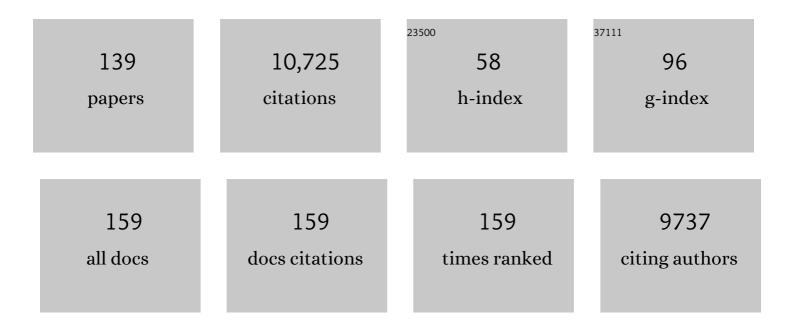
James M Musser

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone emergence. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10078-10083.	3.3	452
2	Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4668-4673.	3.3	406
3	Genome-Wide Analysis of Group A Streptococci Reveals a Mutation That Modulates Global Phenotype and Disease Specificity. PLoS Pathogens, 2006, 2, e5.	2.1	396
4	Virulence control in group A Streptococcus by a two-component gene regulatory system: Global expression profiling and in vivo infection modeling. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13855-13860.	3.3	349
5	Integrating Rapid Pathogen Identification and Antimicrobial Stewardship Significantly Decreases Hospital Costs. Archives of Pathology and Laboratory Medicine, 2013, 137, 1247-1254.	1.2	336
6	Molecular dissection of the evolution of carbapenem-resistant multilocus sequence type 258 <i>Klebsiella pneumoniae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4988-4993.	3.3	325
7	Evolutionary Origin and Emergence of a Highly Successful Clone of Serotype M1 Group AStreptococcusInvolved Multiple Horizontal Gene Transfer Events. Journal of Infectious Diseases, 2005, 192, 771-782.	1.9	312
8	Integrating rapid diagnostics and antimicrobial stewardship improves outcomes in patients with antibiotic-resistant Gram-negative bacteremia. Journal of Infection, 2014, 69, 216-225.	1.7	252
9	Treatment of Coronavirus Disease 2019 (COVID-19) Patients with Convalescent Plasma. American Journal of Pathology, 2020, 190, 1680-1690.	1.9	239
10	Evolutionary pathway to increased virulence and epidemic group A <i>Streptococcus</i> disease derived from 3,615 genome sequences. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1768-76.	3.3	215
11	Genome Sequence of a Serotype M28 Strain of Group AStreptococcus:Potential New Insights into Puerperal Sepsis and Bacterial Disease Specificity. Journal of Infectious Diseases, 2005, 192, 760-770.	1.9	214
12	Molecular genetic anatomy of inter- and intraserotype variation in the human bacterial pathogen group A Streptococcus. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7059-7064.	3.3	203
13	Treatment of Coronavirus Disease 2019 Patients with Convalescent Plasma Reveals a Signal of Significantly Decreased Mortality. American Journal of Pathology, 2020, 190, 2290-2303.	1.9	197
14	Population genetics of pathogenic bacteria. Microbial Pathogenesis, 1987, 3, 1-7.	1.3	191
15	Longitudinal analysis of the group A Streptococcus transcriptome in experimental pharyngitis in cynomolgus macaques. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9014-9019.	3.3	183
16	Progress toward Characterization of the Group AStreptococcusMetagenome: Complete Genome Sequence of a Macrolideâ€Resistant Serotype M6 Strain. Journal of Infectious Diseases, 2004, 190, 727-738.	1.9	172
17	Convalescent plasma anti–SARS-CoV-2 spike protein ectodomain and receptor-binding domain IgG correlate with virus neutralization. Journal of Clinical Investigation, 2020, 130, 6728-6738.	3.9	172
18	Multiple spillovers from humans and onward transmission of SARS-CoV-2 in white-tailed deer. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	164

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19	Signals of Significantly Increased Vaccine Breakthrough, Decreased Hospitalization Rates, and Less Severe Disease in Patients with Coronavirus Disease 2019 Caused by the Omicron Variant of Severe Acute Respiratory Syndrome Coronavirus 2 in Houston,ÂTexas. American Journal of Pathology, 2022, 192, 642-652.	1.9	161
