

Orla O'Sullivan

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

19,386
citations

20817

60
h-index

12597

132
g-index

144
all docs

144
docs citations

144
times ranked

24364
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012, 488, 178-184. | 27.8 | 2,618 |
| 2 | 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 |
| 3 | Exercise and associated dietary extremes impact on gut microbial diversity. <i>Gut</i> , 2014, 63, 1913-1920. | 12.1 | 987 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | The complex microbiota of raw milk. <i>FEMS Microbiology Reviews</i> , 2013, 37, 664-698. | 8.6 | 591 |
| 8 | Gut microbiota depletion from early adolescence in mice: Implications for brain and behaviour. <i>Brain, Behavior, and Immunity</i> , 2015, 48, 165-173. | 4.1 | 572 |
| 9 | M-Coffee: combining multiple sequence alignment methods with T-Coffee. <i>Nucleic Acids Research</i> , 2006, 34, 1692-1699. | 14.5 | 533 |
| 10 | 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 |
| 11 | Short-chain fatty acids: microbial metabolites that alleviate stress-induced brain-gut axis alterations. <i>Journal of Physiology</i> , 2018, 596, 4923-4944. | 2.9 | 460 |
| 12 | The microbiome of professional athletes differs from that of more sedentary subjects in composition and particularly at the functional metabolic level. <i>Gut</i> , 2018, 67, gutjnl-2016-313627. | 12.1 | 333 |
| 13 | Effect of broad- and narrow-spectrum antimicrobials on <i>Clostridium difficile</i> and microbial diversity in a model of the distal colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4639-4644. | 7.1 | 313 |
| 14 | Sequence-based analysis of the bacterial and fungal compositions of multiple kombucha (tea fungus) samples. <i>Food Microbiology</i> , 2014, 38, 171-178. | 4.2 | 303 |
| 15 | 3DCoffee: Combining Protein Sequences and Structures within Multiple Sequence Alignments. <i>Journal of Molecular Biology</i> , 2004, 340, 385-395. | 4.2 | 302 |
| 16 | Exploring a Possible Link between the Intestinal Microbiota and Feed Efficiency in Pigs. <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 3.1 | 258 |
| 17 | The Effects of Freezing on Faecal Microbiota as Determined Using MiSeq Sequencing and Culture-Based Investigations. <i>PLoS ONE</i> , 2015, 10, e0119355. | 2.5 | 241 |
| 18 | High-Throughput Sequencing for Detection of Subpopulations of Bacteria Not Previously Associated with Artisanal Cheeses. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5717-5723. | 3.1 | 236 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | 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 |
| 20 | Gender-dependent consequences of chronic olanzapine in the rat: effects on body weight, inflammatory, metabolic and microbiota parameters. <i>Psychopharmacology</i> , 2012, 221, 155-169. | 3.1 | 231 |
| 21 | Spatial variation of the colonic microbiota in patients with ulcerative colitis and control volunteers. <i>Gut</i> , 2015, 64, 1553-1561. | 12.1 | 226 |
| 22 | Prenatal stress-induced alterations in major physiological systems correlate with gut microbiota composition in adulthood. <i>Psychoneuroendocrinology</i> , 2015, 60, 58-74. | 2.7 | 224 |
| 23 | Genome Sequence of <i>Lactobacillus helveticus</i> , an Organism Distinguished by Selective Gene Loss and Insertion Sequence Element Expansion. <i>Journal of Bacteriology</i> , 2008, 190, 727-735. | 2.2 | 208 |
| 24 | Molecular approaches to analysing the microbial composition of raw milk and raw milk cheese. <i>International Journal of Food Microbiology</i> , 2011, 150, 81-94. | 4.7 | 205 |
| 25 | Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. <i>MSystems</i> , 2016, 1, . | 3.8 | 202 |
| 26 | Antipsychotics and the gut microbiome: olanzapine-induced metabolic dysfunction is attenuated by antibiotic administration in the rat. <i>Translational Psychiatry</i> , 2013, 3, e309-e309. | 4.8 | 201 |
| 27 | Behavioural and neurochemical consequences of chronic gut microbiota depletion during adulthood in the rat. <i>Neuroscience</i> , 2016, 339, 463-477. | 2.3 | 196 |
| 28 | <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 |
| 29 | Sequencing-Based Analysis of the Bacterial and Fungal Composition of Kefir Grains and Milks from Multiple Sources. <i>PLoS ONE</i> , 2013, 8, e69371. | 2.5 | 169 |
| 30 | Impact of dietary fatty acids on metabolic activity and host intestinal microbiota composition in C57BL/6J mice. <i>British Journal of Nutrition</i> , 2014, 111, 1905-1917. | 2.3 | 152 |
| 31 | A Prospective Metagenomic and Metabolomic Analysis of the Impact of Exercise and/or Whey Protein Supplementation on the Gut Microbiome of Sedentary Adults. <i>MSystems</i> , 2018, 3, . | 3.8 | 148 |
| 32 | N-3 Polyunsaturated Fatty Acids (PUFAs) Reverse the Impact of Early-Life Stress on the Gut Microbiota. <i>PLoS ONE</i> , 2015, 10, e0139721. | 2.5 | 143 |
| 33 | Targeting the Microbiota to Address Diet-Induced Obesity: A Time Dependent Challenge. <i>PLoS ONE</i> , 2013, 8, e65790. | 2.5 | 132 |
| 34 | Exercise and the microbiota. <i>Gut Microbes</i> , 2015, 6, 131-136. | 9.8 | 127 |
| 35 | Casein Fermentate of <i>Lactobacillus animalis</i> DPC6134 Contains a Range of Novel Propeptide Angiotensin-Converting Enzyme Inhibitors. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4658-4667. | 3.1 | 125 |
| 36 | Comparative genomics of lactic acid bacteria reveals a niche-specific gene set. <i>BMC Microbiology</i> , 2009, 9, 50. | 3.3 | 122 |

