Jens Walter

List of Publications by Year
in descending order

160 papers	26,308 citations	10351 72 h-index	6979 154 g-index
172 all docs	172 docs citations	172 times ranked	26876 citing authors

#	Article	IF	Citations
1	A taxonomic note on the genus Lactobacillus: Description of 23 novel genera, emended description of the genus Lactobacillus Beijerinck 1901, and union of Lactobacillaceae and Leuconostocaceae. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2782-2858.	0.8	2,775
2	The Impact of Dietary Fiber on Gut Microbiota in Host Health and Disease. Cell Host and Microbe, 2018, 23, 705-715.	5.1	1,441
3	Role of the gut microbiota in nutrition and health. BMJ: British Medical Journal, 2018, 361, k2179.	2.4	1,228
4	Individuality in gut microbiota composition is a complex polygenic trait shaped by multiple environmental and host genetic factors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18933-18938.	3.3	1,113
5	A critical assessment of the â€œsterile wombâ€•and â€œin utero colonizationâ€•hypotheses: implications for research on the pioneer infant microbiome. Microbiome, 2017, 5, 48.	4.9	744
6	The microbiome of uncontacted Amerindians. Science Advances, 2015, 1, .	4.7	721
7	Detection of Lactobacillus, Pediococcus, Leuconostoc , and Weissella Species in Human Feces by Using Group-Specific PCR Primers and Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2001, 67, 2578-2585.	1.4	691
8	Towards a more comprehensive concept for prebiotics. Nature Reviews Gastroenterology and Hepatology, 2015, 12, 303-310.	8.2	679
9	Ecological Role of Lactobacilli in the Gastrointestinal Tract: Implications for Fundamental and Biomedical Research. Applied and Environmental Microbiology, 2008, 74, 4985-4996.	1.4	594
10	The Human Gut Microbiome: Ecology and Recent Evolutionary Changes. Annual Review of Microbiology, 2011, 65, 411-429.	2.9	589
11	Detection and Identification of Gastrointestinal <i>Lactobacillus</i> Species by Using Denaturing Gradient Gel Electrophoresis and Species-Specific PCR Primers. Applied and Environmental Microbiology, 2000, 66, 297-303.	1.4	555
12	Resistant Starches Types 2 and 4 Have Differential Effects on the Composition of the Fecal Microbiota in Human Subjects. PLoS ONE, 2010, 5, e15046.	1.1	508
13	The Gut Microbiota of Rural Papua New Guineans: Composition, Diversity Patterns, and Ecological Processes. Cell Reports, 2015, 11, 527-538.	2.9	475
14	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. Nature Microbiology, 2016, 1, 16131.	5.9	465
15	Gut microbiome composition is linked to whole grain-induced immunological improvements. ISME Journal, 2013, 7, 269-280.	4.4	462
16	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. Cell Host and Microbe, 2019, 25, 789-802.e5.	5.1	441
17	The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. Genetics, 2012, 190, 389-401.	1.2	435
18	Lifestyles in transition: evolution and natural history of the genus Lactobacillus. FEMS Microbiology Reviews, 2017, 41, S27-S48.	3.9	400

#	Article	IF	Citations
19	Prebiotics Reduce Body Fat and Alter Intestinal Microbiota in Children Who Are Overweight or With Obesity. Gastroenterology, 2017, 153, 711-722.	0.6	358
20	Monitoring the Bacterial Population Dynamics in Sourdough Fermentation Processes by Using PCR-Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2003, 69, 475-482.	1.4	345
21	Stable Engraftment of Bifidobacterium longum AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome. Cell Host and Microbe, 2016, 20, 515-526.	5.1	337
22	Innate and Adaptive Immunity Interact to Quench Microbiome Flagellar Motility in the Gut. Cell Host and Microbe, 2013, 14, 571-581.	5.1	321
23	Establishing or Exaggerating Causality for the Gut Microbiome: Lessons from Human Microbiota-Associated Rodents. Cell, 2020, 180, 221-232.	13.5	318
24	Diet-Induced Metabolic Improvements in a Hamster Model of Hypercholesterolemia Are Strongly Linked to Alterations of the Gut Microbiota. Applied and Environmental Microbiology, 2009, 75, 4175-4184.	1.4	299
