestations. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1628-1636.	0.6	7
90	EasyMap - An Interactive Web Tool for Evaluating and Comparing Associations of Clinical Variables and Microbiome Composition. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
91	Impact of antibiotics on off-target infant gut microbiota and resistance genes in cohort studies. <i>Pediatric Research</i> , 2022, 92, 1757-1766.	1.1	9
92	Editorial: Methods for Single-Cell and Microbiome Sequencing Data. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	0
93	Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. <i>ISME Journal</i> , 2022, 16, 1980-1992.	4.4	14
94	Stool and Ruminal Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	12
95	Gut Microbial Stability is Associated with Greater Endurance Performance in Athletes Undertaking Dietary Periodization. <i>MSystems</i> , 2022, 7, e0012922.	1.7	12

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96	Association between gut Microbiota, GROWth and Diet in peripubertal children from the TARGet Kids! cohort (The MiGrowD) study: protocol for studying gut microbiota at a community-based primary healthcare setting. <i>BMJ Open</i> , 2022, 12, e057989.	0.8	0
97	BiGAMi: Bi-Objective Genetic Algorithm Fitness Function for Feature Selection on Microbiome Datasets. <i>Methods and Protocols</i> , 2022, 5, 42.	0.9	1
98	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. <i>Communications Earth & Environment</i> , 2022, 3, .	2.6	13
99	Interaction effect between NAFLD severity and high carbohydrate diet on gut microbiome alteration and hepatic <i>de novo</i> lipogenesis. <i>Gut Microbes</i> , 2022, 14, .	4.3	18
100	The Gut Microbiome of Preterm Infants Treated With Aminophylline Is Closely Related to the Occurrence of Feeding Intolerance and the Weight Gain. <i>Frontiers in Nutrition</i> , 2022, 9, .	1.6	3
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103	Differential expression of single-cell RNA-seq data using Tweedie models. <i>Statistics in Medicine</i> , 2022, 41, 3492-3510.	0.8	11
106	Composition and Functional Potential of the Human Mammary Microbiota Prior to and Following Breast Tumor Diagnosis. <i>MSystems</i> , 2022, 7, .	1.7	10
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108	The epithelial-specific ER stress sensor ERN2/IRE1 ² enables host-microbiota crosstalk to affect colon goblet cell development. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	19
111	Transitory Shifts in Skin Microbiota Composition and Reductions in Bacterial Load and Psoriasis following Ethanol Perturbation. <i>MSphere</i> , 2022, 7, .	1.3	1
112	Different Fecal Microbiota in Hirschsprung's Patients With and Without Associated Enterocolitis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
114	Epithelial HNF4A shapes the intraepithelial lymphocyte compartment via direct regulation of immune signaling molecules. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
115	Long-read PacBio genome sequencing of four environmental saprophytic <i>Sporothrix</i> species spanning the pathogenic clade. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
116	Antibiotic and antifungal use in pediatric leukemia and lymphoma patients are associated with increasing opportunistic pathogens and decreasing bacteria responsible for activities that enhance colonic defense. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6
118	Alterations in infant gut microbiome composition and metabolism after exposure to glyphosate and Roundup and/or a spore-based formulation using the SHIME technology. <i>Gut Microbiome</i> , 2022, 3, .	0.8	4
119	Shift of dietary carbohydrate source from milk to various solid feeds reshapes the rumen and fecal microbiome in calves. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
120	Novel Insights into the Pig Gut Microbiome Using Metagenome-Assembled Genomes. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	16

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121	Metagenomic analysis reveals associations between salivary microbiota and body composition in early childhood. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
122	In Utero Exposure to Caffeine and Acetaminophen, the Gut Microbiome, and Neurodevelopmental Outcomes: A Prospective Birth Cohort Study. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 9357.	1.2	3
123	Progressive microbial adaptation of the bovine rumen and hindgut in response to a step-wise increase in dietary starch and the influence of phytogenic supplementation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	12
124	Source of human milk (mother or donor) is more important than fortifier type (human or bovine) in shaping the preterm infant microbiome. <i>Cell Reports Medicine</i> , 2022, 3, 100712.	3.3	17
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127	The association between early-life gut microbiota and childhood respiratory diseases: a systematic review. <i>Lancet Microbe</i> , The, 2022, 3, e867-e880.	3.4	26
128	Altered gut microbiota is associated with sleep disturbances in patients with minimal hepatic encephalopathy caused by hepatitis B-related liver cirrhosis. <i>Expert Review of Gastroenterology and Hepatology</i> , 2022, 16, 797-807.	1.4	3
129	Alterations of Gut Microbiome, Metabolome, and Lipidome in Takayasu Arteritis. <i>Arthritis and Rheumatology</i> , 2023, 75, 266-278.	2.9	9
130	A multi-omics graph database for data integration and knowledge extraction. , 2022, , .		0
132	Chemotherapy-associated oral microbiome changes in breast cancer patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
133	Characterization of presence and activity of microRNAs in the rumen of cattle hints at possible host-microbiota cross-talk mechanism. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
134	Skin bacterial microbiome diversity predicts lower activity levels in female, but not male, guppies, <i>Poecilia reticulata</i> . <i>Biology Letters</i> , 2022, 18, .	1.0	2
136	Human milk nutrient fortifiers alter the developing gastrointestinal microbiota of very-low-birth-weight infants. <i>Cell Host and Microbe</i> , 2022, 30, 1328-1339.e5.	5.1	12
137	Supplemental Oxygen Alters the Airway Microbiome in Cystic Fibrosis. <i>MSystems</i> , 2022, 7, .	1.7	1
138	Zebra: Static and Dynamic Genome Cover Thresholds with Overlapping References. <i>MSystems</i> , 2022, 7, .	1.7	5
139	Landscape of the gut archaeome in association with geography, ethnicity, urbanization, and diet in the Chinese population. <i>Microbiome</i> , 2022, 10, .	4.9	14
140	Gut dysbiosis and inflammatory blood markers precede HIV with limited changes after early seroconversion. <i>EBioMedicine</i> , 2022, 84, 104286.	2.7	8

