

Trevor D Lawley

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

10,701
citations

76196

40
h-index

138251

58
g-index

70
all docs

70
docs citations

70
times ranked

12729
citing authors

#	ARTICLE	IF	CITATIONS
1	Two microbiota subtypes identified in irritable bowel syndrome with distinct responses to the low FODMAP diet. <i>Gut</i> , 2022, 71, 1821-1830.	6.1	63
2	The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. <i>Cell Host and Microbe</i> , 2022, 30, 124-138.e8.	5.1	59
3	Strain-level characterization of broad host range mobile genetic elements transferring antibiotic resistance from the human microbiome. <i>Nature Communications</i> , 2022, 13, 1445.	5.8	52
4	Identification of gut microbial species linked with disease variability in a widely used mouse model of colitis. <i>Nature Microbiology</i> , 2022, 7, 590-599.	5.9	53
5	Should we modulate the neonatal microbiome and what should be the goal?. <i>Microbiome</i> , 2022, 10, 74.	4.9	6
6	Motherâ€™infant transmission of human microbiota. <i>Current Opinion in Microbiology</i> , 2022, 69, 102173.	2.3	23
7	Massive expansion of human gut bacteriophage diversity. <i>Cell</i> , 2021, 184, 1098-1109.e9.	13.5	331
8	Pangenome analysis reveals genetic isolation in <i>Campylobacter hyointestinalis</i> subspecies adapted to different mammalian hosts. <i>Scientific Reports</i> , 2021, 11, 3431.	1.6	7
9	Identification of bacteria-derived HLA-bound peptides in melanoma. <i>Nature</i> , 2021, 592, 138-143.	13.7	187
10	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. <i>ISME Communications</i> , 2021, 1, .	1.7	228
11	A novel technique capable of taking â€™protectedâ€™™ biopsies for reliable assessment of the distribution of microbiota along the colonic mucosa. <i>Journal of Microbiological Methods</i> , 2021, 185, 106204.	0.7	1
12	Host adaptation in gut Firmicutes is associated with sporulation loss and altered transmission cycle. <i>Genome Biology</i> , 2021, 22, 204.	3.8	25
13	<i>Citrobacter amalonaticus</i> Inhibits the Growth of <i>Citrobacter rodentium</i> in the Gut Lumen. <i>MBio</i> , 2021, 12, e0241021.	1.8	9
14	Gut-educated IgA plasma cells defend the meningeal venous sinuses. <i>Nature</i> , 2020, 587, 472-476.	13.7	167
15	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020, 21, 343-353.	7.0	175
16	Adaptation of host transmission cycle during <i>Clostridium difficile</i> speciation. <i>Nature Genetics</i> , 2019, 51, 1315-1320.	9.4	41
17	High-resolution mapping reveals that microniches in the gastric glands control <i>Helicobacter pylori</i> colonization of the stomach. <i>PLoS Biology</i> , 2019, 17, e3000231.	2.6	72
18	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	13.7	901

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19	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. <i>Nature</i> , 2019, 574, 117-121.	13.7	617
20	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019, 37, 186-192.	9.4	420
21	Culturing of female bladder bacteria reveals an interconnected urogenital microbiota. <i>Nature Communications</i> , 2018, 9, 1557.	5.8	241
22	Commensal Koch's postulates: establishing causation in human microbiota research. <i>Current Opinion in Microbiology</i> , 2018, 42, 47-52.	2.3	84
23	Interleukin-22 promotes phagolysosomal fusion to induce protection against <i>Salmonella enterica</i> Typhimurium in human epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10118-10123.	3.3	33
24	Proteomic identification of Axc, a novel beta-lactamase with carbapenemase activity in a meropenem-resistant clinical isolate of <i>Achromobacter xylosoxidans</i> . <i>Scientific Reports</i> , 2018, 8, 8181.	1.6	10
25	Transmission of the gut microbiota: spreading of health. <i>Nature Reviews Microbiology</i> , 2017, 15, 531-543.	13.6	150
26	Distinct <i>Campylobacter fetus</i> lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <i>Nature Communications</i> , 2017, 8, 1367.	5.8	56
27	Culturing of "unculturable" human microbiota reveals novel taxa and extensive sporulation. <i>Nature</i> , 2016, 533, 543-546.	13.7	958
28	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. <i>Nucleic Acids Research</i> , 2016, 44, D604-D609.	6.5	60
29	A Modified R-Type Bacteriocin Specifically Targeting <i>Clostridium difficile</i> Prevents Colonization of Mice without Affecting Gut Microbiota Diversity. <i>MBio</i> , 2015, 6, .	1.8	115
30	<i>Clostridium sordellii</i> genome analysis reveals plasmid localized toxin genes encoded within pathogenicity loci. <i>BMC Genomics</i> , 2015, 16, 392.	1.2	39
31	Defining the Roles of TcdA and TcdB in Localized Gastrointestinal Disease, Systemic Organ Damage, and the Host Response during <i>Clostridium difficile</i> Infections. <i>MBio</i> , 2015, 6, e00551.	1.8	228
32	Systematic discovery of probiotics. <i>Nature Biotechnology</i> , 2015, 33, 47-48.	9.4	16
33	High-Throughput Analysis of Gene Essentiality and Sporulation in <i>Clostridium difficile</i> . <i>MBio</i> , 2015, 6, e02383.	1.8	157
34	Complete genome sequence of BS49 and draft genome sequence of BS34A, <i>Bacillus subtilis</i> strains carrying Tn916. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-4.	0.7	13
35	Pathogen Resistance Mediated by IL-22 Signaling at the Epithelial-Microbiota Interface. <i>Journal of Molecular Biology</i> , 2015, 427, 3676-3682.	2.0	52
36	Pathogens' Exploitation of the Intestinal Food Web. <i>Cell Host and Microbe</i> , 2014, 16, 703-705.	5.1	7

