

Alan Walker

List of Publications by Year in descending order

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103
papers

16,438
citations

41344

49
h-index

34986

98
g-index

110
all docs

110
docs citations

110
times ranked

23923
citing authors

#	ARTICLE	IF	CITATIONS
1	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. BMC Biology, 2014, 12, 87.	3.8	2,677
2	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. ISME Journal, 2011, 5, 220-230.	9.8	1,352
3	Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 2017, 35, 833-844.	17.5	1,196
4	Salmonella enterica Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. PLoS Biology, 2007, 5, e244.	5.6	905
5	pH and Peptide Supply Can Radically Alter Bacterial Populations and Short-Chain Fatty Acid Ratios within Microbial Communities from the Human Colon. Applied and Environmental Microbiology, 2005, 71, 3692-3700.	3.1	596
6	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. BMC Microbiology, 2011, 11, 7.	3.3	596
7	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing Clostridium difficile Disease in Mice. PLoS Pathogens, 2012, 8, e1002995.	4.7	504
8	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. Nature Genetics, 2013, 45, 450-455.	21.4	500
9	Intestinal colonization resistance. Immunology, 2013, 138, 1-11.	4.4	466
10	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. Nature Communications, 2018, 9, 870.	12.8	405
11	Gut inflammation can boost horizontal gene transfer between pathogenic and commensal <i>Enterobacteriaceae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1269-1274.	7.1	398
12	The Intestinal Microbiota Contributes to the Ability of Helminths to Modulate Allergic Inflammation. Immunity, 2015, 43, 998-1010.	14.3	362
13	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. Nature Biotechnology, 2019, 37, 953-961.	17.5	353
14	Antibiotic Treatment of <i>Clostridium difficile</i> Carrier Mice Triggers a Supershedder State, Spore-Mediated Transmission, and Severe Disease in Immunocompromised Hosts. Infection and Immunity, 2009, 77, 3661-3669.	2.2	315
15	Modulation of the human gut microbiota by dietary fibres occurs at the species level. BMC Biology, 2016, 14, 3.	3.8	308
16	The Transcription Factor T-bet Regulates Intestinal Inflammation Mediated by Interleukin-7 Receptor+ Innate Lymphoid Cells. Immunity, 2012, 37, 674-684.	14.3	305
17	Selective colonization of insoluble substrates by human faecal bacteria. Environmental Microbiology, 2007, 9, 667-679.	3.8	238
18	The Impact of Different DNA Extraction Kits and Laboratories upon the Assessment of Human Gut Microbiota Composition by 16S rRNA Gene Sequencing. PLoS ONE, 2014, 9, e88982.	2.5	236

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19	Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. ISME Journal, 2011, 5, 780-791.	9.8	222
20	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. Genome Biology, 2014, 15, R76.	9.6	219
21	16S rRNA gene-based profiling of the human infant gut microbiota is strongly influenced by sample processing and PCR primer choice. Microbiome, 2015, 3, 26.	11.1	208
22	Phylogeny, culturing, and metagenomics of the human gut microbiota. Trends in Microbiology, 2014, 22, 267-274.	7.7	194
23	Dietary Uncoupling of Gut Microbiota and Energy Harvesting from Obesity and Glucose Tolerance in Mice. Cell Reports, 2017, 21, 1521-1533.	6.4	177
24	Bacterial microbiota of the upper respiratory tract and childhood asthma. Journal of Allergy and Clinical Immunology, 2017, 139, 826-834.e13.	2.9	165
25	Patent Human Infections with the Whipworm, <i>Trichuris trichiura</i> , Are Not Associated with Alterations in the Faecal Microbiota. PLoS ONE, 2013, 8, e76573.	2.5	159
26	Therapeutic modulation of intestinal dysbiosis. Pharmacological Research, 2013, 69, 75-86.	7.1	142
27	The impact of the Fungus-Host-Microbiota interplay upon <i>Candida albicans</i> infections: current knowledge and new perspectives. FEMS Microbiology Reviews, 2021, 45, .	8.6	139
28	Lung function and microbiota diversity in cystic fibrosis. Microbiome, 2020, 8, 45.	11.1	138
29	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. Environmental Microbiology, 2008, 10, 3275-3283.	3.8	135
30	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. Environmental Microbiology, 2016, 18, 2214-2225.	3.8	119
31	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> . Applied and Environmental Microbiology, 2006, 72, 6371-6376.	3.1	113
32	A non-endoscopic device to sample the oesophageal microbiota: a case-control study. The Lancet Gastroenterology and Hepatology, 2017, 2, 32-42.	8.1	111
33	Gut microbiota trajectory in early life may predict development of celiac disease. Microbiome, 2018, 6, 36.	11.1	107
34	The Bacteriology of Pouchitis. Annals of Surgery, 2010, 252, 90-98.	4.2	99
35	Fighting Obesity with Bacteria. Science, 2013, 341, 1069-1070.	12.6	98
36	Respiratory microbiota resistance and resilience to pulmonary exacerbation and subsequent antimicrobial intervention. ISME Journal, 2016, 10, 1081-1091.	9.8	92

