

Trevor D Lawley

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

10,701
citations

76326

40
h-index

138484

58
g-index

70
all docs

70
docs citations

70
times ranked

12729
citing authors

#	ARTICLE	IF	CITATIONS
1	Culturing of "unculturable"™ human microbiota reveals novel taxa and extensive sporulation. <i>Nature</i> , 2016, 533, 543-546.	27.8	958
2	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	27.8	901
3	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . <i>Nature Genetics</i> , 2013, 45, 109-113.	21.4	669
4	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. <i>Nature</i> , 2019, 574, 117-121.	27.8	617
5	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.	4.7	504
6	Intestinal colonization resistance. <i>Immunology</i> , 2013, 138, 1-11.	4.4	466
7	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.	9.6	431
8	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019, 37, 186-192.	17.5	420
9	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.	7.1	346
10	Massive expansion of human gut bacteriophage diversity. <i>Cell</i> , 2021, 184, 1098-1109.e9.	28.9	331
11	The <i>Clostridium difficile</i> <i>spo0A</i> Gene Is a Persistence and Transmission Factor. <i>Infection and Immunity</i> , 2012, 80, 2704-2711.	2.2	324
12	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.	2.2	315
13	Genome-Wide Screen for <i>Salmonella</i> Genes Required for Long-Term Systemic Infection of the Mouse. <i>PLoS Pathogens</i> , 2006, 2, e11.	4.7	300
14	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.	2.2	263
15	Culturing of female bladder bacteria reveals an interconnected urogenital microbiota. <i>Nature Communications</i> , 2018, 9, 1557.	12.8	241
16	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. <i>Cell Host and Microbe</i> , 2014, 16, 504-516.	11.0	237
17	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.	4.1	228
18	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. <i>ISME Communications</i> , 2021, 1, .	4.2	228

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19	Global Analysis of the Sporulation Pathway of <i>Clostridium difficile</i> . <i>PLoS Genetics</i> , 2013, 9, e1003660.	3.5	219
20	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. <i>Journal of Bacteriology</i> , 2009, 191, 5377-5386.	2.2	210
21	Identification of bacteria-derived HLA-bound peptides in melanoma. <i>Nature</i> , 2021, 592, 138-143.	27.8	187
22	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020, 21, 343-353.	14.5	175
23	Gut-educated IgA plasma cells defend the meningeal venous sinuses. <i>Nature</i> , 2020, 587, 472-476.	27.8	167
24	High-Throughput Analysis of Gene Essentiality and Sporulation in <i>Clostridium difficile</i> . <i>MBio</i> , 2015, 6, e02383.	4.1	157
25	Transmission of the gut microbiota: spreading of health. <i>Nature Reviews Microbiology</i> , 2017, 15, 531-543.	28.6	150
26	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	2.8	145
27	SpoIVA and SipL Are <i>Clostridium difficile</i> Spore Morphogenetic Proteins. <i>Journal of Bacteriology</i> , 2013, 195, 1214-1225.	2.2	129
28	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.	3.1	120
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, .	4.1	115
30	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.	2.2	99
31	Emerging insights on intestinal dysbiosis during bacterial infections. <i>Current Opinion in Microbiology</i> , 2014, 17, 67-74.	5.1	94
32	Commensal Koch's postulates: establishing causation in human microbiota research. <i>Current Opinion in Microbiology</i> , 2018, 42, 47-52.	5.1	84
33	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.	5.6	72
34	Two microbiota subtypes identified in irritable bowel syndrome with distinct responses to the low FODMAP diet. <i>Gut</i> , 2022, 71, 1821-1830.	12.1	63
35	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. <i>Nucleic Acids Research</i> , 2016, 44, D604-D609.	14.5	60
36	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.	11.0	59

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37	Distinct <i>Campylobacter fetus</i> lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <i>Nature Communications</i> , 2017, 8, 1367.	12.8	56
38	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.	13.3	53
39	Proteomic Comparison of Historic and Recently Emerged Hypervirulent <i>Clostridium difficile</i> Strains. <i>Journal of Proteome Research</i> , 2013, 12, 1151-1161.	3.7	52
40	Pathogen Resistance Mediated by IL-22 Signaling at the Epithelial-Microbiota Interface. <i>Journal of Molecular Biology</i> , 2015, 427, 3676-3682.	4.2	52
41	Strain-level characterization of broad host range mobile genetic elements transferring antibiotic resistance from the human microbiome. <i>Nature Communications</i> , 2022, 13, 1445.	12.8	52
42	Bacteriotherapy for the treatment of intestinal dysbiosis caused by <i>Clostridium difficile</i> infection. <i>Current Opinion in Microbiology</i> , 2013, 16, 596-601.	5.1	41
43	Adaptation of host transmission cycle during <i>Clostridium difficile</i> speciation. <i>Nature Genetics</i> , 2019, 51, 1315-1320.	21.4	41
44	<i>Clostridium sordellii</i> genome analysis reveals plasmid localized toxin genes encoded within pathogenicity loci. <i>BMC Genomics</i> , 2015, 16, 392.	2.8	39
45	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.	7.1	33
46	Murine models to study <i>Clostridium difficile</i> infection and transmission. <i>Anaerobe</i> , 2013, 24, 94-97.	2.1	29
47	Host adaptation in gut Firmicutes is associated with sporulation loss and altered transmission cycle. <i>Genome Biology</i> , 2021, 22, 204.	8.8	25
48	Mother-infant transmission of human microbiota. <i>Current Opinion in Microbiology</i> , 2022, 69, 102173.	5.1	23
49	Systematic discovery of probiotics. <i>Nature Biotechnology</i> , 2015, 33, 47-48.	17.5	16
50	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.	1.8	14
51	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.	1.8	13
52	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.	3.3	10
53	<i>Citrobacter amalonaticus</i> Inhibits the Growth of <i>Citrobacter rodentium</i> in the Gut Lumen. <i>MBio</i> , 2021, 12, e0241021.	4.1	9
54	Pathogens' Exploitation of the Intestinal Food Web. <i>Cell Host and Microbe</i> , 2014, 16, 703-705.	11.0	7

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55	Pangenome analysis reveals genetic isolation in <i>Campylobacter hyointestinalis</i> subspecies adapted to different mammalian hosts. <i>Scientific Reports</i> , 2021, 11, 3431.	3.3	7
56	Should we modulate the neonatal microbiome and what should be the goal?. <i>Microbiome</i> , 2022, 10, 74.	11.1	6
57	Infection and immunity from a lifecourse perspective: Life Study Enhancement. <i>Lancet, The</i> , 2013, 382, S35.	13.7	2
58	A novel technique capable of taking "protected" biopsies for reliable assessment of the distribution of microbiota along the colonic mucosa. <i>Journal of Microbiological Methods</i> , 2021, 185, 106204.	1.6	1
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.	1.1	1