

Willem M De Vos

List of Publications by Year in descending order

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723
papers

114,049
citations

135

159
h-index

250

301
g-index

749
all docs

749
docs citations

749
times ranked

68537
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
2	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
3	Cross-talk between <i>Akkermansia muciniphila</i> and intestinal epithelium controls diet-induced obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9066-9071.	3.3	3,474
4	Duodenal Infusion of Donor Feces for Recurrent <i>Clostridium difficile</i> . <i>New England Journal of Medicine</i> , 2013, 368, 407-415.	13.9	3,157
5	Transfer of Intestinal Microbiota From Lean Donors Increases Insulin Sensitivity in Individuals With Metabolic Syndrome. <i>Gastroenterology</i> , 2012, 143, 913-916.e7.	0.6	2,287
6	<i>Akkermansia muciniphila</i> gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1469-1476.	0.8	1,566
7	A purified membrane protein from <i>Akkermansia muciniphila</i> or the pasteurized bacterium improves metabolism in obese and diabetic mice. <i>Nature Medicine</i> , 2017, 23, 107-113.	15.2	1,451
8	Complete genome sequence of <i>Lactobacillus plantarum</i> WCFS1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1990-1995.	3.3	1,326
9	Supplementation with <i>Akkermansia muciniphila</i> in overweight and obese human volunteers: a proof-of-concept exploratory study. <i>Nature Medicine</i> , 2019, 25, 1096-1103.	15.2	1,281
10	Temperature Gradient Gel Electrophoresis Analysis of 16S rRNA from Human Fecal Samples Reveals Stable and Host-Specific Communities of Active Bacteria. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3854-3859.	1.4	1,186
11	The first 1000 cultured species of the human gastrointestinal microbiota. <i>FEMS Microbiology Reviews</i> , 2014, 38, 996-1047.	3.9	923
12	Global and Deep Molecular Analysis of Microbiota Signatures in Fecal Samples From Patients With Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2011, 141, 1792-1801.	0.6	885
13	Responses of Gut Microbiota and Glucose and Lipid Metabolism to Prebiotics in Genetic Obese and Diet-Induced Leptin-Resistant Mice. <i>Diabetes</i> , 2011, 60, 2775-2786.	0.3	881
14	European consensus conference on faecal microbiota transplantation in clinical practice. <i>Gut</i> , 2017, 66, 569-580.	6.1	793
15	<i>Akkermansia muciniphila</i> and its role in regulating host functions. <i>Microbial Pathogenesis</i> , 2017, 106, 171-181.	1.3	775
16	Findings From a Randomized Controlled Trial of Fecal Transplantation for Patients With Ulcerative Colitis. <i>Gastroenterology</i> , 2015, 149, 110-118.e4.	0.6	769
17	Fat, fibre and cancer risk in African Americans and rural Africans. <i>Nature Communications</i> , 2015, 6, 6342.	5.8	761
18	Controlled gene expression systems for <i>Lactococcus lactis</i> with the food-grade inducer nisin. <i>Applied and Environmental Microbiology</i> , 1996, 62, 3662-3667.	1.4	752

