

Alan Walker

List of Publications by Citations

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89
papers

11,387
citations

43
h-index

106
g-index

110
ext. papers

14,508
ext. citations

11
avg, IF

6.25
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 89 | Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. <i>BMC Biology</i> , 2014 , 12, 87 | 7.3 | 1745 |
| 88 | Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011 , 5, 220-30 | 11.9 | 1081 |
| 87 | Salmonella enterica serovar typhimurium exploits inflammation to compete with the intestinal microbiota. <i>PLoS Biology</i> , 2007 , 5, 2177-89 | 9.7 | 736 |
| 86 | Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017 , 35, 833-844 | 44.5 | 643 |
| 85 | pH and peptide supply can radically alter bacterial populations and short-chain fatty acid ratios within microbial communities from the human colon. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 3692-700 | 4.8 | 485 |
| 84 | High-throughput clone library analysis of the mucosa-associated microbiota reveals dysbiosis and differences between inflamed and non-inflamed regions of the intestine in inflammatory bowel disease. <i>BMC Microbiology</i> , 2011 , 11, 7 | 4.5 | 455 |
| 83 | Targeted restoration of the intestinal microbiota with a simple, defined bacteriotherapy resolves relapsing <i>Clostridium difficile</i> disease in mice. <i>PLoS Pathogens</i> , 2012 , 8, e1002995 | 7.6 | 403 |
| 82 | Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. <i>Nature Genetics</i> , 2013 , 45, 450-5, 455e1 | 36.3 | 366 |
| 81 | Intestinal colonization resistance. <i>Immunology</i> , 2013 , 138, 1-11 | 7.8 | 323 |
| 80 | Gut inflammation can boost horizontal gene transfer between pathogenic and commensal Enterobacteriaceae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1269-74 | 11.5 | 277 |
| 79 | Antibiotic treatment of <i>clostridium difficile</i> carrier mice triggers a supershedder state, spore-mediated transmission, and severe disease in immunocompromised hosts. <i>Infection and Immunity</i> , 2009 , 77, 3661-9 | 3.7 | 265 |
| 78 | The Intestinal Microbiota Contributes to the Ability of Helminths to Modulate Allergic Inflammation. <i>Immunity</i> , 2015 , 43, 998-1010 | 32.3 | 260 |
| 77 | The transcription factor T-bet regulates intestinal inflammation mediated by interleukin-7 receptor+ innate lymphoid cells. <i>Immunity</i> , 2012 , 37, 674-84 | 32.3 | 244 |
| 76 | Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018 , 9, 870 | 17.4 | 237 |
| 75 | Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016 , 14, 3 | 7.3 | 214 |
| 74 | Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , 2007 , 9, 667-79 | 5.2 | 197 |
| 73 | The impact of different DNA extraction kits and laboratories upon the assessment of human gut microbiota composition by 16S rRNA gene sequencing. <i>PLoS ONE</i> , 2014 , 9, e88982 | 3.7 | 177 |