25	Precision Microbiome Modulation with Discrete Dietary Fiber Structures Directs Short-Chain Fatty Acid Production. Cell Host and Microbe, 2020, 27, 389-404.e6.	5.1	298
26	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. BMC Microbiology, 2014, 14, 189.	1.3	292
27	Host-microbial symbiosis in the vertebrate gastrointestinal tract and the <i>Lactobacillus reuteri</i> paradigm. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4645-4652.	3.3	283
28	The Evolution of Host Specialization in the Vertebrate Gut Symbiont Lactobacillus reuteri. PLoS Genetics, 2011, 7, e1001314.	1.5	270
29	Barcoded Pyrosequencing Reveals That Consumption of Galactooligosaccharides Results in a Highly Specific Bifidogenic Response in Humans. PLoS ONE, 2011, 6, e25200.	1.1	263
30	Diversification of the gut symbiont <i>Lactobacillus reuteri</i> as a result of host-driven evolution. ISME Journal, 2010, 4, 377-387.	4.4	254
31	Depletion of luminal iron alters the gut microbiota and prevents Crohn's disease-like ileitis. Gut, 2011, 60, 325-333.	6.1	251
32	InÂvitro characterization of the impact of selected dietary fibers on fecal microbiota composition and short chain fatty acid production. Anaerobe, 2013, 23, 74-81.	1.0	235
33	Probiotic Bifidobacterium strains and galactooligosaccharides improve intestinal barrier function in obese adults but show no synergism when used together as synbiotics. Microbiome, 2018, 6, 121.	4.9	202
34	Intake of <i>Lactobacillus reuteri</i> Improves Incretin and Insulin Secretion in Glucose-Tolerant Humans: A Proof of Concept. Diabetes Care, 2015, 38, 1827-1834.	4.3	194
35	Human Microbiota-Associated Mice: A Model with Challenges. Cell Host and Microbe, 2016, 19, 575-578.	5.1	190
36	Characterization of Reutericyclin Produced by Lactobacillus reuteri LTH2584. Applied and Environmental Microbiology, 2000, 66, 4325-4333.	1.4	182

#	Article	IF	Citations
37	Associations between infant fungal and bacterial dysbiosis and childhood atopic wheeze in a nonindustrialized setting. Journal of Allergy and Clinical Immunology, 2018, 142, 424-434.e10.	1.5	181
38	Diet-Induced Alterations of Host Cholesterol Metabolism Are Likely To Affect the Gut Microbiota Composition in Hamsters. Applied and Environmental Microbiology, 2013, 79, 516-524.	1.4	180
39	In vitro study of Prebiotic Properties of Levan-type Exopolysaccharides from Lactobacilli and Non-digestible Carbohydrates Using Denaturing Gradient Gel Electrophoresis. Systematic and Applied Microbiology, 2001, 24, 232-237.	1.2	178
40	Mucosal Barrier Depletion and Loss of Bacterial Diversity are Primary Abnormalities in Paediatric Ulcerative Colitis. Journal of Crohn's and Colitis, 2016, 10, 462-471.	0.6	178
41	Dietary selenium affects host selenoproteome expression by influencing the gut microbiota. FASEB Journal, 2011, 25, 2492-2499.	0.2	175
42	A dose dependent impact of prebiotic galactooligosaccharides on the intestinal microbiota of healthy adults. International Journal of Food Microbiology, 2010, 144, 285-292.	2.1	170
43	Establishing What Constitutes a Healthy Human Gut Microbiome: State of the Science, Regulatory Considerations, and Future Directions. Journal of Nutrition, 2019, 149, 1882-1895.	1.3	163
44	Molecular Characterization of Host-Specific Biofilm Formation in a Vertebrate Gut Symbiont. PLoS Genetics, 2013, 9, e1004057.	1.5	162
45	Strain-specific diversity of mucus-binding proteins in the adhesion and aggregation properties of Lactobacillus reuteri. Microbiology (United Kingdom), 2010, 156, 3368-3378.	0.7	157
46	The Fiber Gap and the Disappearing Gut Microbiome: Implications for Human Nutrition. Trends in Endocrinology and Metabolism, 2016, 27, 239-242.	3.1	155
47	Long-Term Temporal Analysis of the Human Fecal Microbiota Revealed a Stable Core of Dominant Bacterial Species. PLoS ONE, 2013, 8, e69621.	1.1	152