20	Contribution of Exogenous Genetic Elements to the Group A Streptococcus Metagenome. PLoS ONE, 2007, 2, e800.	1.1	155
21	Molecular complexity of successive bacterial epidemics deconvoluted by comparative pathogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4371-4376.	3.3	153
22	Genome-wide protective response used by group A Streptococcus to evade destruction by human polymorphonuclear leukocytes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1996-2001.	3.3	148
23	Molecular differentiation of historic phage-type 80/81 and contemporary epidemic <i>Staphylococcus aureus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18091-18096.	3.3	139
24	Developing an in silico minimum inhibitory concentration panel test for Klebsiella pneumoniae. Scientific Reports, 2018, 8, 421.	1.6	136
25	Genetic Inactivation of an Extracellular Cysteine Protease (SpeB) Expressed by <i>Streptococcus pyogenes</i> Decreases Resistance to Phagocytosis and Dissemination to Organs. Infection and Immunity, 1998, 66, 771-776.	1.0	132
26	Significantly Decreased Mortality in a Large Cohort of Coronavirus Disease 2019 (COVID-19) Patients Transfused Early with Convalescent Plasma Containing High-Titer Anti–Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Spike Protein IgG. American Journal of Pathology, 2021, 191, 90-107.	1.9	131
27	The Effect of Convalescent Plasma Therapy on Mortality Among Patients With COVID-19: Systematic Review and Meta-analysis. Mayo Clinic Proceedings, 2021, 96, 1262-1275.	1.4	129
28	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. MBio, 2017, 8, .	1.8	124
29	PBP2a Mutations Causing High-Level Ceftaroline Resistance in Clinical Methicillin-Resistant Staphylococcus aureus Isolates. Antimicrobial Agents and Chemotherapy, 2014, 58, 6668-6674.	1.4	120
30	A molecular trigger for intercontinental epidemics of group A Streptococcus. Journal of Clinical Investigation, 2015, 125, 3545-3559.	3.9	119
31	Molecular Pathogenesis of Necrotizing Fasciitis. Annual Review of Pathology: Mechanisms of Disease, 2010, 5, 1-31.	9.6	117
32	Multi High-Throughput Approach for Highly Selective Identification of Vaccine Candidates: the Group A Streptococcus Case. Molecular and Cellular Proteomics, 2012, 11, M111.015693.	2.5	115
33	The role of complex carbohydrate catabolism in the pathogenesis of invasive streptococci. Trends in Microbiology, 2008, 16, 318-325.	3.5	109
34	CovS Simultaneously Activates and Inhibits the CovR-Mediated Repression of Distinct Subsets of Group A <i>Streptococcus</i> Virulence Factor-Encoding Genes. Infection and Immunity, 2009, 77, 3141-3149.	1.0	106
35	Molecular mechanisms underlying group A streptococcal pathogenesis. Cellular Microbiology, 2009, 11, 1-12.	1.1	99
36	Decreased necrotizing fasciitis capacity caused by a single nucleotide mutation that alters a multiple gene virulence axis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 888-893.	3.3	99

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37	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area. MBio, 2020, 11, .	1.8	99
38	Rgg Influences the Expression of Multiple Regulatory Loci To Coregulate Virulence Factor Expression in Streptococcus pyogenes. Infection and Immunity, 2002, 70, 762-770.	1.0	94
39	Distinct signatures of diversifying selection revealed by genome analysis of respiratory tract and invasive bacterial populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5039-5044.	3.3	90
40	Delta Variants of SARS-CoV-2 Cause Significantly Increased Vaccine Breakthrough COVID-19 Cases in Houston, Texas. American Journal of Pathology, 2022, 192, 320-331.	1.9	90