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19	Molecular Monitoring of Succession of Bacterial Communities in Human Neonates. <i>Applied and Environmental Microbiology</i> , 2002, 68, 219-226.	1.4	730
20	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. <i>PLoS ONE</i> , 2009, 4, e6669.	1.1	719
21	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
22	Mucosa-Associated Bacteria in the Human Gastrointestinal Tract Are Uniformly Distributed along the Colon and Differ from the Community Recovered from Feces. <i>Applied and Environmental Microbiology</i> , 2002, 68, 3401-3407.	1.4	716
23	Next-Generation Beneficial Microbes: The Case of <i>Akkermansia muciniphila</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1765.	1.5	713
24	Quorum sensing by peptide pheromones and two-component signal transduction systems in Gram-positive bacteria. <i>Molecular Microbiology</i> , 1997, 24, 895-904.	1.2	710
25	Demonstration of safety of probiotics – a review. <i>International Journal of Food Microbiology</i> , 1998, 44, 93-106.	2.1	701
26	Improvement of Insulin Sensitivity after Lean Donor Feces in Metabolic Syndrome Is Driven by Baseline Intestinal Microbiota Composition. <i>Cell Metabolism</i> , 2017, 26, 611-619.e6.	7.2	689
27	Gut microbiome and health: mechanistic insights. <i>Gut</i> , 2022, 71, 1020-1032.	6.1	661
28	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a human-mucus binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17193-17198.	3.3	654
29	Quorum sensing-controlled gene expression in lactic acid bacteria. <i>Journal of Biotechnology</i> , 1998, 64, 15-21.	1.9	641
30	Insight into the prebiotic concept: lessons from an exploratory, double blind intervention study with inulin-type fructans in obese women. <i>Gut</i> , 2013, 62, 1112-1121.	6.1	632
31	Molecular Diversity of <i>Lactobacillus</i> spp. and Other Lactic Acid Bacteria in the Human Intestine as Determined by Specific Amplification of 16S Ribosomal DNA. <i>Applied and Environmental Microbiology</i> , 2002, 68, 114-123.	1.4	619
32	The gut microbiota plays a protective role in the host defence against pneumococcal pneumonia. <i>Gut</i> , 2016, 65, 575-583.	6.1	601
33	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
34	Intestinal microbiota in human health and disease: the impact of probiotics. <i>Genes and Nutrition</i> , 2011, 6, 209-240.	1.2	557
35	Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. <i>Nature Communications</i> , 2016, 7, 10410.	5.8	557
36	Microbes inside – from diversity to function: the case of <i>Akkermansia</i> . <i>ISME Journal</i> , 2012, 6, 1449-1458.	4.4	551

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37	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	4.4	544
38	Intestinal Integrity and <i>Akkermansia muciniphila</i> , a Mucin-Degrading Member of the Intestinal Microbiota Present in Infants, Adults, and the Elderly. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7767-7770.	1.4	540
39	High-throughput diversity and functionality analysis of the gastrointestinal tract microbiota. <i>Gut</i> , 2008, 57, 1605-1615.	6.1	528
40	The Mucin Degrader <i>Akkermansia muciniphila</i> Is an Abundant Resident of the Human Intestinal Tract. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1646-1648.	1.4	517
41	S layer protein A of <i>Lactobacillus acidophilus</i> NCFM regulates immature dendritic cell and T cell functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19474-19479.	3.3	515
42	Butyrate-producing <i>Clostridium</i> cluster XIVa species specifically colonize mucins in an <i>in vitro</i> gut model. <i>ISME Journal</i> , 2013, 7, 949-961.	4.4	501
43	Characterization of the nisin gene cluster nisABTCIPR of <i>Lactococcus lactis</i> . Requirement of expression of the nisA and nisI genes for development of immunity. <i>FEBS Journal</i> , 1993, 216, 281-291.	0.2	495
44	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. <i>ISME Journal</i> , 2014, 8, 2218-2230.	4.4	489
45	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	5.8	488
46	Diversity of the human gastrointestinal tract microbiota revisited. <i>Environmental Microbiology</i> , 2007, 9, 2125-2136.	1.8	485
47	Autoregulation of Nisin Biosynthesis in <i>Lactococcus lactis</i> by Signal Transduction. <i>Journal of Biological Chemistry</i> , 1995, 270, 27299-27304.	1.6	483
48	Comparative analysis of fecal DNA extraction methods with phylogenetic microarray: Effective recovery of bacterial and archaeal DNA using mechanical cell lysis. <i>Journal of Microbiological Methods</i> , 2010, 81, 127-134.	0.7	480
49	CRISPR Immunity Relies on the Consecutive Binding and Degradation of Negatively Supercoiled Invader DNA by Cascade and Cas3. <i>Molecular Cell</i> , 2012, 46, 595-605.	4.5	475
50	Impact of oral vancomycin on gut microbiota, bile acid metabolism, and insulin sensitivity. <i>Journal of Hepatology</i> , 2014, 60, 824-831.	1.8	475
51	Human intestinal microbiota composition is associated with local and systemic inflammation in obesity. <i>Obesity</i> , 2013, 21, E607-15.	1.5	469
52	Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. <i>Gut</i> , 2020, 69, 1218-1228.	6.1	465
53	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
54	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442