48	Synbiotic approach restores intestinal homeostasis and prolongs survival in leukaemic mice with cachexia. ISME Journal, 2016, 10, 1456-1470.	4.4	149
49	Experimental evaluation of the importance of colonization history in early-life gut microbiota assembly. ELife, 2018, 7, .	2.8	140
50	Host genetics and diet, but not immunoglobulin A expression, converge to shape compositional features of the gut microbiome in an advanced intercross population of mice. Genome Biology, 2014, 15, 552.	3.8	134
51	Impact of Fecal Microbiota Transplantation on Obesity and Metabolic Syndromeâ€"A Systematic Review. Nutrients, 2019, 11, 2291.	1.7	132
52	Characterization of the Ileal Microbiota in Rejecting and Nonrejecting Recipients of Small Bowel Transplants. American Journal of Transplantation, 2012, 12, 753-762.	2.6	131
53	To engraft or not to engraft: an ecological framework for gut microbiome modulation with live microbes. Current Opinion in Biotechnology, 2018, 49, 129-139.	3.3	131
54	Glucosyltransferase A (GtfA) and inulosucrase (Inu) of Lactobacillus reuteri TMW1.106 contribute to cell aggregation, in vitro biofilm formation, and colonization of the mouse gastrointestinal tract. Microbiology (United Kingdom), 2008, 154, 72-80.	0.7	130

#	Article	IF	Citations
55	d-Alanyl ester depletion of teichoic acids inLactobacillus reuteri100-23 results in impaired colonization of the mouse gastrointestinal tract. Environmental Microbiology, 2007, 9, 1750-1760.	1.8	126
56	Dietary Fructose and Microbiota-Derived Short-Chain Fatty Acids Promote Bacteriophage Production in the Gut Symbiont Lactobacillus reuteri. Cell Host and Microbe, 2019, 25, 273-284.e6.	5.1	126
57	Modulation of the Gastrointestinal Microbiome with Nondigestible Fermentable Carbohydrates To Improve Human Health. Microbiology Spectrum, 2017, 5, .	1.2	125
58	Randomized controlled trial on the impact of early-life intervention with bifidobacteria on the healthy infant fecal microbiota and metabolome. American Journal of Clinical Nutrition, 2017, 106, 1274-1286.	2.2	124
59	Fecal microbial transplantation and fiber supplementation in patients with severe obesity and metabolic syndrome: a randomized double-blind, placebo-controlled phase 2 trial. Nature Medicine, 2021, 27, 1272-1279.	15.2	119
60	Challenges of metabolomics in human gut microbiota research. International Journal of Medical Microbiology, 2016, 306, 266-279.	1.5	117
61	Identification of Lactobacillus reuteri Genes Specifically Induced in the Mouse Gastrointestinal Tract. Applied and Environmental Microbiology, 2003, 69, 2044-2051.	1.4	115
62	Inulin-type fructans improve active ulcerative colitis associated with microbiota changes and increased short-chain fatty acids levels. Gut Microbes, 2019, 10, 334-357.	4.3	114
63	Resistant starch can improve insulin sensitivity independently of the gut microbiota. Microbiome, 2017, 5, 12.	4.9	113
64	A High-Molecular-Mass Surface Protein (Lsp) and Methionine Sulfoxide Reductase B (MsrB) Contribute to the Ecological Performance of Lactobacillus reuteri in the Murine Gut. Applied and Environmental Microbiology, 2005, 71, 979-986.	1.4	110
65	Asymptomatic Intestinal Colonization with Protist<i>Blastocystis</i>Is Strongly Associated with Distinct Microbiome Ecological Patterns. MSystems, 2018, 3, .	1.7	99
66	Structure and functions of exopolysaccharide produced by gut commensal <i>Lactobacillus reuteri</i> 100-23. ISME Journal, 2011, 5, 1115-1124.	4.4	93
67	Faecal microbiota from patients with cirrhosis has a low capacity to ferment nonâ€digestible carbohydrates into shortâ€chain fatty acids. Liver International, 2019, 39, 1437-1447.	1.9	91
68	Ecological Behavior of Lactobacillus reuteri 100-23 Is Affected by Mutation of the luxS Gene. Applied and Environmental Microbiology, 2005, 71, 8419-8425.	1.4	88
69	Experimental Evaluation of Host Adaptation of Lactobacillus reuteri to Different Vertebrate Species. Applied and Environmental Microbiology, 2017, 83, .	1.4	87