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|----|--|-----|-----------|
| 37 | The microbial content of raw and pasteurized cow milk as determined by molecular approaches. <i>Journal of Dairy Science</i> , 2013, 96, 4928-4937. | 3.4 | 122 |
| 38 | High-throughput sequence-based analysis of the bacterial composition of kefir and an associated kefir grain. <i>FEMS Microbiology Letters</i> , 2011, 320, 56-62. | 1.8 | 120 |
| 39 | Contrasting effects of <i>Bifidobacterium breve</i> NCIMB 702258 and <i>Bifidobacterium breve</i> DPC 6330 on the composition of murine brain fatty acids and gut microbiota. <i>American Journal of Clinical Nutrition</i> , 2012, 95, 1278-1287. | 4.7 | 109 |
| 40 | 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 |
| 41 | The altered gut microbiota in adults with cystic fibrosis. <i>BMC Microbiology</i> , 2017, 17, 58. | 3.3 | 104 |
| 42 | A comparison of methods used to extract bacterial DNA from raw milk and raw milk cheese. <i>Journal of Applied Microbiology</i> , 2012, 113, 96-105. | 3.1 | 98 |
| 43 | Post-weaning social isolation of rats leads to long-term disruption of the gut microbiota-immune-brain axis. <i>Brain, Behavior, and Immunity</i> , 2018, 68, 261-273. | 4.1 | 97 |
| 44 | Dietary <i>trans</i> -10, <i>cis</i> -12-conjugated linoleic acid alters fatty acid metabolism and microbiota composition in mice. <i>British Journal of Nutrition</i> , 2015, 113, 728-738. | 2.3 | 89 |
| 45 | The Fungal Frontier: A Comparative Analysis of Methods Used in the Study of the Human Gut Mycobiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1432. | 3.5 | 86 |
| 46 | Gut microbial diversity is reduced and is associated with colonic inflammation in a piglet model of short bowel syndrome. <i>Gut Microbes</i> , 2013, 4, 212-221. | 9.8 | 82 |
| 47 | Exopolysaccharide-Producing Probiotic Lactobacilli Reduce Serum Cholesterol and Modify Enteric Microbiota in ApoE-Deficient Mice. <i>Journal of Nutrition</i> , 2014, 144, 1956-1962. | 2.9 | 80 |
| 48 | Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 3.1 | 78 |
| 49 | Fermented-Food Metagenomics Reveals Substrate-Associated Differences in Taxonomy and Health-Associated and Antibiotic Resistance Determinants. <i>MSystems</i> , 2020, 5, . | 3.8 | 78 |
| 50 | Antimicrobial activity of two peptides casecidin 15 and 17, found naturally in bovine colostrum. <i>Journal of Applied Microbiology</i> , 2009, 106, 233-240. | 3.1 | 77 |
| 51 | Myosin-cross-reactive antigen (MCRA) protein from <i>Bifidobacterium breve</i> is a FAD-dependent fatty acid hydratase which has a function in stress protection. <i>BMC Biochemistry</i> , 2011, 12, 9. | 4.4 | 75 |
| 52 | Bacteriocin Gene-Trait matching across the complete <i>Lactobacillus</i> Pan-genome. <i>Scientific Reports</i> , 2017, 7, 3481. | 3.3 | 75 |
| 53 | In silico analysis highlights the frequency and diversity of type 1 lantibiotic gene clusters in genome sequenced bacteria. <i>BMC Genomics</i> , 2010, 11, 679. | 2.8 | 74 |
| 54 | Nisin H Is a New Nisin Variant Produced by the Gut-Derived Strain <i>Streptococcus hyointestinalis</i> DPC6484. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3953-3960. | 3.1 | 74 |