41	Analysis of the Transcriptome of Group A Streptococcus in Mouse Soft Tissue Infection. American Journal of Pathology, 2006, 169, 927-942.	1.9	86
42	Toward a Genome-Wide Systems Biology Analysis of Host-Pathogen Interactions in Group A Streptococcus. American Journal of Pathology, 2005, 167, 1461-1472.	1.9	85
43	Interacting networks of resistance, virulence and core machinery genes identified by genome-wide epistasis analysis. PLoS Genetics, 2017, 13, e1006508.	1.5	85
44	A decade of molecular pathogenomic analysis of group A Streptococcus. Journal of Clinical Investigation, 2009, 119, 2455-2463.	3.9	80
45	Central role of a bacterial two-component gene regulatory system of previously unknown function in pathogen persistence in human saliva. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16037-16042.	3.3	78
46	Absence of Patient-to-Patient Intrahospital Transmission of Staphylococcus aureus as Determined by Whole-Genome Sequencing. MBio, 2014, 5, e01692-14.	1.8	78
47	Engagement of the Pathogen Survival Response Used by Group A <i>Streptococcus</i> to Avert Destruction by Innate Host Defense. Journal of Immunology, 2004, 173, 1194-1201.	0.4	77
48	Trading Capsule for Increased Cytotoxin Production: Contribution to Virulence of a Newly Emerged Clade of <i>emm89</i> Streptococcus pyogenes. MBio, 2015, 6, e01378-15.	1.8	76
49	Identification of New Candidate Vaccine Antigens Made byStreptococcus pyogenes:Purification and Characterization of 16 Putative Extracellular Lipoproteins. Journal of Infectious Diseases, 2004, 189, 79-89.	1.9	75
50	6 The revival of group A streptococcal diseases, with a commentary on staphylococcal toxic shock syndrome. Biomedical Research Reports, 1998, 1, 185-218.	0.3	73
51	Full-Genome Dissection of an Epidemic of Severe Invasive Disease Caused by a Hypervirulent, Recently Emerged Clone of Group A Streptococcus. American Journal of Pathology, 2012, 180, 1522-1534.	1.9	70
52	Group A Streptococcus emm Gene Types in Pharyngeal Isolates, Ontario, Canada, 2002–2010. Emerging Infectious Diseases, 2011, 17, 2010-7.	2.0	65
53	Integrating Rapid Diagnostics and Antimicrobial Stewardship in Two Community Hospitals Improved Process Measures and Antibiotic Adjustment Time. Infection Control and Hospital Epidemiology, 2016, 37, 425-432.	1.0	65
54	Molecular Analysis of Group A Streptococcus Type emm18 Isolates Temporally Associated with Acute Rheumatic Fever Outbreaks in Salt Lake City, Utah. Journal of Clinical Microbiology, 2002, 40, 1805-1810.	1.8	64

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55	Rapidly Progressive, Fatal, Inhalation Anthrax-like Infection in a Human: Case Report, Pathogen Genome Sequencing, Pathology, and Coordinated Response. Archives of Pathology and Laboratory Medicine, 2011, 135, 1447-1459.	1.2	64
56	Strategy for Rapid Identification and Antibiotic Susceptibility Testing of Gram-Negative Bacteria Directly Recovered from Positive Blood Cultures Using the Bruker MALDI Biotyper and the BD Phoenix System. Journal of Clinical Microbiology, 2012, 50, 2452-2454.	1.8	64
57	Naturally occurring single amino acid replacements in a regulatory protein alter streptococcal gene expression and virulence in mice. Journal of Clinical Investigation, 2011, 121, 1956-1968.	3.9	63
58	M Types of Group A Streptococcal Isolates Submitted to the National Centre for Streptococcus (Canada) from 1993 to 1999. Journal of Clinical Microbiology, 2002, 40, 4466-4471.	1.8	61
59	Protein Array Profiling of Tic Patient Sera Reveals a Broad Range and Enhanced Immune Response against Group A Streptococcus Antigens. PLoS ONE, 2009, 4, e6332.	1.1	60
