Casey M Theriot

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.

46 3,077 23 52 h-index g-index citations papers 8.5 5.84 52 4,415 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
46	Prolonged oral antimicrobial administration prevents doxorubicin-induced loss of active intestinal stem cells <i>Gut Microbes</i> , 2022 , 14, 2018898	8.8	O
45	The Stickland Reaction Precursor -4-Hydroxy-l-Proline Differentially Impacts the Metabolism of Clostridioides difficile and Commensal <i>MSphere</i> , 2022 , e0092621	5	0
44	Mechanisms of Colonization Resistance Against Clostridioides difficile. <i>Journal of Infectious Diseases</i> , 2021 , 223, S194-S200	7	5
43	Clostridioides difficile exploits toxin-mediated inflammation to alter the host nutritional landscape and exclude competitors from the gut microbiota. <i>Nature Communications</i> , 2021 , 12, 462	17.4	26
42	Contribution of Inhibitory Metabolites and Competition for Nutrients to Colonization Resistance against by Commensal. <i>Microorganisms</i> , 2021 , 9,	4.9	3
41	Secondary bile acid ursodeoxycholic acid alters weight, the gut microbiota, and the bile acid pool in conventional mice. <i>PLoS ONE</i> , 2021 , 16, e0246161	3.7	2
40	bile salt hydrolase substrate specificity governs bacterial fitness and host colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	23
39	Salicylanilide Analog Minimizes Relapse of Infection in Mice. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 6898-6908	8.3	5
38	Role of Microbiota-Derived Bile Acids in Enteric Infections. <i>Cell</i> , 2020 , 181, 1452-1454	56.2	8
37	Intestinal bile acids directly modulate the structure and function of TcdB toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 6792-6800	11.5	18
36	Targeting of Clostridioides difficile Using Phage-Delivered CRISPR-Cas3 Antimicrobials. <i>MBio</i> , 2020 , 11,	7.8	50
35	Ursodeoxycholic Acid (UDCA) Mitigates the Host Inflammatory Response during Clostridioides difficile Infection by Altering Gut Bile Acids. <i>Infection and Immunity</i> , 2020 , 88,	3.7	17
34	Complete Genome Sequence of Lactobacillus johnsonii NCK2677, Isolated from Mice. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
33	Diversification of host bile acids by members of the gut microbiota. <i>Gut Microbes</i> , 2020 , 11, 158-171	8.8	95
32	Bile salt hydrolases: Gatekeepers of bile acid metabolism and host-microbiome crosstalk in the gastrointestinal tract. <i>PLoS Pathogens</i> , 2019 , 15, e1007581	7.6	75
31	High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution. <i>Nucleic Acids Research</i> , 2019 , 47, e103	20.1	155
30	Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal Escherichia coli, and the microbiome of steers. <i>PLoS ONE</i> , 2019 , 14, e0223378	3.7	5

(2015-2019)

Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 29 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 28 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 27 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 26 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 25 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal 24 Escherichia coli, and the microbiome of steers 2019, 14, e0223378 Restoration of short chain fatty acid and bile acid metabolism following fecal microbiota 2.8 81 23 transplantation in patients with recurrent Clostridium difficile infection. Anaerobe, 2018, 53, 64-73 Beyond Structure: Defining the Function of the Gut Using Omic Approaches for Rational Design of 7.6 22 2 Personalized Therapeutics. MSystems, 2018, 3, Shifts in the Gut Metabolome and Transcriptome throughout Colonization and Infection in a Mouse 5 2.1 54 Model. MSphere, 2018, 3, A Small Molecule-Screening Pipeline to Evaluate the Therapeutic Potential of 2-Aminoimidazole 5.7 9 Molecules Against. Frontiers in Microbiology, 2018, 9, 1206 The Bile Salt Hydrolase Repertoire Reveals Niche-Specific Adaptation. MSphere, 2018, 3, 19 5 43 Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in 18 5.7 10 Steers. Frontiers in Microbiology, 2018, 9, 2190 Gut microbiome-mediated bile acid metabolism regulates liver cancer via NKT cells. Science, 2018, 17 33.3 503 360, Inhibition of spore germination, growth, and toxin activity of clinically relevant C. difficile strains by 2.8 16 94 gut microbiota derived secondary bile acids. Anaerobe, 2017, 45, 86-100 Cefoperazone-treated Mouse Model of Clinically-relevant Clostridium difficile Strain R20291. 1.6 26 15 Journal of Visualized Experiments, 2016, Antibiotic-Induced Alterations of the Gut Microbiota Alter Secondary Bile Acid Production and Allow for Clostridium difficile Spore Germination and Outgrowth in the Large Intestine. MSphere, 216 14 2016, 1, Impact of microbial derived secondary bile acids on colonization resistance against Clostridium 2.8 68 13 difficile in the gastrointestinal tract. Anaerobe, 2016, 41, 44-50 Effects of tigecycline and vancomycin administration on established Clostridium difficile infection. 12 5.9 10 Antimicrobial Agents and Chemotherapy, 2015, 59, 1596-604

11	Fecal Microbiota Transplantation Eliminates Clostridium difficile in a Murine Model of Relapsing Disease. <i>Infection and Immunity</i> , 2015 , 83, 3838-46	3.7	76
10	Interactions Between the Gastrointestinal Microbiome and Clostridium difficile. <i>Annual Review of Microbiology</i> , 2015 , 69, 445-61	17.5	167
9	Dynamics and establishment of Clostridium difficile infection in the murine gastrointestinal tract. <i>Infection and Immunity</i> , 2015 , 83, 934-41	3.7	100
8	Antibiotic-induced shifts in the mouse gut microbiome and metabolome increase susceptibility to Clostridium difficile infection. <i>Nature Communications</i> , 2014 , 5, 3114	17.4	568
7	Clostridium difficile-induced colitis in mice is independent of leukotrienes. <i>Anaerobe</i> , 2014 , 30, 90-8	2.8	7
6	Alteration of the murine gastrointestinal microbiota by tigecycline leads to increased susceptibility to Clostridium difficile infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 2767-74	5.9	53
5	Microbial and metabolic interactions between the gastrointestinal tract and Clostridium difficile infection. <i>Gut Microbes</i> , 2014 , 5, 86-95	8.8	50
4	Improving the catalytic activity of hyperthermophilic Pyrococcus horikoshii prolidase for detoxification of organophosphorus nerve agents over a broad range of temperatures. <i>Archaea</i> , 2011 , 2011, 565127	2	23
3	Hydrolysis of organophosphorus compounds by microbial enzymes. <i>Applied Microbiology and Biotechnology</i> , 2011 , 89, 35-43	5.7	123
2	Cefoperazone-treated mice as an experimental platform to assess differential virulence of Clostridium difficile strains. <i>Gut Microbes</i> , 2011 , 2, 326-34	8.8	113
1	The interplay between microbiome dynamics and pathogen dynamics in a murine model of Clostridium difficile Infection. <i>Gut Microbes</i> , 2011 , 2, 145-58	8.8	192