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|----|--|------|-----------|
| 55 | Distinct microbiome composition and metabolome exists across subgroups of elite Irish athletes. <i>Journal of Science and Medicine in Sport</i> , 2020, 23, 63-68. | 1.3 | 74 |
| 56 | Sequence-based analysis of the microbial composition of water kefir from multiple sources. <i>FEMS Microbiology Letters</i> , 2013, 348, 79-85. | 1.8 | 70 |
| 57 | Streptozotocin-induced type-1-diabetes disease onset in Spragueâ€Dawley rats is associated with an altered intestinal microbiota composition and decreased diversity. <i>Microbiology (United Kingdom)</i> , 2015, 161, 182-193. | 1.8 | 70 |
| 58 | <i>Thermus</i> and the Pink Discoloration Defect in Cheese. <i>MSystems</i> , 2016, 1, . | 3.8 | 70 |
| 59 | Bacterial Communities Established in Bauxite Residues with Different Restoration Histories. <i>Environmental Science & Technology</i> , 2013, 47, 7110-7119. | 10.0 | 69 |
| 60 | Four men in a boat: Ultra-endurance exercise alters the gut microbiome. <i>Journal of Science and Medicine in Sport</i> , 2019, 22, 1059-1064. | 1.3 | 69 |
| 61 | Genome Mining for Radical SAM Protein Determinants Reveals Multiple Sactibiotic-Like Gene Clusters. <i>PLoS ONE</i> , 2011, 6, e20852. | 2.5 | 68 |
| 62 | Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 214-221. | 3.0 | 67 |
| 63 | FoodMicrobionet: A database for the visualisation and exploration of food bacterial communities based on network analysis. <i>International Journal of Food Microbiology</i> , 2016, 219, 28-37. | 4.7 | 65 |
| 64 | Species classifier choice is a key consideration when analysing low-complexity food microbiome data. <i>Microbiome</i> , 2018, 6, 50. | 11.1 | 65 |
| 65 | Enduring Behavioral Effects Induced by Birth by Caesarean Section in the Mouse. <i>Current Biology</i> , 2020, 30, 3761-3774.e6. | 3.9 | 65 |
| 66 | APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. <i>Bioinformatics</i> , 2003, 19, i215-i221. | 4.1 | 62 |
| 67 | Temporal and Spatial Differences in Microbial Composition during the Manufacture of a Continental-Type Cheese. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2525-2533. | 3.1 | 62 |
| 68 | Early <i>Salmonella</i> Typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. <i>Scientific Reports</i> , 2018, 8, 7788. | 3.3 | 61 |
| 69 | Nigral overexpression of α -synuclein in a rat Parkinsonâ€™s disease model indicates alterations in the enteric nervous system and the gut microbiome. <i>Neurogastroenterology and Motility</i> , 2020, 32, e13726. | 3.0 | 61 |
| 70 | The Potential Impact of Probiotics on the Gut Microbiome of Athletes. <i>Nutrients</i> , 2019, 11, 2270. | 4.1 | 55 |
| 71 | Evaluation of iterative alignment algorithms for multiple alignment. <i>Bioinformatics</i> , 2005, 21, 1408-1414. | 4.1 | 52 |
| 72 | High-Throughput Sequence-Based Analysis of the Intestinal Microbiota of Weanling Pigs Fed Genetically Modified MON810 Maize Expressing <i>Bacillus thuringiensis</i> Cry1Ab (Bt Maize) for 31 Days. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4217-4224. | 3.1 | 52 |