60	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into Streptococcus pyogenes pathogenesis. Nature Genetics, 2019, 51, 548-559.	9.4	58
61	A Combination of Independent Transcriptional Regulators Shapes Bacterial Virulence Gene Expression during Infection. PLoS Pathogens, 2010, 6, e1000817.	2.1	57
62	Contribution of Secreted NADase and Streptolysin O to the Pathogenesis of Epidemic Serotype M1 Streptococcus pyogenes Infections. American Journal of Pathology, 2017, 187, 605-613.	1.9	57
63	Adhesin competence repressor (AdcR) from Streptococcus pyogenes controls adaptive responses to zinc limitation and contributes to virulence. Nucleic Acids Research, 2015, 43, 418-432.	6.5	55
64	Reduced <i>In Vitro</i> Susceptibility of Streptococcus pyogenes to β-Lactam Antibiotics Associated with Mutations in the <i>pbp2x</i> Gene Is Geographically Widespread. Journal of Clinical Microbiology, 2020, 58, .	1.8	55
65	Identification and Characterization of an Antigen I/II Family Protein Produced by Group A Streptococcus. Infection and Immunity, 2006, 74, 4200-4213.	1.0	54
66	Human Disease Isolates of Serotype M4 and M22 Group A Streptococcus Lack Genes Required for Hyaluronic Acid Capsule Biosynthesis. MBio, 2012, 3, e00413-12.	1.8	53
67	Genetic Diversity among Type emm28 Group A Streptococcus Strains Causing Invasive Infections and Pharyngitis. Journal of Clinical Microbiology, 2005, 43, 4083-4091.	1.8	52
68	Lateral gene transfer of streptococcal ICE element RD2 (region of difference 2) encoding secreted proteins. BMC Microbiology, 2011, 11, 65.	1.3	51
69	Analysis of the ARTIC Version 3 and Version 4 SARS-CoV-2 Primers and Their Impact on the Detection of the G142D Amino Acid Substitution in the Spike Protein. Microbiology Spectrum, 2021, 9, e0180321.	1.2	50
70	Characterization of an Extracellular Virulence FactorMade by Group A Streptococcus with Homology to the Listeria monocytogenes Internalin Family ofProteins. Infection and Immunity, 2003, 71, 7043-7052.	1.0	47
71	Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen Streptococcus pyogenes. MBio, 2016, 7, .	1.8	47
72	Leaderless secreted peptide signaling molecule alters global gene expression and increases virulence of a human bacterial pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8498-E8507.	3.3	46

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73	Distinct Single Amino Acid Replacements in the Control of Virulence Regulator Protein Differentially Impact Streptococcal Pathogenesis. PLoS Pathogens, 2011, 7, e1002311.	2.1	42
74	Sequence Analysis of 20,453 Severe Acute Respiratory Syndrome Coronavirus 2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern. American Journal of Pathology, 2021, 191, 983-992.	1.9	42
75	Asymptomatic Carriage of Group A Streptococcus Is Associated with Elimination of Capsule Production. Infection and Immunity, 2014, 82, 3958-3967.	1.0	40
76	Natural Variation in the Promoter of the Gene Encoding the Mga Regulator Alters Host-Pathogen Interactions in Group A Streptococcus Carrier Strains. Infection and Immunity, 2013, 81, 4128-4138.	1.0	36
77	Bacterial Genomics in Infectious Disease and the Clinical Pathology Laboratory. Archives of Pathology and Laboratory Medicine, 2012, 136, 1414-1422.	1.2	34
78	Gene fitness landscape of group A streptococcus during necrotizing myositis. Journal of Clinical Investigation, 2019, 129, 887-901.	3.9	34
79	The Majority of 9,729 Group A Streptococcus Strains Causing Disease Secrete SpeB Cysteine Protease: Pathogenesis Implications. Infection and Immunity, 2015, 83, 4750-4758.	1.0	33
