

Michael A Bachman

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

2,828
citations

361045

20
h-index

344852

36
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all docs

44
docs citations

44
times ranked

3828
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting Direct-Specimen SARS-CoV-2 Assay Performance Using Residual Patient Samples. <i>Journal of Applied Laboratory Medicine</i> , 2022, 7, 661-673.	0.6	3
2	Management of Cytomegalovirus, Epstein-Barr Virus, and HIV Viral Load Quality Control Data Using Unity Real Time. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0167521.	1.8	1
3	The ArcAB Two-Component System: Function in Metabolism, Redox Control, and Infection. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0011021.	2.9	21
4	The ADP-Heptose Biosynthesis Enzyme GmhB is a Conserved Gram-Negative Bacteremia Fitness Factor. <i>Infection and Immunity</i> , 2022, 90, .	1.0	7
5	Comparative study of four SARS-CoV-2 Nucleic Acid Amplification Test (NAAT) platforms demonstrates that ID NOW performance is impaired substantially by patient and specimen type. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 99, 115200.	0.8	41
6	Prolonged Severe Acute Respiratory Syndrome Coronavirus 2 Replication in an Immunocompromised Patient. <i>Journal of Infectious Diseases</i> , 2021, 223, 23-27.	1.9	256
7	Pathogenesis of Gram-Negative Bacteremia. <i>Clinical Microbiology Reviews</i> , 2021, 34, .	5.7	88
8	A systematic analysis of hypermucoviscosity and capsule reveals distinct and overlapping genes that impact <i>Klebsiella pneumoniae</i> fitness. <i>PLoS Pathogens</i> , 2021, 17, e1009376.	2.1	73
9	A plasmid locus associated with <i>Klebsiella</i> clinical infections encodes a microbiome-dependent gut fitness factor. <i>PLoS Pathogens</i> , 2021, 17, e1009537.	2.1	20
10	Risk Factors for and Mechanisms of <i>CO</i> listin <i>R</i> esistance Among <i>E</i> nterobacterales: Getting at the CORE of the Issue. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab145.	0.4	8
11	Measurement of <i>Klebsiella</i> Intestinal Colonization Density To Assess Infection Risk. <i>MSphere</i> , 2021, 6, e0050021.	1.3	18
12	Risk Factors for <i>Klebsiella</i> Infections among Hospitalized Patients with Preexisting Colonization. <i>MSphere</i> , 2021, 6, e0013221.	1.3	16
13	Replication Dynamics for Six Gram-Negative Bacterial Species during Bloodstream Infection. <i>MBio</i> , 2021, 12, e0111421.	1.8	14
14	Stressed erythrophagocytosis induces immunosuppression during sepsis through heme-mediated STAT1 dysregulation. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	31
15	<i>Enterobacterales</i> Infection after Intestinal Dominance in Hospitalized Patients. <i>MSphere</i> , 2020, 5, .	1.3	10
16	Epidemiological and Microbiome Associations Between <i>Klebsiella pneumoniae</i> and Vancomycin-Resistant <i>Enterococcus</i> Colonization in Intensive Care Unit Patients. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa012.	0.4	28
17	Identification of four patients with colistin-resistant <i>Escherichia coli</i> containing the mobile colistin resistance <i>mcr</i> -1 gene from a single health system in Michigan. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 1059-1062.	1.0	15
18	The <i>Klebsiella pneumoniae</i> citrate synthase gene, <i>gltA</i> , influences site specific fitness during infection. <i>PLoS Pathogens</i> , 2019, 15, e1008010.	2.1	27

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19	Twin arginine translocation, ammonia incorporation, and polyamine biosynthesis are crucial for <i>Proteus mirabilis</i> fitness during bloodstream infection. <i>PLoS Pathogens</i> , 2019, 15, e1007653.	2.1	29
20	Iron Acquisition and Siderophore Release by Carbapenem-Resistant Sequence Type 258 <i>Klebsiella pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	1.3	36
21	Unexpected disseminated histoplasmosis detected by bone marrow biopsy in a solid organ transplant patient. <i>Clinical Case Reports (discontinued)</i> , 2018, 6, 49-51.	0.2	3
22	Identification of Pathogenicity-Associated Loci in <i>Klebsiella pneumoniae</i> from Hospitalized Patients. <i>MSystems</i> , 2018, 3, .	1.7	38
23	Colonization, Infection, and the Accessory Genome of <i>Klebsiella pneumoniae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 4.	1.8	515
24	TnseqDiff: identification of conditionally essential genes in transposon sequencing studies. <i>BMC Bioinformatics</i> , 2017, 18, 326.	1.2	42
25	<i>Klebsiella pneumoniae</i> Siderophores Induce Inflammation, Bacterial Dissemination, and HIF-1 α Stabilization during Pneumonia. <i>MBio</i> , 2016, 7, .	1.8	139
26	Molecular Epidemiology of Colonizing and Infecting Isolates of <i>Klebsiella pneumoniae</i> . <i>MSphere</i> , 2016, 1, .	1.3	204
27	Genome-Wide Identification of <i>Klebsiella pneumoniae</i> Fitness Genes during Lung Infection. <i>MBio</i> , 2015, 6, e00775.	1.8	168
28	Diverging roles of bacterial siderophores during infection. <i>Metallomics</i> , 2015, 7, 986-995.	1.0	214
29	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 43816 KPPR1, a Rifampin-Resistant Mutant Commonly Used in Animal, Genetic, and Molecular Biology Studies. <i>Genome Announcements</i> , 2014, 2, .	0.8	52
30	Bacterial Siderophores That Evade or Overwhelm Lipocalin 2 Induce Hypoxia Inducible Factor 1 α and Proinflammatory Cytokine Secretion in Cultured Respiratory Epithelial Cells. <i>Infection and Immunity</i> , 2014, 82, 3826-3836.	1.0	54
31	Interaction of Lipocalin 2, Transferrin, and Siderophores Determines the Replicative Niche of <i>Klebsiella pneumoniae</i> during Pneumonia. <i>MBio</i> , 2012, 3, .	1.8	116
32	<i>Klebsiella pneumoniae</i> Yersiniabactin Promotes Respiratory Tract Infection through Evasion of Lipocalin 2. <i>Infection and Immunity</i> , 2011, 79, 3309-3316.	1.0	227
33	Mucosal Lipocalin 2 Has Pro-Inflammatory and Iron-Sequestering Effects in Response to Bacterial Enterobactin. <i>PLoS Pathogens</i> , 2009, 5, e1000622.	2.1	148
34	Genetic Evidence that <i>Legionella pneumophila</i> RpoS Modulates Expression of the Transmission Phenotype in Both the Exponential Phase and the Stationary Phase. <i>Infection and Immunity</i> , 2004, 72, 2468-2476.	1.0	81
35	The LetE Protein Enhances Expression of Multiple LetA/LetS-Dependent Transmission Traits by <i>Legionella pneumophila</i> . <i>Infection and Immunity</i> , 2004, 72, 3284-3293.	1.0	68