Paul W O'toole

List of Publications by Year in descending order

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Version: 2024-02-01

275 papers

36,576 citations

85 h-index 180 g-index

288 all docs 288 docs citations

288 times ranked

38093 citing authors

#	Article	IF	Citations
1	Geographical and Seasonal Analysis of the Honeybee Microbiome. Microbial Ecology, 2023, 85, 765-778.	1.4	8
2	Altered Skin and Gut Microbiome in Hidradenitis Suppurativa. Journal of Investigative Dermatology, 2022, 142, 459-468.e15.	0.3	35
3	Next-Generation Food Research: Use of Meta-Omic Approaches for Characterizing Microbial Communities Along the Food Chain. Annual Review of Food Science and Technology, 2022, 13, 361-384.	5.1	21
4	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
5	Altered stress responses in adults born by Caesarean section. Neurobiology of Stress, 2022, 16, 100425.	1.9	10
6	Identification of Gut Bacteria such as Lactobacillus johnsonii that Disseminate to Systemic Tissues of Wild Type and MyD88â \in "/â \in " Mice. Gut Microbes, 2022, 14, 2007743.	4.3	1
7	Metabolic rewiring and serotonin depletion in patients with postacute sequelae of COVIDâ€19. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 1623-1625.	2.7	11
8	Colorectal microbiota after removal of colorectal cancer. NAR Cancer, 2022, 4, zcac011.	1.6	5
9	Fermented Foods, Health and the Gut Microbiome. Nutrients, 2022, 14, 1527.	1.7	75
10	Role of the Microbiome in Regulating Bone Metabolism and Susceptibility to Osteoporosis. Calcified Tissue International, 2022, 110, 273-284.	1.5	22
11	The gut microbiome as a modulator of healthy ageing. Nature Reviews Gastroenterology and Hepatology, 2022, 19, 565-584.	8.2	162
12	A high-risk gut microbiota configuration associates with fatal hyperinflammatory immune and metabolic responses to SARS-CoV-2. Gut Microbes, 2022, 14, 2073131.	4.3	40
13	Loss of MMR and TGFBR2 Increases the Susceptibility to Microbiota-Dependent Inflammation-Associated Colon Cancer. Cellular and Molecular Gastroenterology and Hepatology, 2022, 14, 693-717.	2.3	6
14	Microbiome Transfer Partly Overrides Lack of ILâ€1RI Signaling to Alter Hepatic but not Adipose Tissue Phenotype and Lipid Handling following a Highâ€Fat Diet Challenge. Molecular Nutrition and Food Research, 2021, 65, e2000202.	1.5	4
15	Transplanting Microbes for Irritable Bowels or Irritated Microbes or Both?. Gastroenterology, 2021, 160, 15-17.	0.6	1
16	The Healthy Microbiomeâ€"What Is the Definition of a Healthy Gut Microbiome?. Gastroenterology, 2021, 160, 483-494.	0.6	174
17	Understanding the impact of age-related changes in the gut microbiome on chronic diseases and the prospect of elderly-specific dietary interventions. Current Opinion in Biotechnology, 2021, 70, 48-55.	3.3	22
18	A synthetic consortium of 100 gut commensals modulates the composition and function in a colon model of the microbiome of elderly subjects. Gut Microbes, 2021, 13, 1-19.	4.3	8