80	Novel Genes Required for the Fitness of Streptococcus pyogenes in Human Saliva. MSphere, 2017, 2, .	1.3	30
81	Trajectory of Growth of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants in Houston, Texas, January through May 2021, Based on 12,476 Genome Sequences. American Journal of Pathology, 2021, 191, 1754-1773.	1.9	26
82	Seasonal H3N2 influenza A virus fails to enhance <i>Staphylococcus aureus</i> co-infection in a non-human primate respiratory tract infection model. Virulence, 2013, 4, 707-715.	1.8	25
83	Limited window for donation of convalescent plasma with high live-virus neutralizing antibody titers for COVID-19 immunotherapy. Communications Biology, 2021, 4, 267.	2.0	25
84	Genomic Landscape of Intrahost Variation in Group A Streptococcus: Repeated and Abundant Mutational Inactivation of the <i>fabT</i> Gene Encoding a Regulator of Fatty Acid Synthesis. Infection and Immunity, 2016, 84, 3268-3281.	1.0	24
85	Structural and functional analysis of RopB: a major virulence regulator in <scp><i>S</i></scp> <i>treptococcus pyogenes</i> . Molecular Microbiology, 2016, 99, 1119-1133.	1.2	24
86	Intrahost Sequence Variation in the Streptococcal Inhibitor of Complement Gene in Patients with Human Pharyngitis. Journal of Infectious Diseases, 2003, 187, 604-612.	1.9	23
87	Clinical Laboratory Response to a Mock Outbreak of Invasive Bacterial Infections: a Preparedness Study. Journal of Clinical Microbiology, 2014, 52, 4210-4216.	1.8	22
88	Genomic Characteristics Behind the Spread of Bacteremic Group A <i>Streptococcus</i> Type <i>emm</i> 89 in Finland, 2004–2014. Journal of Infectious Diseases, 2016, 214, 1987-1995.	1.9	22
89	Increased Pilus Production Conferred by a Naturally Occurring Mutation Alters Host-Pathogen Interaction in Favor of Carriage in Streptococcus pyogenes. Infection and Immunity, 2017, 85, .	1.0	21
90	New Pathogenesis Mechanisms and Translational Leads Identified by Multidimensional Analysis of Necrotizing Myositis in Primates. MBio, 2020, 11, .	1.8	21

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91	Population Genomic Molecular Epidemiological Study of Macrolide-Resistant Streptococcus pyogenes in Iceland, 1995 to 2016: Identification of a Large Clonal Population with a <i>pbp2x</i> Mutation Conferring Reduced <i>In Vitro</i> β-Lactam Susceptibility. Journal of Clinical Microbiology, 2020, 58, .	1.8	21
92	A Non-Human Primate Model of Acute Group A Streptococcus Pharyngitis. , 2008, 431, 255-267.		21
93	Intergenic Variable-Number Tandem-Repeat Polymorphism Upstream of <i>rocA</i> Alters Toxin Production and Enhances Virulence in Streptococcus pyogenes. Infection and Immunity, 2016, 84, 2086-2093.	1.0	20
94	emm typing of invasive T28 group A streptococci, 1995–2004, Finland. Journal of Medical Microbiology, 2006, 55, 1701-1706.	0.7	19
95	A Naturally Occurring Single Amino Acid Replacement in Multiple Gene Regulator of Group A Streptococcus Significantly Increases Virulence. American Journal of Pathology, 2015, 185, 462-471.	1.9	19
96	Phosphorylation Events in the Multiple Gene Regulator of Group A Streptococcus Significantly Influence Global Gene Expression and Virulence. Infection and Immunity, 2015, 83, 2382-2395.	1.0	18
97	Metal sensing and regulation of adaptive responses to manganese limitation by MtsR is critical for group A streptococcus virulence. Nucleic Acids Research, 2019, 47, 7476-7493.	6.5	18
98	Genome sequence analysis of emm89 Streptococcus pyogenes strains causing infections in Scotland, 2010–2016. Journal of Medical Microbiology, 2017, 66, 1765-1773.	0.7	18