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| 72 | Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. <i>ISME Journal</i> , 2011 , 5, 780-91 | 11.9 | 177 |
| 71 | 16S rRNA gene-based profiling of the human infant gut microbiota is strongly influenced by sample processing and PCR primer choice. <i>Microbiome</i> , 2015 , 3, 26 | 16.6 | 153 |
| 70 | Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <i>Genome Biology</i> , 2014 , 15, R76 | 18.3 | 150 |
| 69 | Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014 , 22, 267-74 | 12.4 | 148 |
| 68 | Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. <i>Nature Biotechnology</i> , 2019 , 37, 953-961 | 44.5 | 146 |
| 67 | Patent human infections with the whipworm, <i>Trichuris trichiura</i> , are not associated with alterations in the faecal microbiota. <i>PLoS ONE</i> , 2013 , 8, e76573 | 3.7 | 118 |
| 66 | Bacterial microbiota of the upper respiratory tract and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 826-834.e13 | 11.5 | 117 |
| 65 | Therapeutic modulation of intestinal dysbiosis. <i>Pharmacological Research</i> , 2013 , 69, 75-86 | 10.2 | 113 |
| 64 | Dietary Uncoupling of Gut Microbiota and Energy Harvesting from Obesity and Glucose Tolerance in Mice. <i>Cell Reports</i> , 2017 , 21, 1521-1533 | 10.6 | 113 |
| 63 | The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008 , 10, 3275-83 | 5.2 | 109 |
| 62 | Molecular diversity, cultivation, and improved detection by fluorescent in situ hybridization of a dominant group of human gut bacteria related to <i>Roseburia</i> spp. or <i>Eubacterium rectale</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6371-6 | 4.8 | 96 |
| 61 | Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. <i>Environmental Microbiology</i> , 2016 , 18, 2214-25 | 5.2 | 86 |
| 60 | The bacteriology of pouchitis: a molecular phylogenetic analysis using 16S rRNA gene cloning and sequencing. <i>Annals of Surgery</i> , 2010 , 252, 90-8 | 7.8 | 85 |
| 59 | Review article: faecal transplantation therapy for gastrointestinal disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2011 , 34, 409-15 | 6.1 | 77 |
| 58 | A non-endoscopic device to sample the oesophageal microbiota: a case-control study. <i>The Lancet Gastroenterology and Hepatology</i> , 2017 , 2, 32-42 | 18.8 | 72 |
| 57 | Gut microbiota trajectory in early life may predict development of celiac disease. <i>Microbiome</i> , 2018 , 6, 36 | 16.6 | 69 |
| 56 | Respiratory microbiota resistance and resilience to pulmonary exacerbation and subsequent antimicrobial intervention. <i>ISME Journal</i> , 2016 , 10, 1081-91 | 11.9 | 68 |
| 55 | Variable alterations of the microbiota, without metabolic or immunological change, following faecal microbiota transplantation in patients with chronic pouchitis. <i>Scientific Reports</i> , 2015 , 5, 12955 | 4.9 | 63 |

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| 54 | Microbiology. Fighting obesity with bacteria. <i>Science</i> , 2013 , 341, 1069-70 | 33.3 | 63 |
| 53 | TLR signaling modulates side effects of anticancer therapy in the small intestine. <i>Journal of Immunology</i> , 2015 , 194, 1983-95 | 5.3 | 62 |
| 52 | A common genomic framework for a diverse assembly of plasmids in the symbiotic nitrogen fixing bacteria. <i>PLoS ONE</i> , 2008 , 3, e2567 | 3.7 | 57 |
| 51 | Studies on the effect of system retention time on bacterial populations colonizing a three-stage continuous culture model of the human large gut using FISH techniques. <i>FEMS Microbiology Ecology</i> , 2006 , 55, 299-310 | 4.3 | 53 |
| 50 | The Ecological Dynamics of Fecal Contamination and Salmonella Typhi and Salmonella Paratyphi A in Municipal Kathmandu Drinking Water. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004346 | 4.8 | 51 |
| 49 | Interleukin 6 Increases Production of Cytokines by Colonic Innate Lymphoid Cells in Mice and Patients With Chronic Intestinal Inflammation. <i>Gastroenterology</i> , 2015 , 149, 456-67.e15 | 13.3 | 50 |
| 48 | Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader <i>Ruminococcus bromii</i> . <i>Environmental Microbiology</i> , 2018 , 20, 324-336 | 5.2 | 46 |
| 47 | Lung function and microbiota diversity in cystic fibrosis. <i>Microbiome</i> , 2020 , 8, 45 | 16.6 | 44 |
| 46 | Assessment of the influence of intrinsic environmental and geographical factors on the bacterial ecology of pit latrines. <i>Microbial Biotechnology</i> , 2016 , 9, 209-23 | 6.3 | 41 |
| 45 | Comparing the microbiota of the cystic fibrosis lung and human gut. <i>Gut Microbes</i> , 2010 , 1, 85-93 | 8.8 | 40 |
| 44 | Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic <i>Escherichia coli</i> and subsequent ciprofloxacin treatment. <i>BMC Genomics</i> , 2016 , 17, 440 | 4.5 | 38 |
| 43 | Enhanced susceptibility to <i>Citrobacter rodentium</i> infection in microRNA-155-deficient mice. <i>Infection and Immunity</i> , 2013 , 81, 723-32 | 3.7 | 34 |
| 42 | Lung infections in cystic fibrosis: deriving clinical insight from microbial complexity. <i>Expert Review of Molecular Diagnostics</i> , 2010 , 10, 187-96 | 3.8 | 33 |
| 41 | Food additives: Assessing the impact of exposure to permitted emulsifiers on bowel and metabolic health - introducing the FADiets study. <i>Nutrition Bulletin</i> , 2019 , 44, 329-349 | 3.5 | 33 |
| 40 | Diet induced obesity is independent of metabolic endotoxemia and TLR4 signalling, but markedly increases hypothalamic expression of the acute phase protein, SerpinA3N. <i>Scientific Reports</i> , 2018 , 8, 15648 | 4.9 | 33 |
| 39 | The impact of the Fungus-Host-Microbiota interplay upon <i>Candida albicans</i> infections: current knowledge and new perspectives. <i>FEMS Microbiology Reviews</i> , 2021 , 45, | 15.1 | 31 |
| 38 | The Impact of NOD2 Variants on Fecal Microbiota in Crohn's Disease and Controls Without Gastrointestinal Disease. <i>Inflammatory Bowel Diseases</i> , 2018 , 24, 583-592 | 4.5 | 28 |
| 37 | Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020 , 21, 138 | 18.3 | 27 |

