

Paul W O'toole

List of Publications by Year in descending order

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276
papers

36,576
citations

4658

85
h-index

3650

180
g-index

288
all docs

288
docs citations

288
times ranked

35277
citing authors

#	ARTICLE	IF	CITATIONS
1	A taxonomic note on the genus <i>Lactobacillus</i> : Description of 23 novel genera, emended description of the genus <i>Lactobacillus</i> Beijerinck 1901, and union of <i>Lactobacillaceae</i> and <i>Leuconostocaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2782-2858.	1.7	2,775
2	Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012, 488, 178-184.	27.8	2,618
3	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4586-4591.	7.1	1,418
4	High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. <i>Gut</i> , 2016, 65, 1812-1821.	12.1	1,092
5	Exercise and associated dietary extremes impact on gut microbial diversity. <i>Gut</i> , 2014, 63, 1913-1920.	12.1	987
6	$\hat{1}^3$ -Aminobutyric acid production by culturable bacteria from the human intestine. <i>Journal of Applied Microbiology</i> , 2012, 113, 411-417.	3.1	871
7	Composition and energy harvesting capacity of the gut microbiota: relationship to diet, obesity and time in mouse models. <i>Gut</i> , 2010, 59, 1635-1642.	12.1	808
8	Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. <i>Nucleic Acids Research</i> , 2010, 38, e200-e200.	14.5	808
9	Gut microbiota and aging. <i>Science</i> , 2015, 350, 1214-1215.	12.6	801
10	An irritable bowel syndrome subtype defined by species-specific alterations in faecal microbiota. <i>Gut</i> , 2012, 61, 997-1006.	12.1	742
11	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.	2.5	719
12	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
13	Bacteriocin production as a mechanism for the anti-infective activity of <i>Lactobacillus salivarius</i> UCC118. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7617-7621.	7.1	690
14	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. <i>Gut</i> , 2017, 66, 633-643.	12.1	623
15	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
16	Next-generation probiotics: the spectrum from probiotics to live biotherapeutics. <i>Nature Microbiology</i> , 2017, 2, 17057.	13.3	553
17	Diversity of <i>Bifidobacteria</i> within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	2.5	512
18	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	12.8	488

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19	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.	12.1	465
20	The oral microbiota in colorectal cancer is distinctive and predictive. <i>Gut</i> , 2018, 67, 1454-1463.	12.1	425
21	Genome-scale analyses of health-promoting bacteria: probiogenomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 61-71.	28.6	400
22	The gut microbiota and its relationship to diet and obesity. <i>Gut Microbes</i> , 2012, 3, 186-202.	9.8	382
23	Intestinal microbiota, diet and health. <i>British Journal of Nutrition</i> , 2014, 111, 387-402.	2.3	371
24	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.	7.1	328
25	Archaea and the human gut: New beginning of an old story. <i>World Journal of Gastroenterology</i> , 2014, 20, 16062.	3.3	308
26	Composition and temporal stability of the gut microbiota in older persons. <i>ISME Journal</i> , 2016, 10, 170-182.	9.8	305
27	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	8.2	297
28	Techniques used to characterize the gut microbiota: a guide for the clinician. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2012, 9, 312-322.	17.8	290
29	The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study. <i>Scientific Reports</i> , 2017, 7, 40597.	3.3	279
30	Molecular dialogue between the human gut microbiota and the host: a <i>Lactobacillus</i> and <i>Bifidobacterium</i> perspective. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 183-203.	5.4	265
31	Functional metagenomic profiling of intestinal microbiome in extreme ageing. <i>Aging</i> , 2013, 5, 902-912.	3.1	263
32	Categorization of the gut microbiota: enterotypes or gradients?. <i>Nature Reviews Microbiology</i> , 2012, 10, 591-592.	28.6	260
33	Phylogenomic Data Support a Seventh Order of Methylophilic Methanogens and Provide Insights into the Evolution of Methanogenesis. <i>Genome Biology and Evolution</i> , 2013, 5, 1769-1780.	2.5	249
34	Comparative genomics highlights the unique biology of Methanomassiliicoccales, a Thermoplasmatales-related seventh order of methanogenic archaea that encodes pyrrolysine. <i>BMC Genomics</i> , 2014, 15, 679.	2.8	246
35	Divergent metabolic outcomes arising from targeted manipulation of the gut microbiota in diet-induced obesity. <i>Gut</i> , 2013, 62, 220-226.	12.1	235
36	Dietary Fibre Modulates the Gut Microbiota. <i>Nutrients</i> , 2021, 13, 1655.	4.1	225