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37	Review article: faecal transplantation therapy for gastrointestinal disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2011, 34, 409-415.	3.7	86
38	TLR Signaling Modulates Side Effects of Anticancer Therapy in the Small Intestine. <i>Journal of Immunology</i> , 2015, 194, 1983-1995.	0.8	83
39	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.	1.8	80
40	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.	3.8	79
41	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.	3.3	76
42	Assessment of the influence of intrinsic environmental and geographical factors on the bacterial ecology of pit latrines. <i>Microbial Biotechnology</i> , 2016, 9, 209-223.	4.2	76
43	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.	8.8	72
44	Interleukin 6 Increases Production of Cytokines by Colonic Innate Lymphoid Cells in Mice and Patients With Chronic Intestinal Inflammation. <i>Gastroenterology</i> , 2015, 149, 456-467.e15.	1.3	71
45	The Ecological Dynamics of Fecal Contamination and <i>Salmonella Typhi</i> and <i>Salmonella Paratyphi A</i> in Municipal Kathmandu Drinking Water. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004346.	3.0	70
46	A Common Genomic Framework for a Diverse Assembly of Plasmids in the Symbiotic Nitrogen Fixing Bacteria. <i>PLoS ONE</i> , 2008, 3, e2567.	2.5	69
47	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020, 5, .	3.8	67
48	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.	3.3	66
49	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.	2.7	59
50	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.	2.8	55
51	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.	3.3	51
52	Comparing the microbiota of the cystic fibrosis lung and human gut. <i>Gut Microbes</i> , 2010, 1, 85-93.	9.8	47
53	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
54	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.	6.0	44

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55	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, 3011-3016.	3.9	43
56	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.	2.3	43
57	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.	3.3	41
58	Microbial lactate utilisation and the stability of the gut microbiome. <i>Gut Microbiome</i> , 2022, 3, .	3.2	41
59	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.	1.9	40
60	Lung infections in cystic fibrosis: deriving clinical insight from microbial complexity. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 187-196.	3.1	38
61	Single-cell genomics. <i>Nature Reviews Microbiology</i> , 2008, 6, 176-177.	28.6	37
62	Enhanced Susceptibility to <i>Citrobacter rodentium</i> Infection in MicroRNA-155-Deficient Mice. <i>Infection and Immunity</i> , 2013, 81, 723-732.	2.2	35
63	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.	3.3	34
64	Microbiota That Affect Risk for Shigellosis in Children in Low-Income Countries. <i>Emerging Infectious Diseases</i> , 2015, 21, 242-250.	4.3	30
65	Implications of multiple freeze-thawing on respiratory samples for culture-independent analyses. <i>Journal of Cystic Fibrosis</i> , 2015, 14, 464-467.	0.7	29
66	Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019, 1, 16.	3.8	29
67	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	28
68	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.	6.2	28
69	Bayesian estimation of bacterial community composition from 454 sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, 5240-5249.	14.5	27
70	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.	4.5	27
71	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.	0.7	27
72	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, 3263-3269.	3.9	25