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| 36 | Time between collection and storage significantly influences bacterial sequence composition in sputum samples from cystic fibrosis respiratory infections. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3011-6 | 9.7 | 27 |
| 35 | Exclusive enteral nutrition mediates gut microbial and metabolic changes that are associated with remission in children with Crohn's disease. <i>Scientific Reports</i> , 2020 , 10, 18879 | 4.9 | 24 |
| 34 | Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 701 | 4.5 | 22 |
| 33 | Chemokine (C-C Motif) Receptor 2 Mediates Dendritic Cell Recruitment to the Human Colon but Is Not Responsible for Differences Observed in Dendritic Cell Subsets, Phenotype, and Function Between the Proximal and Distal Colon. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016 , 2, 22-39, e5 | 7.9 | 22 |
| 32 | 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, 862-77 | 4.1 | 22 |
| 31 | Bayesian estimation of bacterial community composition from 454 sequencing data. <i>Nucleic Acids Research</i> , 2012 , 40, 5240-9 | 20.1 | 22 |
| 30 | Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020 , 5, | 7.6 | 22 |
| 29 | Dietary fibers inhibit obesity in mice, but host responses in the cecum and liver appear unrelated to fiber-specific changes in cecal bacterial taxonomic composition. <i>Scientific Reports</i> , 2018 , 8, 15566 | 4.9 | 22 |
| 28 | Colitis susceptibility in mice with reactive oxygen species deficiency is mediated by mucus barrier and immune defense defects. <i>Mucosal Immunology</i> , 2019 , 12, 1316-1326 | 9.2 | 21 |
| 27 | Implications of multiple freeze-thawing on respiratory samples for culture-independent analyses. <i>Journal of Cystic Fibrosis</i> , 2015 , 14, 464-7 | 4.1 | 20 |
| 26 | Survey of culture, goldengate assay, universal biosensor assay, and 16S rRNA Gene sequencing as alternative methods of bacterial pathogen detection. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 3263-9 | 9.7 | 20 |
| 25 | Microbiota that affect risk for shigellosis in children in low-income countries. <i>Emerging Infectious Diseases</i> , 2015 , 21, 242-50 | 10.2 | 20 |
| 24 | Relative abundance of the <i>Prevotella</i> genus within the human gut microbiota of elderly volunteers determines the inter-individual responses to dietary supplementation with wheat bran arabinoxylan-oligosaccharides. <i>BMC Microbiology</i> , 2020 , 20, 283 | 4.5 | 18 |
| 23 | Reagent contamination can critically impact sequence-based microbiome analyses | | 16 |
| 22 | Application of the dynamic gastrointestinal simulator (simgi) to assess the impact of probiotic supplementation in the metabolism of grape polyphenols. <i>Food Research International</i> , 2020 , 129, 108790 | 7 | 16 |
| 21 | Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019 , 95, | 4.3 | 16 |
| 20 | Studying the Human Microbiota. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 902, 5-32 | 3.6 | 14 |
| 19 | Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019 , 1, 16 | 4.1 | 12 |

