

Alan Walker

List of Publications by Year in descending order

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103
papers

16,438
citations

47409

49
h-index

39744

98
g-index

110
all docs

110
docs citations

110
times ranked

26017
citing authors

#	ARTICLE	IF	CITATIONS
1	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
2	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, .	0.8	8
3	Microbial lactate utilisation and the stability of the gut microbiome. <i>Gut Microbiome</i> , 2022, 3, .	0.8	41
4	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, .	1.2	10
5	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, .	3.9	139
6	<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, .	0.8	13
7	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.	0.4	9
8	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.	0.3	27
9	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.	2.9	28
10	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.	1.3	41
11	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020, 5, .	1.7	67
12	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.	1.6	66
13	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.	3.8	72
14	Lung function and microbiota diversity in cystic fibrosis. <i>Microbiome</i> , 2020, 8, 45.	4.9	138
15	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	28
16	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. <i>Nature Biotechnology</i> , 2019, 37, 953-961.	9.4	353
17	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.	1.1	43
18	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.	2.7	44

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19	A Lot on Your Plate? Well-to-Well Contamination as an Additional Confounder in Microbiome Sequence Analyses. <i>MSystems</i> , 2019, 4, .	1.7	9
20	Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019, 1, 16.	1.5	29
21	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.	0.8	80
22	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.	0.9	40
23	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	5.8	405
24	Sporulation capability and amylozyme 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.	1.8	79
25	Gut microbiota trajectory in early life may predict development of celiac disease. <i>Microbiome</i> , 2018, 6, 36.	4.9	107
26	Studying the microbiome and its complexities: an interview with Alan Walker. <i>BMC Biology</i> , 2018, 16, 134.	1.7	0
27	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.	1.6	51
28	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.	1.6	34
29	A non-endoscopic device to sample the oesophageal microbiota: a case-control study. <i>The Lancet Gastroenterology and Hepatology</i> , 2017, 2, 32-42.	3.7	111
30	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017, 35, 833-844.	9.4	1,196
31	Dietary Uncoupling of Gut Microbiota and Energy Harvesting from Obesity and Glucose Tolerance in Mice. <i>Cell Reports</i> , 2017, 21, 1521-1533.	2.9	177
32	Bacterial microbiota of the upper respiratory tract and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 826-834.e13.	1.5	165
33	TPL-2 restricts Ccl24-dependent immunity to <i>Heligmosomoides polygyrus</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006536.	2.1	7
34	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.	1.2	55
35	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. <i>Environmental Microbiology</i> , 2016, 18, 2214-2225.	1.8	119
36	Studying the Human Microbiota. <i>Advances in Experimental Medicine and Biology</i> , 2016, 902, 5-32.	0.8	20

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37	Editorial: further evidence that proton pump inhibitors may impact on the gut microbiota. <i>Alimentary Pharmacology and Therapeutics</i> , 2016, 43, 1104-1105.	1.9	1
38	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.	2.3	27
39	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.	2.0	76
40	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308
41	Respiratory microbiota resistance and resilience to pulmonary exacerbation and subsequent antimicrobial intervention. <i>ISME Journal</i> , 2016, 10, 1081-1091.	4.4	92
42	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.	0.8	9
43	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.	1.3	70
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.	0.6	71
45	Implications of multiple freeze-thawing on respiratory samples for culture-independent analyses. <i>Journal of Cystic Fibrosis</i> , 2015, 14, 464-467.	0.3	29
46	Whole Genome Amplification of Single Bacterial Cells. <i>Springer Protocols</i> , 2015, , 29-41.	0.1	1
47	TLR Signaling Modulates Side Effects of Anticancer Therapy in the Small Intestine. <i>Journal of Immunology</i> , 2015, 194, 1983-1995.	0.4	83
48	The Human Microbiota and Pathogen Interactions. , 2015, , 347-356.		1
49	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.	4.9	208
50	The Intestinal Microbiota Contributes to the Ability of Helminths to Modulate Allergic Inflammation. <i>Immunity</i> , 2015, 43, 998-1010.	6.6	362
51	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.	1.6	76
52	ARK: Aggregation of Reads by K-Means for Estimation of Bacterial Community Composition. <i>PLoS ONE</i> , 2015, 10, e0140644.	1.1	4
53	Microbiota That Affect Risk for Shigellosis in Children in Low-Income Countries. <i>Emerging Infectious Diseases</i> , 2015, 21, 242-250.	2.0	30
54	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.	1.1	236