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37	Disturbance of the gut microbiota in early-life selectively affects visceral pain in adulthood without impacting cognitive or anxiety-related behaviors in male rats. <i>Neuroscience</i> , 2014, 277, 885-901.	2.3	222
38	Gut microbiota: Changes throughout the lifespan from infancy to elderly. <i>International Dairy Journal</i> , 2010, 20, 281-291.	3.0	218
39	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6718-6723.	7.1	216
40	Forgotten fungi—the gut mycobiome in human health and disease. <i>FEMS Microbiology Reviews</i> , 2017, 41, 479-511.	8.6	216
41	The rumen microbiome: a crucial consideration when optimising milk and meat production and nitrogen utilisation efficiency. <i>Gut Microbes</i> , 2019, 10, 115-132.	9.8	209
42	The microbial eukaryote <i>Blastocystis</i> is a prevalent and diverse member of the healthy human gut microbiota. <i>FEMS Microbiology Ecology</i> , 2014, 90, 326-330.	2.7	208
43	Beneficial modulation of the gut microbiota. <i>FEBS Letters</i> , 2014, 588, 4120-4130.	2.8	204
44	Archaeobiotics. <i>Gut Microbes</i> , 2014, 5, 5-10.	9.8	201
45	Genus-Wide Assessment of Antibiotic Resistance in <i>Lactobacillus</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	190
46	<i>Clostridium difficile</i> Carriage in Elderly Subjects and Associated Changes in the Intestinal Microbiota. <i>Journal of Clinical Microbiology</i> , 2012, 50, 867-875.	3.9	184
47	Diet-Microbiota Interactions and Their Implications for Healthy Living. <i>Nutrients</i> , 2013, 5, 234-252.	4.1	174
48	The Healthy Microbiome—What Is the Definition of a Healthy Gut Microbiome?. <i>Gastroenterology</i> , 2021, 160, 483-494.	1.3	174
49	International Cancer Microbiome Consortium consensus statement on the role of the human microbiome in carcinogenesis. <i>Gut</i> , 2019, 68, 1624-1632.	12.1	173
50	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. <i>Microbial Genomics</i> , 2016, 2, e000043.	2.0	162
51	The gut microbiome as a modulator of healthy ageing. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2022, 19, 565-584.	17.8	162
52	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	11.0	160
53	The genus <i>Lactobacillus</i> —a genomic basis for understanding its diversity. <i>FEMS Microbiology Letters</i> , 2007, 269, 22-28.	1.8	157
54	Genome Sequence of <i>Candidatus Methanomethylophilus alvus</i> Mx1201, a Methanogenic Archaeon from the Human Gut Belonging to a Seventh Order of Methanogens. <i>Journal of Bacteriology</i> , 2012, 194, 6944-6945.	2.2	155