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|----|---|-----|-----------|
| 73 | The changing face of dairy starter culture research: From genomics to economics. <i>International Journal of Dairy Technology</i> , 2010, 63, 149-170. | 2.8 | 50 |
| 74 | Genome analysis of the <i>Clostridium difficile</i> phage ϕ CD6356, a temperate phage of the Siphoviridae family. <i>Gene</i> , 2010, 462, 34-43. | 2.2 | 50 |
| 75 | Fate and efficacy of lacticin 3147-producing <i>Lactococcus lactis</i> in the mammalian gastrointestinal tract. <i>FEMS Microbiology Ecology</i> , 2011, 76, 602-614. | 2.7 | 50 |
| 76 | Nisin J, a Novel Natural Nisin Variant, Is Produced by <i>Staphylococcus capitis</i> Sourced from the Human Skin Microbiota. <i>Journal of Bacteriology</i> , 2020, 202, . | 2.2 | 48 |
| 77 | Moderate-intensity aerobic and resistance exercise is safe and favorably influences body composition in patients with quiescent Inflammatory Bowel Disease: a randomized controlled cross-over trial. <i>BMC Gastroenterology</i> , 2019, 19, 29. | 2.0 | 47 |
| 78 | Bactofencin A, a New Type of Cationic Bacteriocin with Unusual Immunity. <i>MBio</i> , 2013, 4, e00498-13. | 4.1 | 46 |
| 79 | Influence of GABA and GABA-producing <i>Lactobacillus brevis</i> DPC 6108 on the development of diabetes in a streptozotocin rat model. <i>Beneficial Microbes</i> , 2016, 7, 409-420. | 2.4 | 46 |
| 80 | A new phage on the "Mozzarella" block: Bacteriophage 5093 shares a low level of homology with other <i>Streptococcus thermophilus</i> phages. <i>International Dairy Journal</i> , 2011, 21, 963-969. | 3.0 | 45 |
| 81 | Porcine Feed Efficiency-Associated Intestinal Microbiota and Physiological Traits: Finding Consistent Cross-Locational Biomarkers for Residual Feed Intake. <i>MSystems</i> , 2019, 4, . | 3.8 | 45 |
| 82 | 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 |
| 83 | Influence of the Intestinal Microbiota on Colonization Resistance to <i>Salmonella</i> and the Shedding Pattern of Naturally Exposed Pigs. <i>MSystems</i> , 2019, 4, . | 3.8 | 40 |
| 84 | High-throughput DNA sequencing to survey bacterial histidine and tyrosine decarboxylases in raw milk cheeses. <i>BMC Microbiology</i> , 2015, 15, 266. | 3.3 | 39 |
| 85 | The Effect of Dietary Supplementation with Spent Cider Yeast on the Swine Distal Gut Microbiome. <i>PLoS ONE</i> , 2013, 8, e75714. | 2.5 | 37 |
| 86 | Genome of a virulent bacteriophage Lb338-1 that lyses the probiotic <i>Lactobacillus paracasei</i> cheese strain. <i>Gene</i> , 2009, 448, 29-39. | 2.2 | 36 |
| 87 | Marine <i>Pseudovibrio</i> sp. as a Novel Source of Antimicrobials. <i>Marine Drugs</i> , 2014, 12, 5916-5929. | 4.6 | 36 |
| 88 | Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the <i>Pseudovibrio</i> Genus. <i>Frontiers in Microbiology</i> , 2016, 7, 387. | 3.5 | 36 |
| 89 | A pilot study demonstrating the altered gut microbiota functionality in stable adults with Cystic Fibrosis. <i>Scientific Reports</i> , 2017, 7, 6685. | 3.3 | 35 |
| 90 | The Effect of Feeding Bt MON810 Maize to Pigs for 110 Days on Intestinal Microbiota. <i>PLoS ONE</i> , 2012, 7, e33668. | 2.5 | 35 |