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19	The gut virome in Irritable Bowel Syndrome differs from that of controls. Gut Microbes, 2021, 13, 1-15.	4.3	36
20	Macrophage cytokine responses to commensal Gram-positive Lactobacillus salivarius strains are TLR2-independent and Myd88-dependent. Scientific Reports, 2021, 11, 5896.	1.6	12
21	The Influence of Different Physical Activity Behaviours on the Gut Microbiota of Older Irish Adults. Journal of Nutrition, Health and Aging, 2021, 25, 854-861.	1.5	9
22	Dietary Fibre Modulates the Gut Microbiota. Nutrients, 2021, 13, 1655.	1.7	225
23	Effect of Fecal Microbiota Transplantation Combined With Mediterranean Diet on Insulin Sensitivity in Subjects With Metabolic Syndrome. Frontiers in Microbiology, 2021, 12, 662159.	1.5	22
24	The potential of non-starter lactic acid bacteria from Cheddar cheese to colonise the gut. Journal of Functional Foods, 2021, 83, 104425.	1.6	10
25	Seasonality and Geography Have a Greater Influence than the Use of Chlorine-Based Cleaning Agents on the Microbiota of Bulk Tank Raw Milk. Applied and Environmental Microbiology, 2021, 87, e0108121.	1.4	8
26	244 MICROBIOME ANALYSIS OF UPPER DIGESTIVE TRACT BIOPSY SAMPLES FROM INDIVIDUALS ALONG THE METAPLASIA-DYSPLASIA-ADENOCARCINOMA SEQUENCE Ecological Management and Restoration, 2021, 34, .	0.2	0
27	Elevated gut microbiome abundance of <i>Christensenellaceae, Porphyromonadaceae and Rikenellaceae</i> is associated with reduced visceral adipose tissue and healthier metabolic profile in Italian elderly. Gut Microbes, 2021, 13, 1-19.	4.3	127
28	Mapping the colorectal tumor microbiota. Gut Microbes, 2021, 13, 1-10.	4.3	10
29	Vitamin K status and inflammation are associated with cognition in older Irish adults. Nutritional Neuroscience, 2020, 23, 591-599.	1.5	30
30	Differences in Fecal Microbiomes and Metabolomes of People With vs Without Irritable Bowel Syndrome and Bile Acid Malabsorption. Gastroenterology, 2020, 158, 1016-1028.e8.	0.6	122
31	Whole Blueberry and Isolated Polyphenol-Rich Fractions Modulate Specific Gut Microbes in an In Vitro Colon Model and in a Pilot Study in Human Consumers. Nutrients, 2020, 12, 2800.	1.7	30
32	Metagenomic analysis reveals distinct patterns of gut lactobacillus prevalence, abundance, and geographical variation in health and disease. Gut Microbes, 2020, 12, 1822729.	4.3	26
33	Microbiome transfer between IL-1RI- I - and wild-type mice during high or low-fat feeding alters metabolic tissue functionality but not glucose homeostasis Proceedings of the Nutrition Society, 2020, 79, .	0.4	0
34	Baker's yeast (1→3)-Î ² -D-glucan Influences Insulin Sensitivity in Mice with Humanized Obese Diabetic Microbiome in High-Fat Diet-Induced Obesity. Proceedings of the Nutrition Society, 2020, 79, .	0.4	0
35	Gut Microbiota Associations with Metabolic Health and Obesity Status in Older Adults. Nutrients, 2020, 12, 2364.	1.7	34
36	Evaluation of methods for the reduction of contaminating host reads when performing shotgun metagenomic sequencing of the milk microbiome. Scientific Reports, 2020, 10, 21665.	1.6	33