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55	Healthy human gut phageome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10400-10405.	3.3	439
56	Modulation of Mucosal Immune Response, Tolerance, and Proliferation in Mice Colonized by the Mucin-Degrader <i>Akkermansia muciniphila</i> . Frontiers in Microbiology, 2011, 2, 166.	1.5	438
57	<i>Akkermansia muciniphila</i> Adheres to Enterocytes and Strengthens the Integrity of the Epithelial Cell Layer. Applied and Environmental Microbiology, 2015, 81, 3655-3662.	1.4	437
58	Anaerobic Microbial Dehalogenation. Annual Review of Microbiology, 2004, 58, 43-73.	2.9	433
59	Mucin-bacterial interactions in the human oral cavity and digestive tract. Gut Microbes, 2010, 1, 254-268.	4.3	421
60	Development and application of the human intestinal tract chip, a phylogenetic microarray: analysis of universally conserved phylotypes in the abundant microbiota of young and elderly adults. Environmental Microbiology, 2009, 11, 1736-1751.	1.8	420
61	<i>Lactobacillus plantarum</i> survival, functional and potential probiotic properties in the human intestinal tract. International Dairy Journal, 2006, 16, 1018-1028.	1.5	410
62	Homeostasis of the gut barrier and potential biomarkers. American Journal of Physiology - Renal Physiology, 2017, 312, G171-G193.	1.6	408
63	Bifidobacterial Diversity in Human Feces Detected by Genus-Specific PCR and Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2001, 67, 504-513.	1.4	392
64	Mouse models for human intestinal microbiota research: a critical evaluation. Cellular and Molecular Life Sciences, 2018, 75, 149-160.	2.4	380
65	Identification and characterization of the lantibiotic nisin Z, a natural nisin variant. FEBS Journal, 1991, 201, 581-584.	0.2	377
66	Differential Modulation by <i>Akkermansia muciniphila</i> and <i>Faecalibacterium prausnitzii</i> of Host Peripheral Lipid Metabolism and Histone Acetylation in Mouse Gut Organoids. MBio, 2014, 5, .	1.8	376
67	The Gut Microbiota in the First Decade of Life. Trends in Microbiology, 2019, 27, 997-1010.	3.5	368
68	Differential NF- κ B pathways induction by <i>Lactobacillus plantarum</i> in the duodenum of healthy humans correlating with immune tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2371-2376.	3.3	363
69	Maternal prenatal stress is associated with the infant intestinal microbiota. Psychoneuroendocrinology, 2015, 53, 233-245.	1.3	359
70	The function of our microbiota: who is out there and what do they do?. Frontiers in Cellular and Infection Microbiology, 2012, 2, 104.	1.8	352
71	Metagenomics meets time series analysis: unraveling microbial community dynamics. Current Opinion in Microbiology, 2015, 25, 56-66.	2.3	345
72	Probiotic and other functional microbes: from markets to mechanisms. Current Opinion in Biotechnology, 2005, 16, 204-211.	3.3	344