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|-----|--|-----|-----------|
| 91 | The bacteriocin lactofensin A subtly modulates gut microbial populations. <i>Anaerobe</i> , 2016, 40, 41-49. | 2.1 | 34 |
| 92 | Evaluation of methods for the reduction of contaminating host reads when performing shotgun metagenomic sequencing of the milk microbiome. <i>Scientific Reports</i> , 2020, 10, 21665. | 3.3 | 33 |
| 93 | Gut microbiota: implications for sports and exercise medicine. <i>British Journal of Sports Medicine</i> , 2017, 51, 700-701. | 6.7 | 31 |
| 94 | Formicin – a novel broad-spectrum two-component lantibiotic produced by <i>Bacillus paralicheniformis</i> APC 1576. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1662-1671. | 1.8 | 31 |
| 95 | Preparation of a standardised faecal slurry for ex-vivo microbiota studies which reduces inter-individual donor bias. <i>Journal of Microbiological Methods</i> , 2016, 129, 109-116. | 1.6 | 29 |
| 96 | <i>Miscanthus</i> biochar promotes growth of spring barley and shifts bacterial community structures including phosphorus and sulfur mobilizing bacteria. <i>Pedobiologia</i> , 2016, 59, 195-202. | 1.2 | 28 |
| 97 | pEOC01: A plasmid from <i>Pediococcus acidilactici</i> which encodes an identical streptomycin resistance (aadE) gene to that found in <i>Campylobacter jejuni</i> . <i>Plasmid</i> , 2007, 58, 115-126. | 1.4 | 25 |
| 98 | Characterisation of single nucleotide polymorphisms identified in the bovine lactoferrin gene sequences across a range of dairy cow breeds. <i>Biochimie</i> , 2009, 91, 68-75. | 2.6 | 24 |
| 99 | Re: Gut microbiota depletion from early adolescence in mice: Implications for brain and behaviour. <i>Brain, Behavior, and Immunity</i> , 2015, 50, 335-336. | 4.1 | 24 |
| 100 | Relatedness between the two-component lantibiotics lactacin 3147 and staphylococcin C55 based on structure, genetics and biological activity. <i>BMC Microbiology</i> , 2007, 7, 24. | 3.3 | 23 |
| 101 | In silico analysis of Ardmore, a novel mycobacteriophage isolated from soil. <i>Gene</i> , 2010, 453, 9-23. | 2.2 | 22 |
| 102 | Correlation of rRNA gene amplicon pyrosequencing and bacterial culture for microbial compositional analysis of faecal samples from elderly Irish subjects. <i>Journal of Applied Microbiology</i> , 2011, 111, 467-473. | 3.1 | 21 |
| 103 | “Microbes in sport” – The potential role of the gut microbiota in athlete health and performance. <i>British Journal of Sports Medicine</i> , 2017, 51, 698-699. | 6.7 | 21 |
| 104 | Next-Generation Food Research: Use of Meta-Omic Approaches for Characterizing Microbial Communities Along the Food Chain. <i>Annual Review of Food Science and Technology</i> , 2022, 13, 361-384. | 9.9 | 21 |
| 105 | Genome sequence of the phage clP1, which infects the beer spoilage bacterium <i>Pediococcus damnosus</i> . <i>Gene</i> , 2012, 504, 53-63. | 2.2 | 18 |
| 106 | More than a gut feeling: What is the role of the gastrointestinal tract in female athlete health?. <i>European Journal of Sport Science</i> , 2022, 22, 755-764. | 2.7 | 16 |
| 107 | Sequence-Based Analysis of the Intestinal Microbiota of Sows and Their Offspring Fed Genetically Modified Maize Expressing a Truncated Form of <i>Bacillus thuringiensis</i> Cry1Ab Protein (Bt Maize). <i>Applied and Environmental Microbiology</i> , 2013, 79, 7735-7744. | 3.1 | 15 |
| 108 | Microbiota of Raw Milk and Raw Milk Cheeses. , 2017, , 301-316. | | 15 |