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55	Comparative and Functional Analysis of Sortase-Dependent Proteins in the Predicted Secretome of <i>Lactobacillus salivarius</i> UCC118. Applied and Environmental Microbiology, 2006, 72, 4143-4153.	3.1	145
56	The Bifidobacterium dentium Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. PLoS Genetics, 2009, 5, e1000785.	3.5	141
57	Effect of Lactobacillus salivarius Bacteriocin Abp118 on the Mouse and Pig Intestinal Microbiota. PLoS ONE, 2012, 7, e31113.	2.5	136
58	Targeting the Microbiota to Address Diet-Induced Obesity: A Time Dependent Challenge. PLoS ONE, 2013, 8, e65790.	2.5	132
59	Combating inflammaging through a Mediterranean whole diet approach: The NU-AGE project's conceptual framework and design. Mechanisms of Ageing and Development, 2014, 136-137, 3-13.	4.6	131
60	Isolation and biochemical and molecular analyses of a species-specific protein antigen from the gastric pathogen Helicobacter pylori. Journal of Bacteriology, 1991, 173, 505-513.	2.2	130
61	Novel Chromosomally Encoded Multidrug Efflux Transporter MdeA in <i>Staphylococcus aureus</i> . Antimicrobial Agents and Chemotherapy, 2004, 48, 909-917.	3.2	128
62	Probiotic Bacteria Influence the Composition and Function of the Intestinal Microbiota. Interdisciplinary Perspectives on Infectious Diseases, 2008, 2008, 1-9.	1.4	128
63	Potentially modifiable determinants of malnutrition in older adults: A systematic review. Clinical Nutrition, 2019, 38, 2477-2498.	5.0	127
64	Elevated gut microbiome abundance of <i>Christensenellaceae</i> , <i>Porphyromonadaceae</i> and <i>Rikenellaceae</i> is associated with reduced visceral adipose tissue and healthier metabolic profile in Italian elderly. Gut Microbes, 2021, 13, 1-19.	9.8	127
65	Potential of methicillin activity against methicillin-resistant <i>Staphylococcus aureus</i> by diterpenes. FEMS Microbiology Letters, 1999, 179, 233-239.	1.8	124
66	A clinician's guide to microbiome analysis. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 585-595.	17.8	124
67	Feeding the microbiota: transducer of nutrient signals for the host. Gut, 2017, 66, 1709-1717.	12.1	124
68	<i>APOE</i> genotype influences the gut microbiome structure and function in humans and mice: relevance for Alzheimer's disease pathophysiology. FASEB Journal, 2019, 33, 8221-8231.	0.5	124
69	Differences in Fecal Microbiomes and Metabolomes of People With vs Without Irritable Bowel Syndrome and Bile Acid Malabsorption. Gastroenterology, 2020, 158, 1016-1028.e8.	1.3	122
70	Diversity of the genus Lactobacillus revealed by comparative genomics of five species. Microbiology (United Kingdom), 2006, 152, 3185-3196.	1.8	118
71	Many group A streptococcal strains express two different immunoglobulin-binding proteins, encoded by closely linked genes: characterization of the proteins expressed by four strains of different M-type. Molecular Microbiology, 1992, 6, 1185-1194.	2.5	116
72	Diet influences the functions of the human intestinal microbiome. Scientific Reports, 2020, 10, 4247.	3.3	115