99	Natural Variant of Collagen-Like Protein A in Serotype M3 Group A Streptococcus Increases Adherence and Decreases Invasive Potential. Infection and Immunity, 2015, 83, 1122-1129.	1.0	17
100	A Single Amino Acid Replacement in the Sensor Kinase LiaS Contributes to a Carrier Phenotype in Group A Streptococcus. Infection and Immunity, 2015, 83, 4237-4246.	1.0	17
101	Contribution of AmyA, an extracellular αâ€glucan degrading enzyme, to group A streptococcal host–pathogen interaction. Molecular Microbiology, 2009, 74, 159-174.	1.2	16
102	Integrated whole-genome sequencing and temporospatial analysis of a continuing Group A <i>Streptococcus</i> epidemic. Emerging Microbes and Infections, 2013, 2, 1-8.	3.0	16
103	RocA Has Serotype-Specific Gene Regulatory and Pathogenesis Activities in Serotype M28 Group A Streptococcus. Infection and Immunity, 2018, 86, .	1.0	14
104	Human M1 macrophages express unique innate immune response genes after mycobacterial infection to defend against tuberculosis. Communications Biology, 2022, 5, 480.	2.0	14
105	Signaling by a Conserved Quorum Sensing Pathway Contributes to Growth <i>Ex Vivo</i> and Oropharyngeal Colonization of Human Pathogen Group A Streptococcus. Infection and Immunity, 2018, 86, .	1.0	13
106	A Single Amino Acid Replacement in Penicillin-Binding Protein 2X in Streptococcus pyogenes Significantly Increases Fitness on Subtherapeutic Benzylpenicillin Treatment in a Mouse Model of NecrotizingÂMyositis. American Journal of Pathology, 2020, 190, 1625-1631.	1.9	13
107	Transmission history of SARS-CoV-2 in humans and white-tailed deer. Scientific Reports, 2022, 12, .	1.6	13
108	Whole-Genome Sequencing of a Human Clinical Isolate of emm28 Streptococcus pyogenes Causing Necrotizing Fasciitis Acquired Contemporaneously with Hurricane Harvey. Genome Announcements, 2017, 5, .	0.8	11

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109	Real-world Assessment of 2,879 COVID-19 Patients Treated with Monoclonal Antibody Therapy: A Propensity Score-Matched Cohort Study. Open Forum Infectious Diseases, 2021, 8, ofab512.	0.4	11
110	Integrative Reverse Genetic Analysis Identifies Polymorphisms Contributing to Decreased Antimicrobial Agent Susceptibility in <i>Streptococcus pyogenes</i> . MBio, 2022, 13, e0361821.	1.8	11
111	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
112	Evaluation of large genotypic Mycobacterium tuberculosis clusters: contributions from remote and recent transmission. Tuberculosis, 2013, 93, S38-S46.	0.8	10
113	Genetic Basis Underlying the Hyperhemolytic Phenotype of Streptococcus agalactiae Strain CNCTC10/84. Journal of Bacteriology, 2020, 202, .	1.0	10
114	Genome-Wide Assessment of Streptococcus agalactiae Genes Required for Survival in Human Whole Blood and Plasma. Infection and Immunity, 2020, 88, .	1.0	9
115	Genome-Wide Screens Identify Group A Streptococcus Surface Proteins Promoting Female Genital Tract Colonization and Virulence. American Journal of Pathology, 2020, 190, 862-873.	1.9	9
116	Genetic heterogeneity of the Spy1336/R28—Spy1337 virulence axis in Streptococcus pyogenes and effect on gene transcript levels and pathogenesis. PLoS ONE, 2020, 15, e0229064.	1.1	9
117	Phenotypic Variation in the Group A <i>Streptococcus</i> Due to Natural Mutation of the Accessory Protein-Encoding Gene <i>rocA</i> . MSphere, 2018, 3, .	1.3	8
118	Functional Insights into the High-Molecular-Mass Penicillin-Binding Proteins of Streptococcus agalactiae Revealed by Gene Deletion and Transposon Mutagenesis Analysis. Journal of Bacteriology, 2021, 203, e0023421.	1.0	8
119	Streptococcus pyogenes genes that promote pharyngitis in primates. JCI Insight, 2020, 5, .	2.3	8