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73	Pili-like proteins of <i>Akkermansia muciniphila</i> modulate host immune responses and gut barrier function. <i>PLoS ONE</i> , 2017, 12, e0173004.	1.1	340
74	A microbial world within us.. <i>Molecular Microbiology</i> , 2006, 59, 1639-1650.	1.2	335
75	Role of the intestinal microbiome in health and disease: from correlation to causation. <i>Nutrition Reviews</i> , 2012, 70, S45-S56.	2.6	333
76	Diversity, Dynamics, and Activity of Bacterial Communities during Production of an Artisanal Sicilian Cheese as Evaluated by 16S rRNA Analysis. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1882-1892.	1.4	332
77	Homology modelling and protein engineering strategy of subtilases, the family of subtilisin-like serine proteinases. <i>Protein Engineering, Design and Selection</i> , 1991, 4, 719-737.	1.0	331
78	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11217-11222.	3.3	328
79	The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degrader, and Its Use in Exploring Intestinal Metagenomes. <i>PLoS ONE</i> , 2011, 6, e16876.	1.1	328
80	Functional analysis of promoters in the nisin gene cluster of <i>Lactococcus lactis</i> . <i>Journal of Bacteriology</i> , 1996, 178, 3434-3439.	1.0	316
81	Microbiota conservation and BMI signatures in adult monozygotic twins. <i>ISME Journal</i> , 2013, 7, 707-717.	4.4	311
82	Clinical trial: multispecies probiotic supplementation alleviates the symptoms of irritable bowel syndrome and stabilizes intestinal microbiota. <i>Alimentary Pharmacology and Therapeutics</i> , 2008, 27, 48-57.	1.9	309
83	Characterization of the <i>Lactococcus lactis</i> nisin A operon genes <i>nisP</i> , encoding a subtilisin-like serine protease involved in precursor processing, and <i>nisR</i> , encoding a regulatory protein involved in nisin biosynthesis. <i>Journal of Bacteriology</i> , 1993, 175, 2578-2588.	1.0	305
84	Intestinal Microbiota in Healthy Adults: Temporal Analysis Reveals Individual and Common Core and Relation to Intestinal Symptoms. <i>PLoS ONE</i> , 2011, 6, e23035.	1.1	302
85	<i>Akkermansia muciniphila</i> in the Human Gastrointestinal Tract: When, Where, and How?. <i>Microorganisms</i> , 2018, 6, 75.	1.6	286
86	Phylogenetic Analysis of Dysbiosis in Ulcerative Colitis During Remission. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 481-488.	0.9	285
87	The therapeutic potential of manipulating gut microbiota in obesity and type 2 diabetes mellitus. <i>Diabetes, Obesity and Metabolism</i> , 2012, 14, 112-120.	2.2	283
88	Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena?. <i>American Journal of Gastroenterology</i> , 2015, 110, 278-287.	0.2	283
89	Faecal microbiota composition and host-microbe cross-talk following gastroenteritis and in postinfectious irritable bowel syndrome. <i>Gut</i> , 2014, 63, 1737-1745.	6.1	282
90	Functional Analysis of <i>Lactobacillus rhamnosus</i> GG Pili in Relation to Adhesion and Immunomodulatory Interactions with Intestinal Epithelial Cells. <i>Applied and Environmental Microbiology</i> , 2012, 78, 185-193.	1.4	274

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91	Aberrant gut microbiota composition at the onset of type 1 diabetes in young children. <i>Diabetologia</i> , 2014, 57, 1569-1577.	2.9	274
92	Improvement of solubility and stability of the antimicrobial peptide nisin by protein engineering. <i>Applied and Environmental Microbiology</i> , 1995, 61, 2873-2878.	1.4	274
93	Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin of <i>Lactobacillus plantarum</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6128-6136.	1.0	272
94	The environment within: how gut microbiota may influence metabolism and body composition. <i>Diabetologia</i> , 2010, 53, 606-613.	2.9	270
95	<i>Akkermansia muciniphila</i> induces gut microbiota remodelling and controls islet autoimmunity in NOD mice. <i>Gut</i> , 2018, 67, 1445-1453.	6.1	270
96	Microbial Metabolic Networks at the Mucus Layer Lead to Diet-Independent Butyrate and Vitamin B ₁₂ Production by Intestinal Symbionts. <i>MBio</i> , 2017, 8, .	1.8	269
97	Altered Gut Microbiota and Endocannabinoid System Tone in Obese and Diabetic Leptin-Resistant Mice: Impact on Apelin Regulation in Adipose Tissue. <i>Frontiers in Microbiology</i> , 2011, 2, 149.	1.5	267
98	Analysis of Growth of <i>Lactobacillus plantarum</i> WCFS1 on a Complex Medium Using a Genome-scale Metabolic Model. <i>Journal of Biological Chemistry</i> , 2006, 281, 40041-40048.	1.6	261
99	Molecular characterization of the plasmid-encoded <i>eps</i> gene cluster essential for exopolysaccharide biosynthesis in <i>Lactococcus lactis</i> . <i>Molecular Microbiology</i> , 1997, 24, 387-397.	1.2	257
100	The micro-Petri dish, a million-well growth chip for the culture and high-throughput screening of microorganisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18217-18222.	3.3	255
101	High temporal and inter-individual variation detected in the human ileal microbiota. <i>Environmental Microbiology</i> , 2010, 12, 3213-3227.	1.8	254
102	Post-natal development of the porcine microbiota composition and activities. <i>Environmental Microbiology</i> , 2006, 8, 1191-1199.	1.8	253
103	Multiparametric Flow Cytometry and Cell Sorting for the Assessment of Viable, Injured, and Dead <i>Bifidobacterium</i> Cells during Bile Salt Stress. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5209-5216.	1.4	252
104	The Lrp family of transcriptional regulators. <i>Molecular Microbiology</i> , 2003, 48, 287-294.	1.2	252
105	Cell to cell communication by autoinducing peptides in gram-positive bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 233-243.	0.7	248
106	Do nutrient-gut microbiota interactions play a role in human obesity, insulin resistance and type 2 diabetes?. <i>Obesity Reviews</i> , 2011, 12, 272-281.	3.1	248
107	Identification of mesophilic lactic acid bacteria by using polymerase chain reaction-amplified variable regions of 16S rRNA and specific DNA probes. <i>Applied and Environmental Microbiology</i> , 1991, 57, 3390-3393.	1.4	247
108	Colonic Microbiota Signatures across Five Northern European Countries. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4153-4155.	1.4	243