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73	Say hello to our little friends. <i>Nature Reviews Microbiology</i> , 2007, 5, 572-573.	28.6	22
74	Studying the Human Microbiota. <i>Advances in Experimental Medicine and Biology</i> , 2016, 902, 5-32.	1.6	20
75	Welcome to the plasmidome. <i>Nature Reviews Microbiology</i> , 2012, 10, 379-379.	28.6	18
76	<i>Ruminococcoides bili</i> 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, .	1.7	13
77	Faecal matters. <i>Nature Reviews Microbiology</i> , 2006, 4, 572-573.	28.6	11
78	Adding genomic 'foliage' to the tree of life. <i>Nature Reviews Microbiology</i> , 2014, 12, 78-78.	28.6	11
79	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	2.0	10
80	Survival Strategies and Metabolic Interactions between <i>Ruminococcus gauvreauii</i> and <i>Ruminococcoides bili</i> , Isolated from Human Bile. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	10
81	A glut from the gut: metagenomics takes a giant step forward. <i>Nature Reviews Microbiology</i> , 2010, 8, 315-315.	28.6	9
82	A Lot on Your Plate? Well-to-Well Contamination as an Additional Confounder in Microbiome Sequence Analyses. <i>MSystems</i> , 2019, 4, .	3.8	9
83	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, 2106-2106.	1.7	9
84	Dietary fibre complexity and its influence on functional groups of the human gut microbiota. <i>Proceedings of the Nutrition Society</i> , 2021, 80, 386-397.	1.0	9
85	Higher total faecal short-chain fatty acid concentrations correlate with increasing proportions of butyrate and decreasing proportions of branched-chain fatty acids across multiple human studies. <i>Gut Microbiome</i> , 2022, 3, .	3.2	8
86	TPL-2 restricts Ccl24-dependent immunity to <i>Heligmosomoides polygyrus</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006536.	4.7	7
87	Does my genome look big in this?. <i>Nature Reviews Microbiology</i> , 2008, 6, 878-879.	28.6	6
88	Gut metagenomics goes viral. <i>Nature Reviews Microbiology</i> , 2010, 8, 841-841.	28.6	6
89	Probiotics stick it to the man. <i>Nature Reviews Microbiology</i> , 2009, 7, 843-843.	28.6	5
90	ARK: Aggregation of Reads by K-Means for Estimation of Bacterial Community Composition. <i>PLoS ONE</i> , 2015, 10, e0140644.	2.5	4

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91	Milk and two oligosaccharides. Nature Reviews Microbiology, 2009, 7, 483-483.	28.6	3
92	This place is big enough for both of us. Nature Reviews Microbiology, 2007, 5, 90-92.	28.6	2
93	Opportunity knocks. Nature Reviews Microbiology, 2008, 6, 652-653.	28.6	2
94	Singled out. Nature Reviews Microbiology, 2011, 9, 485-485.	28.6	1
95	Deep-sea striving. Nature Reviews Microbiology, 2013, 11, 364-364.	28.6	1
96	Whole Genome Amplification of Single Bacterial Cells. Springer Protocols, 2015, , 29-41.	0.3	1
97	The Human Microbiota and Pathogen Interactions. , 2015, , 347-356.		1
98	Editorial: further evidence that proton pump inhibitors may impact on the gut microbiota. Alimentary Pharmacology and Therapeutics, 2016, 43, 1104-1105.	3.7	1
99	Intestinal Microbiology and Ecology in Inflammatory Bowel Disease. , 2012, , 85-95.		1
100	It's hip to be square!. Nature Reviews Microbiology, 2007, 5, 400-401.	28.6	0
101	Urbane decay. Nature Reviews Microbiology, 2007, 5, 748-749.	28.6	0
102	Ileal Pouch Microbial Diversity. Annals of Surgery, 2011, 254, 669-670.	4.2	0
103	Studying the microbiome and its complexities: an interview with Alan Walker. BMC Biology, 2018, 16, 134.	3.8	0