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37	The probiotic <i>L. casei</i> LC-XCALâ,,¢ improves metabolic health in a diet-induced obesity mouse model without altering the microbiome. Gut Microbes, 2020, 12, 1747330.	4.3	16
38	Microbiome alterations in IBS. Gut, 2020, 69, 2263-2264.	6.1	10
39	Diet influences the functions of the human intestinal microbiome. Scientific Reports, 2020, 10, 4247.	1.6	115
40	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. Cell Host and Microbe, 2020, 28, 258-272.e6.	5.1	160
41	Microbiome and health implications for ethnic minorities after enforced lifestyle changes. Nature Medicine, 2020, 26, 1089-1095.	15.2	48
42	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. Gut, 2020, 69, 1218-1228.	6.1	465
43	Mutagenesis by Microbe: the Role of the Microbiota in Shaping the Cancer Genome. Trends in Cancer, 2020, 6, 277-287.	3.8	45
44	The role of the microbiota in sedentary lifestyle disorders and ageing: lessons from the animal kingdom. Journal of Internal Medicine, 2020, 287, 271-282.	2.7	44
45	Archaea, specific genetic traits, and development of improved bacterial live biotherapeutic products: another face of next-generation probiotics. Applied Microbiology and Biotechnology, 2020, 104, 4705-4716.	1.7	18
46	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
47	Adjusting for age improves identification of gut microbiome alterations in multiple diseases. ELife, 2020, 9, .	2.8	113
48	Dose-interval study of a dual probiotic in preterm infants. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2019, 104, F159-F164.	1.4	15
49	The microbiota of the mother at birth and its influence on the emerging infant oral microbiota from birth to 1 year of age: a cohort study. Journal of Oral Microbiology, 2019, 11, 1599652.	1.2	23
50	Gut microbiota alterations associated with reduced bone mineral density in older adults. Rheumatology, 2019, 58, 2295-2304.	0.9	106
51	Exploratory analysis of covariation of microbiota-derived vitamin K and cognition in older adults. American Journal of Clinical Nutrition, 2019, 110, 1404-1415.	2.2	26
52	Retention of Microbiota Diversity by Lactose-Free Milk in a Mouse Model of Elderly Gut Microbiota. Journal of Agricultural and Food Chemistry, 2019, 67, 2098-2112.	2.4	11
53	Heterologous gene expression in the human gut bacteria Eubacterium rectale and Roseburia inulinivorans by means of conjugative plasmids. Anaerobe, 2019, 59, 131-140.	1.0	8
54	Schistosoma mansoni Worm Infection Regulates the Intestinal Microbiota and Susceptibility to Colitis. Infection and Immunity, $2019,87,\ldots$	1.0	52

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55	Analysis of Health Benefits Conferred by Lactobacillus Species from Kefir. Nutrients, 2019, 11, 1252.	1.7	109
56	International Cancer Microbiome Consortium consensus statement on the role of the human microbiome in carcinogenesis. Gut, 2019, 68, 1624-1632.	6.1	173
57	Volatile organic compounds emitted from faeces as a biomarker for colorectal cancer. Alimentary Pharmacology and Therapeutics, 2019, 49, 1005-1012.	1.9	57
58	Prebiotic supplementation in frail older people affects specific gut microbiota taxa but not global diversity. Microbiome, 2019, 7, 39.	4.9	72
59	<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.	0.2	124
60	The Gut Microbiota in Causation, Detection, and Treatment of Cancer. American Journal of Gastroenterology, 2019, 114, 1036-1042.	0.2	25
61	The rumen microbiome: a crucial consideration when optimising milk and meat production and nitrogen utilisation efficiency. Gut Microbes, 2019, 10, 115-132.	4.3	209
62	Prevalence of malnutrition using harmonized definitions in older adults from different settings – A MaNuEL study. Clinical Nutrition, 2019, 38, 2389-2398.	2.3	56
63	Gut and Whole-Body Microbiota of the Honey Bee Separate Thriving and Non-thriving Hives. Microbial Ecology, 2019, 78, 195-205.	1.4	39
64	Comparison of the salivary and dentinal microbiome of children with severe-early childhood caries to the salivary microbiome of caries-free children. BMC Oral Health, 2019, 19, 13.	0.8	86
65	Potentially modifiable determinants of malnutrition in older adults: AÂsystematic review. Clinical Nutrition, 2019, 38, 2477-2498.	2.3	127
66	Genus-Wide Assessment of Antibiotic Resistance in <i>Lactobacillus</i> spp. Applied and Environmental Microbiology, 2019, 85, .	1.4	190
67	The viability of probiotics in water, breast milk, and infant formula. European Journal of Pediatrics, 2018, 177, 867-870.	1.3	13
68	Tumour-associated and non-tumour-associated microbiota: Addendum. Gut Microbes, 2018, 9, 1-5.	4.3	25
69	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	5.9	717
70	Selected aspects of the human gut microbiota. Cellular and Molecular Life Sciences, 2018, 75, 81-82.	2.4	19
71	Microbiome–health interactions in older people. Cellular and Molecular Life Sciences, 2018, 75, 119-128.	2.4	80
72	The oral microbiota in colorectal cancer is distinctive and predictive. Gut, 2018, 67, 1454-1463.	6.1	425