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109	Akkermansia muciniphila: paradigm for next-generation beneficial microorganisms. Nature Reviews Gastroenterology and Hepatology, 2022, 19, 625-637.	8.2	239
110	Gelatinase biosynthesis-activating pheromone: a peptide lactone that mediates a quorum sensing in Enterococcus faecalis. Molecular Microbiology, 2001, 41, 145-154.	1.2	234
111	Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology (United Kingdom), 2010, 156, 3205-3215.	0.7	231
112	Controlled gene expression systems for lactic acid bacteria: transferable nisin-inducible expression cassettes for Lactococcus, Leuconostoc, and Lactobacillus spp. Applied and Environmental Microbiology, 1997, 63, 4581-4584.	1.4	231
113	Exploring Lactobacillus plantarum Genome Diversity by Using Microarrays. Journal of Bacteriology, 2005, 187, 6119-6127.	1.0	229
114	Significant Correlation Between the Infant Gut Microbiome and Rotavirus Vaccine Response in Rural Ghana. Journal of Infectious Diseases, 2017, 215, 34-41.	1.9	227
115	Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis subsp. lactis MG1363. Gene, 1990, 95, 155-160.	1.0	222
116	Inulin-type fructans modulate intestinal Bifidobacterium species populations and decrease fecal short-chain fatty acids in obese women. Clinical Nutrition, 2015, 34, 501-507.	2.3	220
117	Tipping elements in the human intestinal ecosystem. Nature Communications, 2014, 5, 4344.	5.8	217
118	Cofactor Engineering: a Novel Approach to Metabolic Engineering in <i>Lactococcus lactis</i> by Controlled Expression of NADH Oxidase. Journal of Bacteriology, 1998, 180, 3804-3808.	1.0	217
119	Intestinal Microbiota of Infants With Colic: Development and Specific Signatures. Pediatrics, 2013, 131, e550-e558.	1.0	213
120	Identification of Lactobacillus plantarum Genes That Are Induced in the Gastrointestinal Tract of Mice. Journal of Bacteriology, 2004, 186, 5721-5729.	1.0	211
121	Identification of Prebiotic Fructooligosaccharide Metabolism in Lactobacillus plantarum WCFS1 through Microarrays. Applied and Environmental Microbiology, 2007, 73, 1753-1765.	1.4	210
122	Controlled overproduction of proteins by lactic acid bacteria. Trends in Biotechnology, 1997, 15, 135-140.	4.9	208
123	The microbial eukaryote <i>Blastocystis</i> is a prevalent and diverse member of the healthy human gut microbiota. FEMS Microbiology Ecology, 2014, 90, 326-330.	1.3	208
124	Quantification of 16S rRNAs in Complex Bacterial Communities by Multiple Competitive Reverse Transcription-PCR in Temperature Gradient Gel Electrophoresis Fingerprints. Applied and Environmental Microbiology, 1998, 64, 4581-4587.	1.4	205
125	Characterization of the novel nisin-sucrose conjugative transposon Tn5276 and its insertion in Lactococcus lactis. Journal of Bacteriology, 1992, 174, 1280-1287.	1.0	204
126	Fecal microbiota transplantation as novel therapy in gastroenterology: A systematic review. World Journal of Gastroenterology, 2015, 21, 5359.	1.4	204