70	Resistant starches for the management of metabolic diseases. Current Opinion in Clinical Nutrition and Metabolic Care, 2015, 18, 559-565.	1.3	84
71	From Prediction to Function Using Evolutionary Genomics: Human-Specific Ecotypes of Lactobacillus reuteri Have Diverse Probiotic Functions. Genome Biology and Evolution, 2014, 6, 1772-1789.	1.1	83
72	Gut microbiota modulation with long-chain corn bran arabinoxylan in adults with overweight and obesity is linked to an individualized temporal increase in fecal propionate. Microbiome, 2020, 8, 118.	4.9	81

#	Article	IF	Citations
73	Increased Complexity of the Species Composition of Lactic Acid Bacteria in Human Feces Revealed by Alternative Incubation Condition. Microbial Ecology, 2003, 45, 455-463.	1.4	78
74	Engineering the Campylobacter jejuni N-glycan to create an effective chicken vaccine. Scientific Reports, 2016, 6, 26511.	1.6	70
75	Construction, Analysis, and Î²-Glucanase Screening of a Bacterial Artificial Chromosome Library from the Large-Bowel Microbiota of Mice. Applied and Environmental Microbiology, 2005, 71, 2347-2354.	1.4	68
76	Biomarkers for assessment of intestinal permeability in clinical practice. American Journal of Physiology - Renal Physiology, 2021, 321, G11-G17.	1.6	65
77	Rethinking healthy eating in light of the gut microbiome. Cell Host and Microbe, 2022, 30, 764-785.	5.1	65
78	The pan-genome of Lactobacillus reuteri strains originating from the pig gastrointestinal tract. BMC Genomics, 2015, 16, 1023.	1.2	64
79	Dietary non-fermentable fiber prevents autoimmune neurological disease by changing gut metabolic and immune status. Scientific Reports, 2018, 8, 10431.	1.6	63
80	Supplementation with a probiotic mixture accelerates gut microbiome maturation and reduces intestinal inflammation in extremely preterm infants. Cell Host and Microbe, 2022, 30, 696-711.e5.	5.1	63
81	Sucrose utilization and impact of sucrose on glycosyltransferase expression in Lactobacillus reuteri. Systematic and Applied Microbiology, 2007, 30, 433-443.	1.2	61
82	Low-Density Lipoprotein Receptor Signaling Mediates the Triglyceride-Lowering Action of <i>Akkermansia muciniphila</i> in Genetic-Induced Hyperlipidemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1448-1456.	1.1	60
83	Limosilactobacillus balticus sp. nov., Limosilactobacillus agrestis sp. nov., Limosilactobacillus albertensis sp. nov., Limosilactobacillus rudii sp. nov. and Limosilactobacillus fastidiosus sp. nov., five novel Limosilactobacillus species isolated from the vertebrate gastrointestinal tract, and proposal of six subspecies of Limosilactobacillus reuteri adapted to the gastrointestinal tract of specific vertebrate hosts. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	60
84	Responders and non-responders to probiotic interventions. Gut Microbes, 2010, 1, 200-204.	4.3	59
85	Intestinal Origin of Sourdough <i>Lactobacillus reuteri</i> Isolates as Revealed by Phylogenetic, Genetic, and Physiological Analysis. Applied and Environmental Microbiology, 2012, 78, 6777-6780.	1.4	57
86	Genetic Determinants of Reutericyclin Biosynthesis in Lactobacillus reuteri. Applied and Environmental Microbiology, 2015, 81, 2032-2041.	1.4	56
87	Comparison of the Colonization Ability of Autochthonous and Allochthonous Strains of Lactobacilli in the Human Gastrointestinal Tract. Advances in Microbiology, 2012, 02, 399-409.	0.3	51
88	Bifidobacterium animalis causes extensive duodenitis and mild colonic inflammation in monoassociated interleukin-10-deficient mice. Inflammatory Bowel Diseases, 2009, 15, 1022-1031.	0.9	48
89	Ability of the gut microbiota to produce PUFAâ€derived bacterial metabolites: Proof of concept in germâ€free versus conventionalized mice. Molecular Nutrition and Food Research, 2015, 59, 1603-1613.	1.5	48
90	Role of dietary fiber in promoting immune healthâ€"An <scp>EAACI</scp> position paper. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 3185-3198.	2.7	48