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73	Draft Genome Sequence of Lactobacillus fermentum Lf2, an Exopolysaccharide-Producing Strain Isolated from Argentine Cheese. Microbiology Resource Announcements, 2018, 7, .	0.3	3
74	Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. Emerging Topics in Life Sciences, 2018, 2, 607-618.	1.1	22
75	The Evolution of Living Beings Started with Prokaryotes and in Interaction with Prokaryotes. , 2018, , 241-338.		2
76	Genomic Characterization of Sulphite Reducing Bacteria Isolated From the Dairy Production Chain. Frontiers in Microbiology, 2018, 9, 1507.	1.5	9
77	Changes in microbiota composition, bile and fatty acid metabolism, in successful faecal microbiota transplantation for Clostridioides difficile infection. BMC Gastroenterology, 2018, 18, 131.	0.8	67
78	The Genomic Basis of Lactobacilli as Health-Promoting Organisms. , 2018, , 49-71.		0
79	Comparative Genomics of the Genus Lactobacillus Reveals Robust Phylogroups That Provide the Basis for Reclassification. Applied and Environmental Microbiology, 2018, 84, .	1.4	93
80	The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study. Scientific Reports, 2017, 7, 40597.	1.6	279
81	From Culture to High-Throughput Sequencing and Beyond. Gastroenterology Clinics of North America, 2017, 46, 9-17.	1.0	13
82	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. Gut, 2017, 66, 633-643.	6.1	623
83	Glycomacropeptide Sustains Microbiota Diversity and Promotes Specific Taxa in an Artificial Colon Model of Elderly Gut Microbiota. Journal of Agricultural and Food Chemistry, 2017, 65, 1836-1846.	2.4	35
84	Forgotten fungiâ€"the gut mycobiome in human health and disease. FEMS Microbiology Reviews, 2017, 41, 479-511.	3.9	216
85	Next-generation probiotics: the spectrum from probiotics to live biotherapeutics. Nature Microbiology, 2017, 2, 17057.	5.9	553
86	When regulation challenges innovation: The case of the genus Lactobacillus. Trends in Food Science and Technology, 2017, 66, 187-194.	7.8	39
87	Fecal microbiota variation across the lifespan of the healthy laboratory rat. Gut Microbes, 2017, 8, 428-439.	4.3	93
88	High-throughput metataxonomic characterization of the raw milk microbiota identifies changes reflecting lactation stage and storage conditions. International Journal of Food Microbiology, 2017, 255, 1-6.	2.1	36
89	Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076.	9.4	581
90	Core fecal microbiota of domesticated herbivorous ruminant, hindgut fermenters, and monogastric animals. MicrobiologyOpen, 2017, 6, e00509.	1.2	83

