Michael A Bachman

List of Publications by Year
in descending order

35 papers	2,828 citations	361413 20 h-index	345221 36 g-index
44 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. journal of applied laboratory medicine, The, 2022, 7, 661-673.	1.3	3
2	Management of Cytomegalovirus, Epstein-Barr Virus, and HIV Viral Load Quality Control Data Using Unity Real Time. Journal of Clinical Microbiology, 2022, 60, JCM0167521.	3.9	1
3	The ArcAB Two-Component System: Function in Metabolism, Redox Control, and Infection. Microbiology and Molecular Biology Reviews, 2022, 86, e0011021.	6.6	21
4	The ADP-Heptose Biosynthesis Enzyme GmhB is a Conserved Gram-Negative Bacteremia Fitness Factor. Infection and Immunity, 2022, 90, .	2.2	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. Diagnostic Microbiology and Infectious Disease, 2021, 99, 115200.	1.8	41
6	Prolonged Severe Acute Respiratory Syndrome Coronavirus 2 Replication in an Immunocompromised Patient. Journal of Infectious Diseases, 2021, 223, 23-27.	4.0	256
7	Pathogenesis of Gram-Negative Bacteremia. Clinical Microbiology Reviews, 2021, 34, .	13.6	88
8	A systematic analysis of hypermucoviscosity and capsule reveals distinct and overlapping genes that impact Klebsiella pneumoniae fitness. PLoS Pathogens, 2021, 17, e1009376.	4.7	73
9	A plasmid locus associated with Klebsiella clinical infections encodes a microbiome-dependent gut fitness factor. PLoS Pathogens, 2021, 17, e1009537.	4.7	20
10	Risk Factors for and Mechanisms of *CO*listin *R*esistance Among *E*nterobacterales: Getting at the CORE of the Issue. Open Forum Infectious Diseases, 2021, 8, ofab145.	0.9	8
11	Measurement of Klebsiella Intestinal Colonization Density To Assess Infection Risk. MSphere, 2021, 6, e0050021.	2.9	18
12	Risk Factors for Klebsiella Infections among Hospitalized Patients with Preexisting Colonization. MSphere, 2021, 6, e0013221.	2.9	16
13	Replication Dynamics for Six Gram-Negative Bacterial Species during Bloodstream Infection. MBio, 2021, 12, e0111421.	4.1	14
14	Stressed erythrophagocytosis induces immunosuppression during sepsis through heme-mediated STAT1 dysregulation. Journal of Clinical Investigation, 2021, 131, .	8.2	31
15	*Enterobacterales* Infection after Intestinal Dominance in Hospitalized Patients. MSphere, 2020, 5, .	2.9	10
16	Epidemiological and Microbiome Associations Between Klebsiella pneumoniae and Vancomycin-Resistant Enterococcus Colonization in Intensive Care Unit Patients. Open Forum Infectious Diseases, 2020, 7, ofaa012.	0.9	28
17	Identification of four patients with colistin-resistant *Escherichia coli* containing the mobile colistin resistance *mcr*-1 gene from a single health system in Michigan. Infection Control and Hospital Epidemiology, 2019, 40, 1059-1062.	1.8	15
18	The Klebsiella pneumoniae citrate synthase gene, gltA, influences site specific fitness during infection. PLoS Pathogens, 2019, 15, e1008010.	4.7	27

#	ARTICLE	IF	CITATIONS
19	Twin arginine translocation, ammonia incorporation, and polyamine biosynthesis are crucial for Proteus mirabilis fitness during bloodstream infection. PLoS Pathogens, 2019, 15, e1007653.	4.7	29
20	Iron Acquisition and Siderophore Release by Carbapenem-Resistant Sequence Type 258 Klebsiella pneumoniae. MSphere, 2018, 3, .	2.9	36
21	Unexpected disseminated histoplasmosis detected by bone marrow biopsy in a solid organ transplant patient. Clinical Case Reports (discontinued), 2018, 6, 49-51.	0.5	3
22	Identification of Pathogenicity-Associated Loci in Klebsiella pneumoniae from Hospitalized Patients. MSystems, 2018, 3, .	3.8	38
23	Colonization, Infection, and the Accessory Genome of Klebsiella pneumoniae. Frontiers in Cellular and Infection Microbiology, 2018, 8, 4.	3.9	515
24	TnseqDiff: identification of conditionally essential genes in transposon sequencing studies. BMC Bioinformatics, 2017, 18, 326.	2.6	42
25	Klebsiella pneumoniae Siderophores Induce Inflammation, Bacterial Dissemination, and HIF-1α Stabilization during Pneumonia. MBio, 2016, 7, .	4.1	139
26	Molecular Epidemiology of Colonizing and Infecting Isolates of Klebsiella pneumoniae. MSphere, 2016, 1, .	2.9	204
27	Genome-Wide Identification of Klebsiella pneumoniae Fitness Genes during Lung Infection. MBio, 2015, 6, e00775.	4.1	168
28	Diverging roles of bacterial siderophores during infection. Metallomics, 2015, 7, 986-995.	2.4	214
29	Complete Genome Sequence of Klebsiella pneumoniae Strain ATCC 43816 KPPR1, a Rifampin-Resistant Mutant Commonly Used in Animal, Genetic, and Molecular Biology Studies. Genome Announcements, 2014, 2, .	0.8	52
30	Bacterial Siderophores That Evade or Overwhelm Lipocalin 2 Induce Hypoxia Inducible Factor 1α and Proinflammatory Cytokine Secretion in Cultured Respiratory Epithelial Cells. Infection and Immunity, 2014, 82, 3826-3836.	2.2	54
31	Interaction of Lipocalin 2, Transferrin, and Siderophores Determines the Replicative Niche of Klebsiella pneumoniae during Pneumonia. MBio, 2012, 3, .	4.1	116
32	Klebsiella pneumoniae Yersiniabactin Promotes Respiratory Tract Infection through Evasion of Lipocalin 2. Infection and Immunity, 2011, 79, 3309-3316.	2.2	227
33	Mucosal Lipocalin 2 Has Pro-Inflammatory and Iron-Sequestering Effects in Response to Bacterial Enterobactin. PLoS Pathogens, 2009, 5, e1000622.	4.7	148
34	Genetic Evidence that Legionella pneumophila RpoS Modulates Expression of the Transmission Phenotype in Both the Exponential Phase and the Stationary Phase. Infection and Immunity, 2004, 72, 2468-2476.	2.2	81
35	The LetE Protein Enhances Expression of Multiple LetA/LetS-Dependent Transmission Traits by Legionella pneumophila. Infection and Immunity, 2004, 72, 3284-3293.	2.2	68