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73	Adjusting for age improves identification of gut microbiome alterations in multiple diseases. <i>ELife</i> , 2020, 9, .	6.0	113
74	In silico identification of bacteriocin gene clusters in the gastrointestinal tract, based on the Human Microbiome Project's reference genome database. <i>BMC Microbiology</i> , 2015, 15, 183.	3.3	112
75	Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. <i>ISME Journal</i> , 2017, 11, 2059-2074.	9.8	112
76	Probiotic properties of <i>Lactobacillus salivarius</i> and closely related <i>Lactobacillus</i> species. <i>Future Microbiology</i> , 2010, 5, 759-774.	2.0	109
77	Analysis of Health Benefits Conferred by <i>Lactobacillus</i> Species from Kefir. <i>Nutrients</i> , 2019, 11, 1252.	4.1	109
78	Gut microbiota alterations associated with reduced bone mineral density in older adults. <i>Rheumatology</i> , 2019, 58, 2295-2304.	1.9	106
79	The individual-specific and diverse nature of the preterm infant microbiota. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2013, 98, F334-F340.	2.8	105
80	Non-motile mutants of <i>Helicobacter pylori</i> and <i>Helicobacter mustelae</i> defective in flagellar hook production. <i>Molecular Microbiology</i> , 1994, 14, 691-703.	2.5	104
81	Impacts of Seasonal Housing and Teat Preparation on Raw Milk Microbiota: a High-Throughput Sequencing Study. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	104
82	The microbiota link to irritable bowel syndrome. <i>Gut Microbes</i> , 2012, 3, 572-576.	9.8	102
83	Genomic Diversity of <i>Lactobacillus salivarius</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 954-965.	3.1	101
84	High-affinity binding of the basement membrane proteins collagen type IV and laminin to the gastric pathogen <i>Helicobacter pylori</i> . <i>Infection and Immunity</i> , 1991, 59, 4398-4404.	2.2	100
85	<i>Lactobacillus</i> phylogenomics - towards a reclassification of the genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2945-2954.	1.7	95
86	Fecal microbiota variation across the lifespan of the healthy laboratory rat. <i>Gut Microbes</i> , 2017, 8, 428-439.	9.8	93
87	Comparative Genomics of the Genus <i>Lactobacillus</i> Reveals Robust Phylogroups That Provide the Basis for Reclassification. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	93
88	The putative neuraminylactose-binding hemagglutinin HpaA of <i>Helicobacter pylori</i> CCUG 17874 is a lipoprotein. <i>Journal of Bacteriology</i> , 1995, 177, 6049-6057.	2.2	92
89	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. <i>Letters in Applied Microbiology</i> , 2013, 57, 492-501.	2.2	90
90	Comparison of the salivary and dentinal microbiome of children with severe-early childhood caries to the salivary microbiome of caries-free children. <i>BMC Oral Health</i> , 2019, 19, 13.	2.3	86

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91	Phylogenomics and comparative genomics of <i>Lactobacillus salivarius</i> , a mammalian gut commensal. <i>Microbial Genomics</i> , 2017, 3, e000115.	2.0	86
92	The gamma-hemolysin locus of <i>Staphylococcus aureus</i> comprises three linked genes, two of which are identical to the genes for the F and S components of leukocidin. <i>Infection and Immunity</i> , 1993, 61, 768-771.	2.2	86
93	Genome Sequence of <i>Candidatus</i> <i>Methanomassiliicoccus intestinalis</i> Issoire-Mx1, a Third <i>Thermoplasmatales</i> -Related Methanogenic Archaeon from Human Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	85
94	Core fecal microbiota of domesticated herbivorous ruminant, hindgut fermenters, and monogastric animals. <i>MicrobiologyOpen</i> , 2017, 6, e00509.	3.0	83
95	Two major classes in the M protein family in group A streptococci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 8661-8665.	7.1	82
96	Microbiome-health interactions in older people. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 119-128.	5.4	80
97	Allelic Variation of Bile Salt Hydrolase Genes in <i>Lactobacillus salivarius</i> Does Not Determine Bile Resistance Levels. <i>Journal of Bacteriology</i> , 2009, 191, 5743-5757.	2.2	78
98	Characterization of Pro-Inflammatory Flagellin Proteins Produced by <i>Lactobacillus ruminis</i> and Related Motile <i>Lactobacilli</i> . <i>PLoS ONE</i> , 2012, 7, e40592.	2.5	76
99	Nucleotide sequence of the epidermolytic toxin A gene of <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 1987, 169, 3910-3915.	2.2	75
100	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3130-3146.	3.1	75
101	<i>Lactobacillus salivarius</i> modulates cytokine induction and virulence factor gene expression in <i>Helicobacter pylori</i> . <i>Journal of Medical Microbiology</i> , 2009, 58, 996-1005.	1.8	75
102	Mechanism of protection of transepithelial barrier function by <i>Lactobacillus salivarius</i> : strain dependence and attenuation by bacteriocin production. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, G1029-G1041.	3.4	75
103	Fermented Foods, Health and the Gut Microbiome. <i>Nutrients</i> , 2022, 14, 1527.	4.1	75
104	Microbial diversity in the human intestine and novel insights from metagenomics. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 3214.	3.0	72
105	Maintenance of a healthy trajectory of the intestinal microbiome during aging: A dietary approach. <i>Mechanisms of Ageing and Development</i> , 2014, 136-137, 70-75.	4.6	72
106	Prebiotic supplementation in frail older people affects specific gut microbiota taxa but not global diversity. <i>Microbiome</i> , 2019, 7, 39.	11.1	72
107	<i>Helicobacter pylori</i> motility. <i>Microbes and Infection</i> , 2000, 2, 1207-1214.	1.9	71
108	Resource partitioning in relation to cohabitation of <i>Lactobacillus</i> species in the mouse forestomach. <i>ISME Journal</i> , 2012, 6, 927-938.	9.8	69