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91	Metagenomeâ€based surveillance and diagnostic approaches to studying the microbial ecology of food production and processing environments. Environmental Microbiology, 2017, 19, 4382-4391.	1.8	40
92	The contribution of microbial biotechnology to sustainable development goals: microbiome therapies. Microbial Biotechnology, 2017, 10, 1066-1069.	2.0	19
93	A clinician's guide to microbiome analysis. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 585-595.	8.2	124
94	Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. ISME Journal, 2017, 11, 2059-2074.	4.4	112
95	Feeding the microbiota: transducer of nutrient signals for the host. Gut, 2017, 66, 1709-1717.	6.1	124
96	Impacts of Seasonal Housing and Teat Preparation on Raw Milk Microbiota: a High-Throughput Sequencing Study. Applied and Environmental Microbiology, 2017, 83, .	1.4	104
97	The Genomic Basis of Lactobacilli as Health-Promoting Organisms. Microbiology Spectrum, 2017, 5, .	1.2	29
98	Phylogenomics and comparative genomics of Lactobacillus salivarius, a mammalian gut commensal. Microbial Genomics, 2017, 3, e000115.	1.0	86
99	A long and abundant non-coding RNA in Lactobacillus salivarius. Microbial Genomics, 2017, 3, e000126.	1.0	6
100	A Profile Hidden Markov Model to investigate the distribution and frequency of LanB-encoding lantibiotic modification genes in the human oral and gut microbiome. PeerJ, 2017, 5, e3254.	0.9	24
101	The Microbiome in Aging. , 2016, , 185-222.		1
102	Studying the Microbiome: "Omics―Made Accessible. Seminars in Liver Disease, 2016, 36, 306-311.	1.8	4
103	Effect of room temperature transport vials on DNA quality and phylogenetic composition of faecal microbiota of elderly adults and infants. Microbiome, 2016, 4, 19.	4.9	51
104	Signatures of early frailty in the gut microbiota. Genome Medicine, 2016, 8, 8.	3.6	297
105	High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. Gut, 2016, 65, 1812-1821.	6.1	1,092
106	Composition and temporal stability of the gut microbiota in older persons. ISME Journal, 2016, 10, 170-182.	4.4	305
107	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. Microbial Genomics, 2016, 2, e000043.	1.0	162
108	High-resolution structures of Lactobacillus salivarius transketolase in the presence and absence of thiamine pyrophosphate. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1327-1334.	0.4	1

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109	The Gut Microbiota Composition in Dichorionic Triplet Sets Suggests a Role for Host Genetic Factors. PLoS ONE, 2015, 10, e0122561.	1.1	35
110	Helicobacter pylori, HIV and Gastric Hypochlorhydria in the Malawian Population. PLoS ONE, 2015, 10, e0132043.	1.1	12
111	Detection and Genomic Characterization of Motility in Lactobacillus curvatus: Confirmation of Motility in a Species outside the Lactobacillus salivarius Clade. Applied and Environmental Microbiology, 2015, 81, 1297-1308.	1.4	67
112	The role of the microbiota in ageing: current state and perspectives. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 131-138.	6.6	14
113	Gut microbiota and aging. Science, 2015, 350, 1214-1215.	6.0	801
114	Neonatal Sulfhemoglobinemia and Hemolytic Anemia Associated With Intestinal <i>Morganella morganii</i> . Pediatrics, 2015, 136, e1641-e1645.	1.0	27
115	In silico identification of bacteriocin gene clusters in the gastrointestinal tract, based on the Human Microbiome Project's reference genome database. BMC Microbiology, 2015, 15, 183.	1.3	112
116	Dietary glycaemic load associated with cognitive performance in elderly subjects. European Journal of Nutrition, 2015, 54, 557-568.	1.8	22
117	Molecular methods for studying methanogens of the human gastrointestinal tract: current status and future directions. Applied Microbiology and Biotechnology, 2015, 99, 5801-5815.	1.7	24
118	Carbohydrate catabolic diversity of bifidobacteria and lactobacilli of human origin. International Journal of Food Microbiology, 2015, 203, 109-121.	2.1	63
119	The neonatal gut harbours distinct bifidobacterial strains. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2015, 100, F405-F410.	1.4	29
120	Lactobacillus ruminis strains cluster according to their mammalian gut source. BMC Microbiology, 2015, 15, 80.	1.3	34
121	In-vitro model for studying methanogens in human gut microbiota. Anaerobe, 2015, 34, 50-52.	1.0	10
122	National survey to determine current practices, training and attitudes towards advanced polypectomy in the UK. Frontline Gastroenterology, 2015, 6, 85-93.	0.9	8
123	Impact of diet on the human intestinal microbiota. Current Opinion in Food Science, 2015, 2, 71-77.	4.1	44
124	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. Nature Communications, 2015, 6, 8322.	5.8	488
125	Unique Characteristics of the Pyrrolysine System in the 7th Order of Methanogens: Implications for the Evolution of a Genetic Code Expansion Cassette. Archaea, 2014, 2014, 1-11.	2.3	58
126	Archaea and the human gut: New beginning of an old story. World Journal of Gastroenterology, 2014, 20, 16062.	1.4	308

