

Jessica R Galloway-Pea

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43 papers	3,233 citations	20 h-index	48 g-index
48 ext. papers	4,395 ext. citations	7.3 avg, IF	4.79 L-index

#	Paper	IF	Citations
43	Oral and Stool Microbiome Coalescence and Its Association With Antibiotic Exposure in Acute Leukemia Patients.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 848580	5.9	
42	Characterization of the Type I Restriction Modification System Broadly Conserved among Group A Streptococci. <i>MSphere</i> , 2021 , e0079921	5	1
41	Identification of bacteria-derived HLA-bound peptides in melanoma. <i>Nature</i> , 2021 , 592, 138-143	50.4	52
40	Alterations of the Oral Microbiome and Cumulative Carbapenem Exposure Are Associated With Stenotrophomonas maltophilia Infection in Patients With Acute Myeloid Leukemia Receiving Chemotherapy. <i>Clinical Infectious Diseases</i> , 2021 , 72, 1507-1513	11.6	9
39	IS26-mediated amplification of blaOXA-1 and blaCTX-M-15 with concurrent outer membrane porin disruption associated with de novo carbapenem resistance in a recurrent bacteraemia cohort. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 385-395	5.1	8
38	Tools for Analysis of the Microbiome. <i>Digestive Diseases and Sciences</i> , 2020 , 65, 674-685	4	22
37	The gut mycobiome: The overlooked constituent of clinical outcomes and treatment complications in patients with cancer and other immunosuppressive conditions. <i>PLoS Pathogens</i> , 2020 , 16, e1008353	7.6	11
36	Compositional zero-inflated network estimation for microbiome data. <i>BMC Bioinformatics</i> , 2020 , 21, 581	3.6	2
35	Gut Microbiome Signatures Are Predictive of Infectious Risk Following Induction Therapy for Acute Myeloid Leukemia. <i>Clinical Infectious Diseases</i> , 2020 , 71, 63-71	11.6	34
34	Observational Cohort Study of Oral Mycobiome and Interkingdom Interactions over the Course of Induction Therapy for Leukemia. <i>MSphere</i> , 2020 , 5,	5	8
33	Fecal Microbiome, Metabolites, and Stem Cell Transplant Outcomes: A Single-Center Pilot Study. <i>Open Forum Infectious Diseases</i> , 2019 , 6, ofz173	1	20
32	2674. Microbiome and Cumulative Antibiotic Use as Predictors of Stenotrophomonas maltophilia Infection in Patients with Acute Myeloid Leukemia Receiving Remission-Induction Chemotherapy. <i>Open Forum Infectious Diseases</i> , 2019 , 6, S938-S938	1	78
31	2682. Prophylaxis-Driven Molecular Epidemiology of Pseudomonas aeruginosa Bloodstream Infections in Adults With Leukemia. <i>Open Forum Infectious Diseases</i> , 2019 , 6, S942-S942	1	78
30	What Are the Effects of Irreversible Electroporation on a Staphylococcus aureus Rabbit Model of Osteomyelitis?. <i>Clinical Orthopaedics and Related Research</i> , 2019 , 477, 2367-2377	2.2	2
29	Clonal Emergence of Invasive Multidrug-Resistant Staphylococcus epidermidis Deconvoluted via a Combination of Whole-Genome Sequencing and Microbiome Analyses. <i>Clinical Infectious Diseases</i> , 2018 , 67, 398-406	11.6	16
28	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018 , 359, 97-103	33.3	1895
27	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. <i>Psychoneuroendocrinology</i> , 2018 , 89, 203-208	5	7