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|-----|---|------|-----------|
| 109 | The effects of sustained fitness improvement on the gut microbiome: A longitudinal, repeated measures caseâ€study approach. <i>Translational Sports Medicine</i> , 2021, 4, 174-192. | 1.1 | 14 |
| 110 | The Lung Microbiome in Young Children with Cystic Fibrosis: A Prospective Cohort Study. <i>Microorganisms</i> , 2021, 9, 492. | 3.6 | 12 |
| 111 | Encapsulated cyclosporine does not change the composition of the human microbiota when assessed ex vivo and in vivo. <i>Journal of Medical Microbiology</i> , 2020, 69, 854-863. | 1.8 | 12 |
| 112 | Metabolic phenotyping of the human microbiome. <i>F1000Research</i> , 2019, 8, 1956. | 1.6 | 12 |
| 113 | Investigating the Role of Diet and Exercise in Gut Microbe-Host Cometabolism. <i>MSystems</i> , 2020, 5, . | 3.8 | 11 |
| 114 | Instances of altered gut microbiomes among Irish cricketers over periods of travel in the lead up to the 2016 World Cup: A sequencing analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 35, 101553. | 3.0 | 11 |
| 115 | Best Practices for Probiotic Research in Athletic and Physically Active Populations: Guidance for Future Randomized Controlled Trials. <i>Frontiers in Nutrition</i> , 2022, 9, 809983. | 3.7 | 11 |
| 116 | <i>Lactobacillus gasseri</i> APC 678 Reduces Shedding of the Pathogen <i>Clostridium difficile</i> in a Murine Model. <i>Frontiers in Microbiology</i> , 2019, 10, 273. | 3.5 | 9 |
| 117 | In vitroâ€in vivo Validation of Stimulatory Effect of Oat Ingredients on Lactobacilli. <i>Pathogens</i> , 2021, 10, 235. | 2.8 | 8 |
| 118 | Seasonality and Geography Have a Greater Influence than the Use of Chlorine-Based Cleaning Agents on the Microbiota of Bulk Tank Raw Milk. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0108121. | 3.1 | 8 |
| 119 | In Vitro and In Silico Based Approaches to Identify Potential Novel Bacteriocins from the Athlete Gut Microbiome of an Elite Athlete Cohort. <i>Microorganisms</i> , 2022, 10, 701. | 3.6 | 8 |
| 120 | Further Identification of Novel Lantibiotic Operons Using LanM-Based Genome Mining. <i>Probiotics and Antimicrobial Proteins</i> , 2011, 3, 27-40. | 3.9 | 7 |
| 121 | Impact of nisin on <i>Clostridioides difficile</i> and microbiota composition in a faecal fermentation model of the human colon. <i>Journal of Applied Microbiology</i> , 2022, 132, 1397-1408. | 3.1 | 7 |
| 122 | Alpha-synuclein alters the faecal viromes of rats in a gut-initiated model of Parkinsonâ€™s disease. <i>Communications Biology</i> , 2021, 4, 1140. | 4.4 | 6 |
| 123 | A Graph-Based Molecular Communications Model Analysis of the Human Gut Bacteriome. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 3567-3577. | 6.3 | 5 |
| 124 | Complete Genome Sequence of vB_EcoM_112, a T-Even-Type Bacteriophage Specific for <i>Escherichia coli</i> O157:H7. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 3 |
| 125 | A SAT-Based Approach to Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2003, , 940-944. | 1.3 | 3 |
| 126 | Author response: linking lifestyle and microbes. <i>Gut</i> , 2015, 64, 520.1-520. | 12.1 | 2 |

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|-----|---|-----|-----------|
| 127 | The metabolic role of the microbiota. <i>Clinical Liver Disease</i> , 2015, 5, 91-93. | 2.1 | 2 |
| 128 | Infographic. Athlete health and performance: no guts no glory. <i>British Journal of Sports Medicine</i> , 2020, 54, 250-250. | 6.7 | 1 |
| 129 | Binding Process Analysis of Bacterial-based AND Logic Gates. , 2021, , . | | 1 |
| 130 | Prospective case-control study describing the lower airway microbiome in pre-school children with cystic fibrosis. , 2018, , . | | 1 |
| 131 | Identification of Gut Bacteria such as <i>Lactobacillus johnsonii</i> that Disseminate to Systemic Tissues of Wild Type and MyD88 ^{-/-} Mice. <i>Gut Microbes</i> , 2022, 14, 2007743. | 9.8 | 1 |
| 132 | 295: Causes of massive obstetric haemorrhage and outcomes of medical and surgical management strategies. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, S93. | 1.3 | 0 |
| 133 | Gut Microbiology – A Relatively Unexplored Domain. , 2018, , 629-648. | | 0 |
| 134 | Draft Genome Sequence of <i>Bacillus thuringiensis</i> DPC6431, Producer of the Bacteriocin Thuricin CD. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.6 | 0 |