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127	MOLECULAR BIOLOGY Genomics., 2014, , 770-779.		O
128	Can prebiotics and probiotics improve therapeutic outcomes for undernourished individuals?. Gut Microbes, 2014, 5, 74-82.	4.3	47
129	Compositional dynamics of the human intestinal microbiota with aging: Implications for health. Journal of Nutrition, Health and Aging, 2014, 18, 773-786.	1.5	64
130	The Genome of the Predominant Equine $\langle i \rangle$ Lactobacillus $\langle i \rangle$ Species, Lactobacillus equi, Is Reflective of Its Lifestyle Adaptations to an Herbivorous Host. Genome Announcements, 2014, 2, .	0.8	1
131	Metaphor: Finding Bi-directional Best Hit homology relationships in (meta)genomic datasets. Genomics, 2014, 104, 459-463.	1.3	5
132	Unusual genome complexity in Lactobacillus salivarius JCM1046. BMC Genomics, 2014, 15, 771.	1.2	44
133	Lactobacillus reuteri 100-23 Modulates Urea Hydrolysis in the Murine Stomach. Applied and Environmental Microbiology, 2014, 80, 6104-6113.	1.4	25
134	Beneficial modulation of the gut microbiota. FEBS Letters, 2014, 588, 4120-4130.	1.3	204
135	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.	2.2	131
136	Gut microbiota in older subjects: variation, health consequences and dietary intervention prospects. Proceedings of the Nutrition Society, 2014, 73, 441-451.	0.4	33
137	Maintenance of a healthy trajectory of the intestinal microbiome during aging: A dietary approach. Mechanisms of Ageing and Development, 2014, 136-137, 70-75.	2.2	72
138	Intestinal microbiota, diet and health. British Journal of Nutrition, 2014, 111, 387-402.	1.2	371
139	Diet-Microbiota-Health Interactions in Older Subjects: Implications for Healthy Aging. Interdisciplinary Topics in Gerontology, 2014, 40, 141-154.	3.6	27
140	Archaebiotics. Gut Microbes, 2014, 5, 5-10.	4.3	201
141	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
142	Disturbance of the gut microbiota in early-life selectively affects visceral pain in adulthood without impacting cognitive or anxiety-related behaviors in male rats. Neuroscience, 2014, 277, 885-901.	1.1	222
143	Comparative genomics highlights the unique biology of Methanomassiliicoccales, a Thermoplasmatales-related seventh order of methanogenic archaea that encodes pyrrolysine. BMC Genomics, 2014, 15, 679.	1.2	246
144	Food and nutrient intake of Irish community-dwelling elderly subjects: Who is at nutritional risk?. Journal of Nutrition, Health and Aging, 2014, 18, 561-572.	1.5	61