#	Article	IF	Citations
91	<i>In Vivo</i> Selection To Identify Bacterial Strains with Enhanced Ecological Performance in Synbiotic Applications. Applied and Environmental Microbiology, 2015, 81, 2455-2465.	1.4	47
92	Coadministration of the Campylobacter jejuni N-Glycan-Based Vaccine with Probiotics Improves Vaccine Performance in Broiler Chickens. Applied and Environmental Microbiology, 2017, 83, .	1.4	47
93	Prebiotic dietary fibre intervention improves fecal markers related to inflammation in obese patients: results from the Food4Gut randomized placebo-controlled trial. European Journal of Nutrition, 2021, 60, 3159-3170.	1.8	46
94	A small variation in diet influences the Lactobacillus strain composition in the crop of broiler chickens. Systematic and Applied Microbiology, 2010, 33, 275-281.	1.2	44
95	Prophages in Lactobacillus reuteri Are Associated with Fitness Trade-Offs but Can Increase Competitiveness in the Gut Ecosystem. Applied and Environmental Microbiology, 2019, 86, .	1.4	44
96	Disparate Metabolic Responses in Mice Fed a High-Fat Diet Supplemented with Maize-Derived Non-Digestible Feruloylated Oligo- and Polysaccharides Are Linked to Changes in the Gut Microbiota. PLoS ONE, 2016, 11, e0146144.	1.1	43
97	A philosophical perspective on the prenatal in utero microbiome debate. Microbiome, 2021, 9, 5.	4.9	42
98	A real-time PCR assay for accurate quantification of the individual members of the Altered Schaedler Flora microbiota in gnotobiotic mice. Journal of Microbiological Methods, 2017, 135, 52-62.	0.7	41
99	A gut pathobiont synergizes with the microbiota to instigate inflammatory disease marked by immunoreactivity against other symbionts but not itself. Scientific Reports, 2017, 7, 17707.	1.6	41
100	Synbiotics for Improved Human Health: Recent Developments, Challenges, and Opportunities. Annual Review of Food Science and Technology, 2018, 9, 451-479.	5.1	40
101	Ecological Importance of Cross-Feeding of the Intermediate Metabolite 1,2-Propanediol between Bacterial Gut Symbionts. Applied and Environmental Microbiology, 2020, 86, .	1.4	40
102	Holobiont nutrition. Gut Microbes, 2013, 4, 340-346.	4.3	34
103	Quantitative evaluation of synbiotic strategies to improve persistence and metabolic activity of Lactobacillus reuteri DSM 17938 in the human gastrointestinal tract. Journal of Functional Foods, 2014, 10, 85-94.	1.6	34
104	Characterization of the ecological role of genes mediating acid resistance in <scp><i>L</i></scp><i>actobacillus reuteri</i> during colonization of the gastrointestinal tract. Environmental Microbiology, 2016, 18, 2172-2184.	1.8	34
105	The evolution of ecological facilitation within mixed-species biofilms in the mouse gastrointestinal tract. ISME Journal, 2018, 12, 2770-2784.	4.4	34
106	Impact of dietary pattern of the fecal donor on in vitro fermentation properties of whole grains and brans. Journal of Functional Foods, 2017, 29, 281-289.	1.6	33
107	Metabolite profiling reveals the interaction of chitin-glucan with the gut microbiota. Gut Microbes, 2020, 12, 1810530.	4.3	31
108	Elucidating the role of the gut microbiota in the physiological effects of dietary fiber. Microbiome, 2022, 10, 77.	4.9	31

#	Article	IF	Citations
109	Identification and characterization of intestinal lactobacilli strains capable of degrading immunotoxic peptides present in gluten. Journal of Applied Microbiology, 2015, 118, 515-527.	1.4	29
110	Murine Gut Microbiotaâ€”Diet Trumps Genes. Cell Host and Microbe, 2015, 17, 3-5.	5.1	28
111	Bacterial AB5 toxins inhibit the growth of gut bacteria by targeting ganglioside-like glycoconjugates. Nature Communications, 2019, 10, 1390.	5.8	28
112	The importance of social networksâ€”An ecological and evolutionary framework to explain the role of microbes in the aetiology of allergy and asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 2248-2251.	2.7	25
113	Experimental evaluation of ecological principles to understand and modulate the outcome of bacterial strain competition in gut microbiomes. ISME Journal, 2022, 16, 1594-1604.	4.4	24