26	Longitudinal Sensitivity of the MD Anderson Symptom Inventory for Acute Myeloid Leukemia. <i>Blood</i> , 2018 , 132, 4825-4825	2.2	
25	Identification of a chimeric emm gene and novel emm pattern in currently circulating strains of emm4 Group A Streptococcus. <i>Microbial Genomics</i> , 2018 , 4,	4.4	8
24	1055. Epidemiology and Mechanisms of Carbapenem Resistance in Recurrent Extended-Spectrum β -Lactamase- Producing Enterobacteriaceae Bacteremia. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S315-S315	1.5	78
23	Hypervirulent group A Streptococcus emergence in an acapsular background is associated with marked remodeling of the bacterial cell surface. <i>PLoS ONE</i> , 2018 , 13, e0207897	3.7	8
22	An integrative Bayesian Dirichlet-multinomial regression model for the analysis of taxonomic abundances in microbiome data. <i>BMC Bioinformatics</i> , 2017 , 18, 94	3.6	34
21	Can Consideration of the Microbiome Improve Antimicrobial Utilization and Treatment Outcomes in the Oncology Patient?. <i>Clinical Cancer Research</i> , 2017 , 23, 3263-3268	12.9	21
20	Characterization of oral and gut microbiome temporal variability in hospitalized cancer patients. <i>Genome Medicine</i> , 2017 , 9, 21	14.4	51
19	Impact of the Microbiota on Bacterial Infections during Cancer Treatment. <i>Trends in Microbiology</i> , 2017 , 25, 992-1004	12.4	23
18	A Multi-Serotype Approach Clarifies the Catabolite Control Protein A Regulon in the Major Human Pathogen Group A Streptococcus. <i>Scientific Reports</i> , 2016 , 6, 32442	4.9	6
17	The role of the gastrointestinal microbiome in infectious complications during induction chemotherapy for acute myeloid leukemia. <i>Cancer</i> , 2016 , 122, 2186-96	6.4	85
16	Application of Whole-Genome Sequencing to an Unusual Outbreak of Invasive Group A Streptococcal Disease. <i>Open Forum Infectious Diseases</i> , 2016 , 3, ofw042	1	11
15	Sequence type 1 group B Streptococcus, an emerging cause of invasive disease in adults, evolves by small genetic changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6431-6	11.5	63
14	The identification and functional characterization of WxL proteins from Enterococcus faecium reveal surface proteins involved in extracellular matrix interactions. <i>Journal of Bacteriology</i> , 2015 , 197, 882-92	3.5	19
13	Implementation of a Pan-Genomic Approach to Investigate Holobiont-Infecting Microbe Interaction: A Case Report of a Leukemic Patient with Invasive Mucormycosis. <i>PLoS ONE</i> , 2015 , 10, e0139851	3.7	42
12	Enterococcus faecalis reconfigures its transcriptional regulatory network activation at different copper levels. <i>Metallomics</i> , 2014 , 6, 572-81	4.5	18
11	Species-level assessment of the molecular basis of fluoroquinolone resistance among viridans group streptococci causing bacteraemia in cancer patients. <i>International Journal of Antimicrobial Agents</i> , 2014 , 43, 558-62	14.3	7
10	125Single Nucleotide Polymorphisms Drive Phenotypic Diversity Among Sequence Type 1 Group B Streptococcus, An Emerging Cause of Invasive Disease in Adult Humans. <i>Open Forum Infectious Diseases</i> , 2014 , 1, S12-S12	1	78
9	GyrB polymorphisms accurately assign invasive viridans group streptococcal species. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 2905-12	9.7	11

8	Molecular characterization of an invasive phenotype of group A Streptococcus arising during human infection using whole genome sequencing of multiple isolates from the same patient. <i>Journal of Infectious Diseases</i> , 2014 , 209, 1520-3	7	19
7	Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. <i>BMC Microbiology</i> , 2012 , 12, 135	4.5	104
6	Genomic and SNP analyses demonstrate a distant separation of the hospital and community-associated clades of Enterococcus faecium. <i>PLoS ONE</i> , 2012 , 7, e30187	3.7	87
5	Diversity of the fsr-gelE region of the Enterococcus faecalis genome but conservation in strains with partial deletions of the fsr operon. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 442-51	4.8	17
4	Analysis of PBP5 of early U.S. isolates of Enterococcus faecium: sequence variation alone does not explain increasing ampicillin resistance over time. <i>Antimicrobial Agents and Chemotherapy</i> , 2011 , 55, 3272-9	5.9	53
3	Molecular epidemiology of vancomycin-resistant Enterococcus faecium: a prospective, multicenter study in South American hospitals. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 1562-9	9.7	67
2	Analysis of clonality and antibiotic resistance among early clinical isolates of Enterococcus faecium in the United States. <i>Journal of Infectious Diseases</i> , 2009 , 200, 1566-73	7	70
1	Concurrence of Porin Loss and Modular Amplification of β -Lactamase Encoding Genes Drives Carbapenem Resistance in a Cohort of Recurrent Enterobacteriales Bacteremia		1