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145	Host–microbe interactions and spatial variation of cancer in the gut. Nature Reviews Cancer, 2014, 14, 511-512.	12.8	16
146	Exercise and associated dietary extremes impact on gut microbial diversity. Gut, 2014, 63, 1913-1920.	6.1	987
147	Molecular dialogue between the human gut microbiota and the host: a Lactobacillus and Bifidobacterium perspective. Cellular and Molecular Life Sciences, 2014, 71, 183-203.	2.4	265
148	Catabolic flexibility of mammalian-associated lactobacilli. Microbial Cell Factories, 2013, 12, 48.	1.9	17
149	Effects of the Intestinal Microbiota on Behavior and Brain Biochemistry. World Review of Nutrition and Dietetics, 2013, , 56-63.	0.1	0
150	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. Letters in Applied Microbiology, 2013, 57, 492-501.	1.0	90
151	Diet-Microbiota Interactions and Their Implications for Healthy Living. Nutrients, 2013, 5, 234-252.	1.7	174
152	The Intestinal Microbiota and Aging. World Review of Nutrition and Dietetics, 2013, , 25-31.	0.1	2
153	Metabolic Syndrome and Obesity in Adults. World Review of Nutrition and Dietetics, 2013, , 103-121.	0.1	1
154	Next-generation sequencing technologies and their impact on microbial genomics. Briefings in Functional Genomics, 2013, 12, 440-453.	1.3	65
155	Divergent metabolic outcomes arising from targeted manipulation of the gut microbiota in diet-induced obesity. Gut, 2013, 62, 220-226.	6.1	235
156	Diet-microbiota-health interactions in older subjects. Free Radical Biology and Medicine, 2013, 65, S4.	1.3	0
157	Isolation and characterization of bacteriocin-producing bacteria from the intestinal microbiota of elderly Irish subjects. Journal of Applied Microbiology, 2013, 114, 886-898.	1.4	43
158	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. Journal of Antimicrobial Chemotherapy, 2013, 68, 214-221.	1.3	67
159	Challenges and Implications for Biomedical Research and Intervention Studies in Older Populations: Insights from the ELDERMET Study. Gerontology, 2013, 59, 114-121.	1.4	21
160	Genome Sequence of " <i>Candidatus</i> Methanomassiliicoccus intestinalis―Issoire-Mx1, a Third <i>Thermoplasmatales</i> -Related Methanogenic Archaeon from Human Feces. Genome Announcements, 2013, 1, .	0.8	85
161	Phylogenomic Data Support a Seventh Order of Methylotrophic Methanogens and Provide Insights into the Evolution of Methanogenesis. Genome Biology and Evolution, 2013, 5, 1769-1780.	1.1	249
162	The individual-specific and diverse nature of the preterm infant microbiota. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2013, 98, F334-F340.	1.4	105

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163	Microbiota diversity and stability of the preterm neonatal ileum and colon of two infants. MicrobiologyOpen, 2013, 2, 215-225.	1.2	40
164	Prevalence and characterization of Clostridium perfringens from the faecal microbiota of elderly Irish subjects. Journal of Medical Microbiology, 2013, 62, 457-466.	0.7	42
165	Draft Genome Sequence of Lactobacillus crispatus EM-LC1, an Isolate with Antimicrobial Activity Cultured from an Elderly Subject. Genome Announcements, 2013, 1, .	0.8	2
166	Targeting the Microbiota to Address Diet-Induced Obesity: A Time Dependent Challenge. PLoS ONE, 2013, 8, e65790.	1.1	132
167	Functional metagenomic profiling of intestinal microbiome in extreme ageing. Aging, 2013, 5, 902-912.	1.4	263
168	The Human Gut Chip "HuGChipâ€; an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. PLoS ONE, 2013, 8, e62544.	1.1	46
169	Pro-Inflammatory Flagellin Proteins of Prevalent Motile Commensal Bacteria Are Variably Abundant in the Intestinal Microbiome of Elderly Humans. PLoS ONE, 2013, 8, e68919.	1.1	42
170	Influence of Adhesion and Bacteriocin Production by Lactobacillus salivarius on the Intestinal Epithelial Cell Transcriptional Response. Applied and Environmental Microbiology, 2012, 78, 5196-5203.	1.4	43
171	Genome Sequence of "Candidatus Methanomethylophilus alvus―Mx1201, a Methanogenic Archaeon from the Human Gut Belonging to a Seventh Order of Methanogens. Journal of Bacteriology, 2012, 194, 6944-6945.	1.0	155
172	Transcriptional and Metabolomic Consequences of <i>luxS</i> Inactivation Reveal a Metabolic Rather than Quorum-Sensing Role for LuxS in Lactobacillus reuteri 100-23. Journal of Bacteriology, 2012, 194, 1743-1746.	1.0	31
173	The microbiota link to irritable bowel syndrome. Gut Microbes, 2012, 3, 572-576.	4.3	102
174	Subspecies diversity in bacteriocin production by intestinal <i>Lactobacillus salivarius </i> strains. Gut Microbes, 2012, 3, 468-473.	4.3	29
175	The gut microbiota and its relationship to diet and obesity. Gut Microbes, 2012, 3, 186-202.	4.3	382
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