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55	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <i>Genome Biology</i> , 2014, 15, R76.	13.9	219
56	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. <i>BMC Biology</i> , 2014, 12, 87.	1.7	2,677
57	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014, 22, 267-274.	3.5	194
58	Adding genomic 'foliage' to the tree of life. <i>Nature Reviews Microbiology</i> , 2014, 12, 78-78.	13.6	11
59	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.	1.8	43
60	Fighting Obesity with Bacteria. <i>Science</i> , 2013, 341, 1069-1070.	6.0	98
61	Therapeutic modulation of intestinal dysbiosis. <i>Pharmacological Research</i> , 2013, 69, 75-86.	3.1	142
62	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, 450-455.	9.4	500
63	Intestinal colonization resistance. <i>Immunology</i> , 2013, 138, 1-11.	2.0	466
64	Deep-sea striving. <i>Nature Reviews Microbiology</i> , 2013, 11, 364-364.	13.6	1
65	Enhanced Susceptibility to <i>Citrobacter rodentium</i> Infection in MicroRNA-155-Deficient Mice. <i>Infection and Immunity</i> , 2013, 81, 723-732.	1.0	35
66	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.	1.8	25
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.	1.1	159
68	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.	2.1	504
69	Bayesian estimation of bacterial community composition from 454 sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, 5240-5249.	6.5	27
70	Gut inflammation can boost horizontal gene transfer between pathogenic and commensal <i>Enterobacteriaceae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1269-1274.	3.3	398
71	The Transcription Factor T-bet Regulates Intestinal Inflammation Mediated by Interleukin-7 Receptor+ Innate Lymphoid Cells. <i>Immunity</i> , 2012, 37, 674-684.	6.6	305
72	Welcome to the plasmidome. <i>Nature Reviews Microbiology</i> , 2012, 10, 379-379.	13.6	18

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73	Fibrinogenâ€binding and plateletâ€aggregation activities of a <i>Lactobacillus salivarius</i> septicaemia isolate are mediated by a novel fibrinogenâ€binding protein. <i>Molecular Microbiology</i> , 2012, 85, 862-877.	1.2	45
74	Intestinal Microbiology and Ecology in Inflammatory Bowel Disease. , 2012, , 85-95.		1
75	Ileal Pouch Microbial Diversity. <i>Annals of Surgery</i> , 2011, 254, 669-670.	2.1	0
76	Review article: faecal transplantation therapy for gastrointestinal disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2011, 34, 409-415.	1.9	86
77	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011, 5, 220-230.	4.4	1,352
78	Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. <i>ISME Journal</i> , 2011, 5, 780-791.	4.4	222
79	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.	1.3	596
80	Singled out. <i>Nature Reviews Microbiology</i> , 2011, 9, 485-485.	13.6	1
81	The Bacteriology of Pouchitis. <i>Annals of Surgery</i> , 2010, 252, 90-98.	2.1	99
82	A glut from the gut: metagenomics takes a giant step forward. <i>Nature Reviews Microbiology</i> , 2010, 8, 315-315.	13.6	9
83	Gut metagenomics goes viral. <i>Nature Reviews Microbiology</i> , 2010, 8, 841-841.	13.6	6
84	Lung infections in cystic fibrosis: deriving clinical insight from microbial complexity. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 187-196.	1.5	38
85	Comparing the microbiota of the cystic fibrosis lung and human gut. <i>Gut Microbes</i> , 2010, 1, 85-93.	4.3	47
86	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, 3661-3669.	1.0	315
87	Milk and two oligosaccharides. <i>Nature Reviews Microbiology</i> , 2009, 7, 483-483.	13.6	3
88	Probiotics stick it to the man. <i>Nature Reviews Microbiology</i> , 2009, 7, 843-843.	13.6	5
89	Single-cell genomics. <i>Nature Reviews Microbiology</i> , 2008, 6, 176-177.	13.6	37
90	Opportunity knocks. <i>Nature Reviews Microbiology</i> , 2008, 6, 652-653.	13.6	2

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91	Does my genome look big in this?. <i>Nature Reviews Microbiology</i> , 2008, 6, 878-879.	13.6	6
92	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008, 10, 3275-3283.	1.8	135
93	A Common Genomic Framework for a Diverse Assembly of Plasmids in the Symbiotic Nitrogen Fixing Bacteria. <i>PLoS ONE</i> , 2008, 3, e2567.	1.1	69
94	<i>Salmonella enterica</i> Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e244.	2.6	905
95	This place is big enough for both of us. <i>Nature Reviews Microbiology</i> , 2007, 5, 90-92.	13.6	2
96	It's hip to be square!. <i>Nature Reviews Microbiology</i> , 2007, 5, 400-401.	13.6	0
97	Say hello to our little friends. <i>Nature Reviews Microbiology</i> , 2007, 5, 572-573.	13.6	22
98	Urbane decay. <i>Nature Reviews Microbiology</i> , 2007, 5, 748-749.	13.6	0
99	Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , 2007, 9, 667-679.	1.8	238
100	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.	1.3	59
101	Faecal matters. <i>Nature Reviews Microbiology</i> , 2006, 4, 572-573.	13.6	11
102	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, 6371-6376.	1.4	113
103	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, 3692-3700.	1.4	596