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109	Strain-specific inhibition of <i>Helicobacter pylori</i> by <i>Lactobacillus salivarius</i> and other lactobacilli. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 831-834.	3.0	68
110	Isolation of lactobacilli with probiotic properties from the human stomach. <i>Letters in Applied Microbiology</i> , 2008, 47, 269-274.	2.2	67
111	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 214-221.	3.0	67
112	Detection and Genomic Characterization of Motility in <i>Lactobacillus curvatus</i> : Confirmation of Motility in a Species outside the <i>Lactobacillus salivarius</i> Clade. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1297-1308.	3.1	67
113	Changes in microbiota composition, bile and fatty acid metabolism, in successful faecal microbiota transplantation for <i>Clostridioides difficile</i> infection. <i>BMC Gastroenterology</i> , 2018, 18, 131.	2.0	67
114	Genome sequences and comparative genomics of two <i>Lactobacillus ruminis</i> strains from the bovine and human intestinal tracts. <i>Microbial Cell Factories</i> , 2011, 10, S13.	4.0	65
115	Next-generation sequencing technologies and their impact on microbial genomics. <i>Briefings in Functional Genomics</i> , 2013, 12, 440-453.	2.7	65
116	Compositional dynamics of the human intestinal microbiota with aging: Implications for health. <i>Journal of Nutrition, Health and Aging</i> , 2014, 18, 773-786.	3.3	64
117	Carbohydrate catabolic diversity of bifidobacteria and lactobacilli of human origin. <i>International Journal of Food Microbiology</i> , 2015, 203, 109-121.	4.7	63
118	<i>Lactobacillus</i> : Host-Microbe Relationships. <i>Current Topics in Microbiology and Immunology</i> , 2011, 358, 119-154.	1.1	61
119	Changes in the intestinal microbiota from adulthood through to old age. <i>Clinical Microbiology and Infection</i> , 2012, 18, 44-46.	6.0	61
120	Food and nutrient intake of Irish community-dwelling elderly subjects: Who is at nutritional risk?. <i>Journal of Nutrition, Health and Aging</i> , 2014, 18, 561-572.	3.3	61
121	Evidence for ethnic tropism of <i>Helicobacter pylori</i> . <i>Infection and Immunity</i> , 1997, 65, 3708-3712.	2.2	59
122	Production of Multiple Bacteriocins from a Single Locus by Gastrointestinal Strains of <i>Lactobacillus salivarius</i> . <i>Journal of Bacteriology</i> , 2011, 193, 6973-6982.	2.2	58
123	Unique Characteristics of the Pyrrolysine System in the 7th Order of Methanogens: Implications for the Evolution of a Genetic Code Expansion Cassette. <i>Archaea</i> , 2014, 2014, 1-11.	2.3	58
124	Volatile organic compounds emitted from faeces as a biomarker for colorectal cancer. <i>Alimentary Pharmacology and Therapeutics</i> , 2019, 49, 1005-1012.	3.7	57
125	Prevalence of malnutrition using harmonized definitions in older adults from different settings – A MaNuEL study. <i>Clinical Nutrition</i> , 2019, 38, 2389-2398.	5.0	56
126	Molecular cloning and expression of the epidermolytic toxin A gene of <i>Staphylococcus aureus</i> . <i>Microbial Pathogenesis</i> , 1986, 1, 583-594.	2.9	53