120	Polymorphisms in Regulator of Cov Contribute to the Molecular Pathogenesis of Serotype M28 Group A Streptococcus. American Journal of Pathology, 2019, 189, 2002-2018.	1.9	7
121	Opacification Domain of Serum Opacity Factor Inhibits Beta-Hemolysis and Contributes to Virulence of Streptococcus pyogenes. MSphere, 2017, 2, .	1.3	6
122	Rapid Emergence of a New Clone Impacts the Population at Risk and Increases the Incidence of Type emm89 Group A Streptococcus Invasive Disease. Open Forum Infectious Diseases, 2017, 4, ofx042.	0.4	4
123	Postpartum Group A Streptococcus Case Series: Reach Out to Infection Prevention!. Open Forum Infectious Diseases, 2018, 5, ofy159.	0.4	4
124	Draft Genome Sequence of Candida auris Strain LOM, a Human Clinical Isolate from Greater Metropolitan Houston, Texas. Microbiology Resource Announcements, 2019, 8, .	0.3	4
125	Single Amino Acid Replacements in RocA Disrupt Protein-Protein Interactions To Alter the Molecular Pathogenesis of Group A <i>Streptococcus</i> . Infection and Immunity, 2020, 88, .	1.0	4
126	Deletion of <i>ato</i> R from <i>Streptococcus pyogenes</i> Results in Hypervirulence in a Mouse Model of Sepsis and is LuxS Independent. Polish Journal of Microbiology, 2017, 66, 17-24.	0.6	4

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127	Musser et al. Reply to "Emergence of the Same Successful Clade among Distinct Populations of <i>emm</i> 89 Streptococcus pyogenes in Multiple Geographic Regionsâ€: MBio, 2015, 6, e01838-15.	1.8	3
128	Predicting β-lactam resistance using whole genome sequencing in Klebsiella pneumoniae: the challenge of β-lactamase inhibitors. Diagnostic Microbiology and Infectious Disease, 2020, 98, 115149.	0.8	3
129	Development and Evaluation of a Novel Protein-Based Assay for Specific Detection of KPC β-Lactamases from Klebsiella pneumoniae Clinical Isolates. MSphere, 2020, 5, .	1.3	3
130	MOLECULAR MECHANISMS CONTRIBUTING TO FUZZY EPIDEMICS CAUSED BY GROUP A STREPTOCOCCUS, A FLESH-EATING HUMAN BACTERIAL PATHOGEN. Transactions of the American Clinical and Climatological Association, 2020, 131, 356-368.	0.9	3
131	A Chimeric Penicillin Binding Protein 2X Significantly Decreases inÂVitro Beta-Lactam Susceptibility and Increases inÂVivo Fitness of Streptococcus pyogenes. American Journal of Pathology, 2022, 192, 1397-1406.	1.9	2
132	S. Burt Wolbach, Rocky Mountain Spotted Fever, and Blood-Sucking Arthropods. American Journal of Pathology, 2013, 182, 291-293.	1.9	1
133	2558. Predicting β-Lactam Resistance Using Whole Genome Sequencing (WGS) in Klebsiella pneumoniae: The Challenge of β-Lactam Inhibitors. Open Forum Infectious Diseases, 2018, 5, S70-S70.	0.4	1
134	Human Infections Caused by Clonally Related African Clade (Clade III) Strains of Candida auris in the Greater Houston Region. Journal of Clinical Microbiology, 2020, 58, .	1.8	1
135	A Naturally Occurring Single Nucleotide Mutation Significantly Impairs Necrotizing Fasciitis ("Flesh) Tj ETQq1	1	14 ₁ rgBT /Ove
136	Molecular Pathogenesis Lessons from the World of Infectious Diseases Research. American Journal of Pathology, 2015, 185, 1502-1504.	1.9	0
137	A Web-Based Respiratory Pathogen Laboratory Report for Summarizing Key Metrics to Stakeholders. American Journal of Clinical Pathology, 2018, 150, S153-S154.	0.4	0
138	Polymorphisms in regulator of protease B (RopB) alter disease phenotype and strain virulence of serotype M3 Group A Streptococcus. FASEB Journal, 2012, 26, 1034.3.	0.2	0
139	Whole Genome Sequence Analysis of a B. cereus Strain Causing a Fatal Anthrax‣ike Pulmonary Infection. FASEB Journal, 2012, 26, 1034.5.	0.2	0