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141	Microbiome-gut-brain axis in brain development, cognition and behavior during infancy and early childhood. <i>Developmental Review</i> , 2022, 66, 101038.	2.6	7
142	Microbiome dysbiosis inhibits carcinogen-induced murine oral tumorigenesis. <i>Journal of Cancer</i> , 2022, 13, 3051-3060.	1.2	2
143	Alterations of the Composition and Neurometabolic Profile of Human Gut Microbiota in Major Depressive Disorder. <i>Biomedicines</i> , 2022, 10, 2162.	1.4	11
144	COVID-19 patients exhibit unique transcriptional signatures indicative of disease severity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
145	Strain-specific impacts of probiotics are a significant driver of gut microbiome development in very preterm infants. <i>Nature Microbiology</i> , 2022, 7, 1525-1535.	5.9	48
146	Longitudinal analysis of the rectal microbiome in dogs with diabetes mellitus after initiation of insulin therapy. <i>PLoS ONE</i> , 2022, 17, e0273792.	1.1	3
147	Plasticity of the <i>Anemonia viridis</i> microbiota in response to different levels of combined anthropogenic and environmental stresses. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	3
148	Intercontinental Gut Microbiome Variances in IBD. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10868.	1.8	3
149	Machine Learning and Canine Chronic Enteropathies: A New Approach to Investigate FMT Effects. <i>Veterinary Sciences</i> , 2022, 9, 502.	0.6	5
150	Study of gut microbiota alterations in Alzheimer's dementia patients from Kazakhstan. <i>Scientific Reports</i> , 2022, 12, .	1.6	32
152	Short- and Long-Term Effects of a Prebiotic Intervention with Polyphenols Extracted from European Black Elderberry—Sustained Expansion of <i>Akkermansia</i> spp.. <i>Journal of Personalized Medicine</i> , 2022, 12, 1479.	1.1	7
153	Correlation of gut microbiota and metabolic functions with the antibody response to the BBIBP-CoV vaccine. <i>Cell Reports Medicine</i> , 2022, 3, 100752.	3.3	14
154	Bowel habits, faecal microbiota and faecal bile acid composition of healthy adults consuming fruit pomace fibres: two-arm, randomised, double-blinded, placebo-controlled trials. <i>British Journal of Nutrition</i> , 2023, 130, 42-55.	1.2	2
155	Microbial Interdomain Interactions Delineate the Disruptive Intestinal Homeostasis in <i>Clostridioides difficile</i> Infection. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
156	Longitudinal analysis of exposure to a low concentration of oxytetracycline on the zebrafish gut microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
158	A robust and transformation-free joint model with matching and regularization for metagenomic trajectory and disease onset. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
160	Oral microbial taxa associated with risk for SARS-CoV-2 infection. <i>Frontiers in Oral Health</i> , 0, 3, .	1.2	2
161	Combined IgE neutralization and <i>Bifidobacterium longum</i> supplementation reduces the allergic response in models of food allergy. <i>Nature Communications</i> , 2022, 13, .	5.8	8

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163	Feeding strategy and dietary preference shape the microbiome of epipelagic copepods in a warm nutrient-impoverished ecosystem. <i>Environmental DNA</i> , 2023, 5, 38-55.	3.1	4
164	Investigating differential abundance methods in microbiome data: A benchmark study. <i>PLoS Computational Biology</i> , 2022, 18, e1010467.	1.5	18
165	Disrupted establishment of anaerobe and facultative anaerobe balance in preterm infants with extrauterine growth restriction. <i>Frontiers in Pediatrics</i> , 0, 10, .	0.9	1
168	Rural environment reduces allergic inflammation by modulating the gut microbiota. <i>Gut Microbes</i> , 2022, 14, .	4.3	10
169	Altered gut microbiome diversity and function in patients with propionic acidemia. <i>Molecular Genetics and Metabolism</i> , 2022, 137, 308-322.	0.5	2
170	<i>Bacteroides</i> abundance drives birth mode dependent infant gut microbiota developmental trajectories. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
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