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127	Distribution of Megaplastids in <i>Lactobacillus salivarius</i> and Other Lactobacilli. <i>Journal of Bacteriology</i> , 2007, 189, 6128-6139.	2.2	53
128	<i>Schistosoma mansoni</i> Worm Infection Regulates the Intestinal Microbiota and Susceptibility to Colitis. <i>Infection and Immunity</i> , 2019, 87, .	2.2	52
129	Effect of room temperature transport vials on DNA quality and phylogenetic composition of faecal microbiota of elderly adults and infants. <i>Microbiome</i> , 2016, 4, 19.	11.1	51
130	Polyphasic analysis indicates that <i>Lactobacillus salivarius</i> subsp. <i>salivarius</i> and <i>Lactobacillus salivarius</i> subsp. <i>salicinii</i> do not merit separate subspecies status. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2397-2403.	1.7	50
131	Molecular characterization of a conserved 20-kilodalton membrane-associated lipoprotein antigen of <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 1994, 176, 5938-5948.	2.2	49
132	Microbiome and health implications for ethnic minorities after enforced lifestyle changes. <i>Nature Medicine</i> , 2020, 26, 1089-1095.	30.7	48
133	Can prebiotics and probiotics improve therapeutic outcomes for undernourished individuals?. <i>Gut Microbes</i> , 2014, 5, 74-82.	9.8	47
134	Identification and molecular characterization of a major ring-forming surface protein from the gastric pathogen <i>Helicobacter mustelae</i> . <i>Molecular Microbiology</i> , 1994, 11, 349-361.	2.5	46
135	The FliK protein and flagellar hook-length control. <i>Protein Science</i> , 2007, 16, 769-780.	7.6	46
136	Characterization of Endogenous Plasmids from <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3216-3228.	3.1	46
137	The Human Gut Chip –HuGChip, an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. <i>PLoS ONE</i> , 2013, 8, e62544.	2.5	46
138	Fibrinogen-binding and platelet aggregation activities of a <i>Lactobacillus salivarius</i> septicaemia isolate are mediated by a novel fibrinogen-binding protein. <i>Molecular Microbiology</i> , 2012, 85, 862-877.	2.5	45
139	Mutagenesis by Microbe: the Role of the Microbiota in Shaping the Cancer Genome. <i>Trends in Cancer</i> , 2020, 6, 277-287.	7.4	45
140	Unusual genome complexity in <i>Lactobacillus salivarius</i> JCM1046. <i>BMC Genomics</i> , 2014, 15, 771.	2.8	44
141	Impact of diet on the human intestinal microbiota. <i>Current Opinion in Food Science</i> , 2015, 2, 71-77.	8.0	44
142	The role of the microbiota in sedentary lifestyle disorders and ageing: lessons from the animal kingdom. <i>Journal of Internal Medicine</i> , 2020, 287, 271-282.	6.0	44
143	Molecular Basis of the Interaction between the Flagellar Export Proteins FliI and FliH from <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 508-517.	3.4	43
144	Model for Substrate Interactions in C5a Peptidase from <i>Streptococcus pyogenes</i> : A 1.9 Å... Crystal Structure of the Active Form of ScpA. <i>Journal of Molecular Biology</i> , 2009, 386, 754-772.	4.2	43

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145	Influence of Adhesion and Bacteriocin Production by <i>Lactobacillus salivarius</i> on the Intestinal Epithelial Cell Transcriptional Response. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5196-5203.	3.1	43
146	Isolation and characterization of bacteriocin-producing bacteria from the intestinal microbiota of elderly Irish subjects. <i>Journal of Applied Microbiology</i> , 2013, 114, 886-898.	3.1	43
147	Prevalence and characterization of <i>Clostridium perfringens</i> from the faecal microbiota of elderly Irish subjects. <i>Journal of Medical Microbiology</i> , 2013, 62, 457-466.	1.8	42
148	Pro-Inflammatory Flagellin Proteins of Prevalent Motile Commensal Bacteria Are Variably Abundant in the Intestinal Microbiome of Elderly Humans. <i>PLoS ONE</i> , 2013, 8, e68919.	2.5	42
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