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127	Effects of bowel cleansing on the intestinal microbiota. <i>Gut</i> , 2015, 64, 1562-1568.	6.1	201
128	Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. <i>Nature Communications</i> , 2015, 6, 10062.	5.8	199
129	Intestinal Microbiota in Healthy U.S. Young Children and Adults—A High Throughput Microarray Analysis. <i>PLoS ONE</i> , 2013, 8, e64315.	1.1	196
130	Long-term monitoring of the human intestinal microbiota composition. <i>Environmental Microbiology</i> , 2013, 15, 1146-1159.	1.8	195
131	Maturation pathway of nisin and other lantibiotics: post-translationally modified antimicrobial peptides exported by Gram-positive bacteria. <i>Molecular Microbiology</i> , 1995, 17, 427-437.	1.2	194
132	Mixed-Culture Transcriptome Analysis Reveals the Molecular Basis of Mixed-Culture Growth in <i>Streptococcus thermophilus</i> and <i>Lactobacillus bulgaricus</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 7775-7784.	1.4	194
133	Severity of atopic disease inversely correlates with intestinal microbiota diversity and butyrate-producing bacteria. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 241-244.	2.7	194
134	Fecal Microbiota in Pediatric Inflammatory Bowel Disease and Its Relation to Inflammation. <i>American Journal of Gastroenterology</i> , 2015, 110, 921-930.	0.2	193
135	Properties of nisin Z and distribution of its gene, nisZ, in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 1993, 59, 213-218.	1.4	193
136	Action and function of <i>Akkermansia muciniphila</i> in microbiome ecology, health and disease. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2017, 31, 637-642.	1.0	191
137	Genetic Diversity of Viable, Injured, and Dead Fecal Bacteria Assessed by Fluorescence-Activated Cell Sorting and 16S rRNA Gene Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4679-4689.	1.4	190
138	Mucosal Adhesion Properties of the Probiotic <i>Lactobacillus rhamnosus</i> GG SpaCBA and SpaFED Pilin Subunits. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2049-2057.	1.4	189
139	Harnessing the power of microbial autotrophy. <i>Nature Reviews Microbiology</i> , 2016, 14, 692-706.	13.6	189
140	Maternal Fecal Microbiota Transplantation in Cesarean-Born Infants Rapidly Restores Normal Gut Microbial Development: A Proof-of-Concept Study. <i>Cell</i> , 2020, 183, 324-334.e5.	13.5	188
141	Beyond diversity: functional microbiomics of the human colon. <i>Trends in Microbiology</i> , 2006, 14, 86-91.	3.5	187
142	Genetic marking of <i>Lactococcus lactis</i> shows its survival in the human gastrointestinal tract. <i>Applied and Environmental Microbiology</i> , 1995, 61, 2771-2774.	1.4	187
143	A maturation protein is essential for production of active forms of <i>Lactococcus lactis</i> SK11 serine proteinase located in or secreted from the cell envelope. <i>Journal of Bacteriology</i> , 1989, 171, 2795-2802.	1.0	186
144	Specific Response of a Novel and Abundant <i>Lactobacillus amylovorus</i> -Like Phylotype to Dietary Prebiotics in the Guts of Weaning Piglets. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3821-3830.	1.4	185

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145	Use of the <i>Escherichia coli</i> beta-glucuronidase (<i>gusA</i>) gene as a reporter gene for analyzing promoters in lactic acid bacteria. <i>Applied and Environmental Microbiology</i> , 1994, 60, 587-593.	1.4	185
146	Cloning and characterization of plasmid-encoded genes for the degradation of 1,2-dichloro-, 1,4-dichloro-, and 1,2,4-trichlorobenzene of <i>Pseudomonas</i> sp. strain P51. <i>Journal of Bacteriology</i> , 1991, 173, 6-15.	1.0	183
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