

Blair Lawley

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

797
citations

516710

16
h-index

526287

27
g-index

31
all docs

31
docs citations

31
times ranked

1329
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultraviolet-C Irradiation, Heat, and Storage as Potential Methods of Inactivating SARS-CoV-2 and Bacterial Pathogens on Filtering Facepiece Respirators. <i>Pathogens</i> , 2022, 11, 83.	2.8	6
2	Reduced and highly diverse peripheral HIV-1 reservoir in virally suppressed patients infected with non-B HIV-1 strains in Uganda. <i>Retrovirology</i> , 2022, 19, 1.	2.0	5
3	Characterization of the First SARS-CoV-2 Isolates from Aotearoa New Zealand as Part of a Rapid Response to the COVID-19 Pandemic. <i>Viruses</i> , 2022, 14, 366.	3.3	7
4	Rapid Response to SARS-CoV-2 in Aotearoa New Zealand: Implementation of a Diagnostic Test and Characterization of the First COVID-19 Cases in the South Island. <i>Viruses</i> , 2021, 13, 2222.	3.3	4
5	Uncoupling Molecular Testing for SARS-CoV-2 From International Supply Chains. <i>Frontiers in Public Health</i> , 2021, 9, 808751.	2.7	2
6	Using compositional principal component analysis to describe children's gut microbiota in relation to diet and body composition. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 70-78.	4.7	20
7	Substrate Use Prioritization by a Coculture of Five Species of Gut Bacteria Fed Mixtures of Arabinoxylan, Xyloglucan, β -Glucan, and Pectin. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	28
8	Gut bacteria characteristic of the infant microbiota down-regulate inflammatory transcriptional responses in HT-29 cells. <i>Anaerobe</i> , 2020, 61, 102112.	2.1	8
9	Body composition of New Zealand European and Pacific women is associated with lower dietary fibre intake and gut microbiota diversity. <i>Proceedings of the Nutrition Society</i> , 2020, 79, .	1.0	0
10	Ethnic diversity in infant gut microbiota is apparent before the introduction of complementary diets. <i>Gut Microbes</i> , 2020, 11, 1362-1373.	9.8	34
11	Compositional principal component analysis generates gut microbiota profiles that associate with children's diet and body composition. <i>Proceedings of the Nutrition Society</i> , 2020, 79, .	1.0	2
12	Association between the faecal short-chain fatty acid propionate and infant sleep. <i>European Journal of Clinical Nutrition</i> , 2020, 74, 1362-1365.	2.9	25
13	Fecal Microbiotas of Indonesian and New Zealand Children Differ in Complexity and Bifidobacterial Taxa during the First Year of Life. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	18
14	Oral bacteriome of HIV-1 infected children from Rio de Janeiro, Brazil: Next-generation DNA sequencing analysis. <i>Journal of Clinical Periodontology</i> , 2019, 46, 1192-1204.	4.9	9
15	Predictors Linking Obesity and the Gut Microbiome (the PROMISE Study): Protocol and Recruitment Strategy for a Cross-Sectional Study on Pathways That Affect the Gut Microbiome and Its Impact on Obesity. <i>JMIR Research Protocols</i> , 2019, 8, e14529.	1.0	9
16	Gene Sequence Variation in <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Detected in the Fecal Microbiota of Chinese Infants. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	9
17	<i>Bifidobacterium pseudolongum</i> in the Ceca of Rats Fed Hi-Maize Starch Has Characteristics of a Keystone Species in Bifidobacterial Blooms. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	28
18	Mediation Analysis as a Means of Identifying Dietary Components That Differentially Affect the Fecal Microbiota of Infants Weaned by Modified Baby-Led and Traditional Approaches. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	35

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19	SunGold Kiwifruit Supplementation of Individuals with Prediabetes Alters Gut Microbiota and Improves Vitamin C Status, Anthropometric and Clinical Markers. <i>Nutrients</i> , 2018, 10, 895.	4.1	32
20	Analysis of 16S rRNA Gene Amplicon Sequences Using the QIIME Software Package. <i>Methods in Molecular Biology</i> , 2017, 1537, 153-163.	0.9	61
21	Differentiation of <i>Bifidobacterium longum</i> subspecies <i>longum</i> and <i>infantis</i> by quantitative PCR using functional gene targets. <i>PeerJ</i> , 2017, 5, e3375.	2.0	42
22	Why Don't All Infants Have Bifidobacteria in Their Stool?. <i>Frontiers in Microbiology</i> , 2016, 7, 834.	3.5	36
23	Three-year follow-up of a randomised controlled trial to reduce excessive weight gain in the first two years of life: protocol for the POI follow-up study. <i>BMC Public Health</i> , 2016, 16, 771.	2.9	20
24	Bacterial Succession in the Broiler Gastrointestinal Tract. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2399-2410.	3.1	107
25	<i>Lactobacillus reuteri</i> 100-23 Modulates Urea Hydrolysis in the Murine Stomach. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6104-6113.	3.1	25
26	Whole-Transcriptome Shotgun Sequencing (RNA-seq) Screen Reveals Upregulation of Cellobiose and Motility Operons of <i>Lactobacillus ruminis</i> L5 during Growth on Tetrasaccharides Derived from Barley β -Glucan. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5661-5669.	3.1	27
27	Nucleic Acid-based Methods to Assess the Composition and Function of the Bowel Microbiota. <i>Gastroenterology Clinics of North America</i> , 2012, 41, 855-868.	2.2	5
28	A new macrocyclic antibiotic, fidaxomicin (OPT-80), causes less alteration to the bowel microbiota of <i>Clostridium difficile</i> -infected patients than does vancomycin. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3354-3359.	1.8	191