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|----|--|------|----|
| 18 | Faecal matters. <i>Nature Reviews Microbiology</i> , 2006 , 4, 572-3 | 22.2 | 10 |
| 17 | The genomic and proteomic landscape of the rumen microbiome revealed by comprehensive genome-resolved metagenomics | | 9 |
| 16 | The environmental stress sensitivities of pathogenic <i>Candida</i> species, including <i>Candida auris</i> , and implications for their spread in the hospital setting. <i>Medical Mycology</i> , 2020 , 58, 744-755 | 3.9 | 8 |
| 15 | Objections to the proposed reclassification of <i>Eubacterium rectale</i> as <i>Agathobacter rectalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016 , 66, 2106 | 2.2 | 7 |
| 14 | A Lot on Your Plate? Well-to-Well Contamination as an Additional Confounder in Microbiome Sequence Analyses. <i>MSystems</i> , 2019 , 4, | 7.6 | 6 |
| 13 | Genome watch: probiotics stick it to the man. <i>Nature Reviews Microbiology</i> , 2009 , 7, 843 | 22.2 | 5 |
| 12 | ARK: Aggregation of Reads by K-Means for Estimation of Bacterial Community Composition. <i>PLoS ONE</i> , 2015 , 10, e0140644 | 3.7 | 4 |
| 11 | Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria.. <i>Microbial Genomics</i> , 2022 , 8, | 4.4 | 3 |
| 10 | Dietary fibre complexity and its influence on functional groups of the human gut microbiota. <i>Proceedings of the Nutrition Society</i> , 1-27 | 2.9 | 3 |
| 9 | TPL-2 restricts Ccl24-dependent immunity to <i>Heligmosomoides polygyrus</i> . <i>PLoS Pathogens</i> , 2017 , 13, e1006536 | 7.6 | 2 |
| 8 | gen. nov., sp. nov., a bile-resistant bacterium from human bile with autolytic behavior. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021 , 71, | 2.2 | 2 |
| 7 | The Human Microbiota and Pathogen Interactions 2015 , 347-356 | | 1 |
| 6 | Whole Genome Amplification of Single Bacterial Cells. <i>Springer Protocols</i> , 2015 , 29-41 | 0.3 | 1 |
| 5 | Intestinal Microbiology and Ecology in Inflammatory Bowel Disease 2012 , 85-95 | | 1 |
| 4 | Higher total faecal short chain fatty concentrations correlate with increasing proportions of butyrate and decreasing proportions of branched chain fatty acids across multiple human studies 1-23 | | 1 |
| 3 | Deep-sea striving. <i>Nature Reviews Microbiology</i> , 2013 , 11, 364 | 22.2 | 0 |
| 2 | Ileal Pouch Microbial Diversity. <i>Annals of Surgery</i> , 2011 , 254, 669-670 | 7.8 | |
| 1 | Studying the microbiome and its complexities: an interview with Alan Walker. <i>BMC Biology</i> , 2018 , 16, 134 | 7.3 | |