114	Alteration of the gastrointestinal microbiota of mice by edible blue-green algae. Journal of Applied Microbiology, 2009, 107, 1108-1118.	1.4	23
115	Effectiveness of Probiotic, Prebiotic, and Synbiotic Supplementation to Improve Perinatal Mental Health in Mothers: A Systematic Review and Meta-Analysis. Frontiers in Psychiatry, 2021, 12, 622181.	1.3	23
116	The Effect of Isolated and Synthetic Dietary Fibers on Markers of Metabolic Diseases in Human Intervention Studies: A Systematic Review. Advances in Nutrition, 2020, 11, 420-438.	2.9	22
117	Inducible Gene Expression in Lactobacillus reuteri LTH5531 during Type II Sourdough Fermentation. Applied and Environmental Microbiology, 2005, 71, 5873-5878.	1.4	21
118	Genes Involved in Galactooligosaccharide Metabolism in Lactobacillus reuteri and Their Ecological Role in the Gastrointestinal Tract. Applied and Environmental Microbiology, 2019, 85, .	1.4	21
119	Pros and cons: Is faecal microbiota transplantation a safe and efficient treatment option for gut dysbiosis?. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 2312-2317.	2.7	20
120	Resistant starchâ€”An accessible fiber ingredient acceptable to the Western palate. Comprehensive Reviews in Food Science and Food Safety, 2022, 21, 2930-2955.	5.9	20
121	Voluntary wheel running reveals sex-specific nociceptive factors in murine experimental autoimmune encephalomyelitis. Pain, 2019, 160, 870-881.	2.0	19
122	The Gut Microbiota Profile in Children with Praderâ€“Willi Syndrome. Genes, 2020, 11, 904.	1.0	18
123	Effects of lactose and yeast-dried milk on growth performance, fecal microbiota, and immune parameters of nursery pigs1. Journal of Animal Science, 2012, 90, 3049-3059.	0.2	16
124	Serine-rich repeat protein adhesins from<i>Lactobacillus reuteri</i>display strain specific glycosylation profiles. Glycobiology, 2019, 29, 45-58.	1.3	15
125	Composition and Functions of the Gut Microbiome in Pediatric Obesity: Relationships with Markers of Insulin Resistance. Microorganisms, 2021, 9, 1490.	1.6	15
126	Improving Chicken Responses to Glycoconjugate Vaccination Against Campylobacter jejuni. Frontiers in Microbiology, 2021, 12, 734526.	1.5	15

#	Article	IF	Citations
127	Metagenomic strain detection with SameStr: identification of a persisting core gut microbiota transferable by fecal transplantation. Microbiome, 2022, 10, 53.	4.9	15
128	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. ELife, 2018, 7, .	2.8	14
129	A Phylogenetic View on the Role of Glycerol for Growth Enhancement and Reuterin Formation in Limosilactobacillus reuteri. Frontiers in Microbiology, 2020, 11, 601422.	1.5	11
130	Higher levels of bacterial DNA in serum associate with severe and fatal COVIDâ€19. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 1312-1314.	2.7	11
131	The FiberTAG project: Tagging dietary fibre intake by measuring biomarkers related to the gut microbiota and their interest for health. Nutrition Bulletin, 2020, 45, 59-65.	0.8	10
132	Over-celling fetal microbial exposure. Cell, 2021, 184, 5839-5841.	13.5	10
133	A secondary metabolite drives intraspecies antagonism in a gut symbiont that is inhibited by cell-wall acetylation. Cell Host and Microbe, 2022, 30, 824-835.e6.	5.1	10
134	Nutritional and ecological perspectives of the interrelationships between diet and the gut microbiome in multiple sclerosis: Insights from marmosets. IScience, 2021, 24, 102709.	1.9	9
135	Effect of corn distillers dried grains with solubles on growth performance and health status indicators in weanling pigs1. Journal of Animal Science, 2012, 90, 790-801.	0.2	8
136	Modulation of the Gastrointestinal Microbiome with Nondigestible Fermentable Carbohydrates To Improve Human Health. , 0, , 453-483.		8
137	Development of a Repertoire and a Food Frequency Questionnaire for Estimating Dietary Fiber Intake Considering Prebiotics: Input from the FiberTAG Project. Nutrients, 2020, 12, 2824.	1.7	8