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37	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. <i>Cell Host and Microbe</i> , 2014, 16, 504-516.	5.1	237
38	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	1.2	145
39	Emerging insights on intestinal dysbiosis during bacterial infections. <i>Current Opinion in Microbiology</i> , 2014, 17, 67-74.	2.3	94
40	Proteomic Comparison of Historic and Recently Emerged Hypervirulent <i>Clostridium difficile</i> Strains. <i>Journal of Proteome Research</i> , 2013, 12, 1151-1161.	1.8	52
41	Infection and immunity from a lifecourse perspective: Life Study Enhancement. <i>Lancet</i> , The, 2013, 382, S35.	6.3	2
42	Murine models to study <i>Clostridium difficile</i> infection and transmission. <i>Anaerobe</i> , 2013, 24, 94-97.	1.0	29
43	Bacteriotherapy for the treatment of intestinal dysbiosis caused by <i>Clostridium difficile</i> infection. <i>Current Opinion in Microbiology</i> , 2013, 16, 596-601.	2.3	41
44	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . <i>Nature Genetics</i> , 2013, 45, 109-113.	9.4	669
45	Intestinal colonization resistance. <i>Immunology</i> , 2013, 138, 1-11.	2.0	466
46	The <i>agr</i> Locus Regulates Virulence and Colonization Genes in <i>Clostridium difficile</i> 027. <i>Journal of Bacteriology</i> , 2013, 195, 3672-3681.	1.0	99
47	Global Analysis of the Sporulation Pathway of <i>Clostridium difficile</i> . <i>PLoS Genetics</i> , 2013, 9, e1003660.	1.5	219
48	SpoIVA and SipL Are <i>Clostridium difficile</i> Spore Morphogenetic Proteins. <i>Journal of Bacteriology</i> , 2013, 195, 1214-1225.	1.0	129
49	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
50	The <i>Clostridium difficile</i> spo0A Gene Is a Persistence and Transmission Factor. <i>Infection and Immunity</i> , 2012, 80, 2704-2711.	1.0	324
51	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7527-7532.	3.3	346
52	Use of Purified <i>Clostridium difficile</i> Spores To Facilitate Evaluation of Health Care Disinfection Regimens. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6895-6900.	1.4	120
53	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. <i>Journal of Bacteriology</i> , 2009, 191, 5377-5386.	1.0	210
54	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

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55	Comparative genome and phenotypic analysis of <i>Clostridium difficile</i> O27 strains provides insight into the evolution of a hypervirulent bacterium. <i>Genome Biology</i> , 2009, 10, R102.	13.9	431
56	Host Transmission of <i>Salmonella enterica</i> Serovar Typhimurium Is Controlled by Virulence Factors and Indigenous Intestinal Microbiota. <i>Infection and Immunity</i> , 2008, 76, 403-416.	1.0	263
57	Interaction between the co-inherited TraG coupling protein and the TraJ membrane-associated protein of the H-plasmid conjugative DNA transfer system resembles chromosomal DNA translocases. <i>Microbiology (United Kingdom)</i> , 2007, 153, 428-441.	0.7	14
58	Genome-Wide Screen for <i>Salmonella</i> Genes Required for Long-Term Systemic Infection of the Mouse. <i>PLoS Pathogens</i> , 2006, 2, e11.	2.1	300
59	The Childhood Acute Illness and Nutrition (CHAIN) network nested case-cohort study protocol: a multi-omics approach to understanding mortality among children in sub-Saharan Africa and South Asia. <i>Gates Open Research</i> , 0, 6, 77.	2.0	1