138	Noninvasive monitoring of fibre fermentation in healthy volunteers by analyzing breath volatile metabolites: lessons from the FiberTAG intervention study. Gut Microbes, 2021, 13, 1-16.	4.3	8
139	Breath volatile metabolome reveals the impact of dietary fibres on the gut microbiota: Proof of concept in healthy volunteers. EBioMedicine, 2022, 80, 104051.	2.7	7
140	Detection of Fusobacterium Species in Human Feces Using Genus-Specific PCR Primers and Denaturing Gradient Gel Electrophoresis. Microbial Ecology in Health and Disease, 2002, 14, 129-132.	3.8	6
141	Effects of a yeast-dried milk product in creep and phase-1 nursery diets on growth performance, circulating immunoglobulin A, and fecal microbiota of nursing and nursery pigs1. Journal of Animal Science, 2014, 92, 4518-4530.	0.2	6
142	Draft Genome Sequence of a Novel Lactobacillus salivarius Strain Isolated from Piglet. Genome Announcements, 2014, 2, .	0.8	6
143	Association between gut colonization of vancomycinâ€resistant enterococci and liver transplant outcomes. Transplant Infectious Disease, 2022, 24, .	0.7	6
144	Chitin-glucan supplementation improved postprandial metabolism and altered gut microbiota in subjects at cardiometabolic risk in a randomized trial. Scientific Reports, 2022, 12, .	1.6	6

#	Article	IF	Citations
145	Effects of triclosan on the normal intestinal microbiota and on susceptibility to experimental murine colitis. FASEB Journal, 2009, 23, 977.10.	0.2	5
146	Sorghumâ€based dietary intervention enriches Faecalibacterium prausnitzii in fecal samples of overweight individuals. FASEB Journal, 2013, 27, 1056.12.	0.2	5
147	Grain Sorghum Lipids: Extraction, Characterization, and Health Potential. ACS Symposium Series, 2011, , 149-170.	0.5	4
148	Efficacy of metformin and fermentable fiber combination therapy in adolescents with severe obesity and insulin resistance: study protocol for a double-blind randomized controlled trial. Trials, 2021, 22, 148.	0.7	4
149	Dietary beta-fructans reduce inflammation in patients with mild to moderate Ulcerative Colitis. Inflammatory Bowel Diseases, 2011, 17, S25.	0.9	2
150	Does host cholesterol metabolism impact the gut microbiota and why does it matter?. Future Microbiology, 2013, 8, 571-573.	1.0	2
151	Insights Into the Relationship Between Gut Microbiota and Colorectal Cancer. Current Colorectal Cancer Reports, 2018, 14, 251-265.	1.0	2
152	Influence of the Mediterranean diet on the production of short-chain fatty acids in women at risk for breast cancer (LIBRE). Proceedings of the Nutrition Society, 2020, 79, .	0.4	2
153	When to suspect contamination rather than colonization â€" lessons from a putative fetal sheep microbiome. Gut Microbes, 2022, 14, 2005751.	4.3	2
154	Discovering the molecular foundations of Lactobacillus autochthony in the gastrointestinal tract. Japanese Journal of Lactic Acid Bacteria, 2008, 19, 9-20.	0.1	1
155	Impact of dietary metabolism by gut microbiota on the pathogenesis of spontaneous autoimmune encephalomyelitis. Journal of Neuroimmunology, 2014, 275, 95-96.	1.1	0
156	23 ESTABLISHING THE SPECIFIC CONTRIBUTION OF ADHERENT AND INVASIVE ESCHERICHIA COLI TO THE ONSET OF INFLAMMATORY BOWEL DISEASE. Gastroenterology, 2019, 156, S102.	0.6	0
157	23 ESTABLISHING THE SPECIFIC CONTRIBUTION OF ADHERENT AND INVASIVE <i>ESCHERICHIA COLI</i> TO THE ONSET OF INFLAMMATORY BOWEL DISEASE. Inflammatory Bowel Diseases, 2019, 25, S70-S70.	0.9	0
158	Breath volatile compounds and conjugated polyunsaturated fatty acids as metabolic biomarkers reflecting the interaction between chitin-glucan and the gut microbiota.. Proceedings of the Nutrition Society, 2020, 79, .	0.4	0
159	An Ecological Framework To Understand Gut Microbiota Modulation By Probiotics. , 2018, , .		0
160	Chitin-Glucan Supplementation Altered Gut Microbiota and Improved Postprandial Metabolism in Subjects at Cardiometabolic Risk. Current Developments in Nutrition, 2022, 6, 331.	0.1	0