

# James M Musser

## List of Publications by Year in descending order

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Version: 2024-02-01

139  
papers

10,725  
citations

23500

58  
h-index

37111

96  
g-index

159  
all docs

159  
docs citations

159  
times ranked

9737  
citing authors

#	ARTICLE	IF	CITATIONS
1	Delta Variants of SARS-CoV-2 Cause Significantly Increased Vaccine Breakthrough COVID-19 Cases in Houston, Texas. <i>American Journal of Pathology</i> , 2022, 192, 320-331.	1.9	90
2	Integrative Reverse Genetic Analysis Identifies Polymorphisms Contributing to Decreased Antimicrobial Agent Susceptibility in <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2022, 13, e0361821.	1.8	11
3	Multiple spillovers from humans and onward transmission of SARS-CoV-2 in white-tailed deer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	164
4	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, Texas. <i>American Journal of Pathology</i> , 2022, 192, 642-652.	1.9	161
5	Human M1 macrophages express unique innate immune response genes after mycobacterial infection to defend against tuberculosis. <i>Communications Biology</i> , 2022, 5, 480.	2.0	14
6	A Chimeric Penicillin Binding Protein 2X Significantly Decreases <i>In Vitro</i> Beta-Lactam Susceptibility and Increases <i>In Vivo</i> Fitness of <i>Streptococcus pyogenes</i> . <i>American Journal of Pathology</i> , 2022, 192, 1397-1406.	1.9	2
7	Transmission history of SARS-CoV-2 in humans and white-tailed deer. <i>Scientific Reports</i> , 2022, 12, .	1.6	13
8	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. <i>American Journal of Pathology</i> , 2021, 191, 90-107.	1.9	131
9	Limited window for donation of convalescent plasma with high live-virus neutralizing antibody titers for COVID-19 immunotherapy. <i>Communications Biology</i> , 2021, 4, 267.	2.0	25
10	The Effect of Convalescent Plasma Therapy on Mortality Among Patients With COVID-19: Systematic Review and Meta-analysis. <i>Mayo Clinic Proceedings</i> , 2021, 96, 1262-1275.	1.4	129
11	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. <i>American Journal of Pathology</i> , 2021, 191, 983-992.	1.9	42
12	Functional Insights into the High-Molecular-Mass Penicillin-Binding Proteins of <i>Streptococcus agalactiae</i> Revealed by Gene Deletion and Transposon Mutagenesis Analysis. <i>Journal of Bacteriology</i> , 2021, 203, e0023421.	1.0	8
13	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. <i>American Journal of Pathology</i> , 2021, 191, 1754-1773.	1.9	26
14	Real-world Assessment of 2,879 COVID-19 Patients Treated with Monoclonal Antibody Therapy: A Propensity Score-Matched Cohort Study. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab512.	0.4	11
15	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. <i>Microbiology Spectrum</i> , 2021, 9, e0180321.	1.2	50
16	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
17	Genome-Wide Assessment of <i>Streptococcus agalactiae</i> Genes Required for Survival in Human Whole Blood and Plasma. <i>Infection and Immunity</i> , 2020, 88, .	1.0	9
18	Predicting $\beta$ -lactam resistance using whole genome sequencing in <i>Klebsiella pneumoniae</i> : the challenge of $\beta$ -lactamase inhibitors. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115149.	0.8	3

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19	Treatment of Coronavirus Disease 2019 Patients with Convalescent Plasma Reveals a Signal of Significantly Decreased Mortality. <i>American Journal of Pathology</i> , 2020, 190, 2290-2303.	1.9	197
20	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area. <i>MBio</i> , 2020, 11, .	1.8	99
21	Genetic Basis Underlying the Hyperhemolytic Phenotype of <i>Streptococcus agalactiae</i> Strain CNCTC10/84. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	10
22	Single Amino Acid Replacements in RocA Disrupt Protein-Protein Interactions To Alter the Molecular Pathogenesis of Group A <i>Streptococcus</i> . <i>Infection and Immunity</i> , 2020, 88, .	1.0	4
23	New Pathogenesis Mechanisms and Translational Leads Identified by Multidimensional Analysis of Necrotizing Myositis in Primates. <i>MBio</i> , 2020, 11, .	1.8	21
24	Treatment of Coronavirus Disease 2019 (COVID-19) Patients with Convalescent Plasma. <i>American Journal of Pathology</i> , 2020, 190, 1680-1690.	1.9	239
25	Population Genomic Molecular Epidemiological Study of Macrolide-Resistant <i>Streptococcus pyogenes</i> in Iceland, 1995 to 2016: Identification of a Large Clonal Population with a <i>pbp2x</i> Mutation Conferring Reduced <i>In Vitro</i> $\beta$ -Lactam Susceptibility. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	21
26	A Single Amino Acid Replacement in Penicillin-Binding Protein 2X in <i>Streptococcus pyogenes</i> Significantly Increases Fitness on Subtherapeutic Benzylpenicillin Treatment in a Mouse Model of Necrotizing Myositis. <i>American Journal of Pathology</i> , 2020, 190, 1625-1631.	1.9	13
27	Genome-Wide Screens Identify Group A <i>Streptococcus</i> Surface Proteins Promoting Female Genital Tract Colonization and Virulence. <i>American Journal of Pathology</i> , 2020, 190, 862-873.	1.9	9
28	Genetic heterogeneity of the Spy1336/R28a Spy1337 virulence axis in <i>Streptococcus pyogenes</i> and effect on gene transcript levels and pathogenesis. <i>PLoS ONE</i> , 2020, 15, e0229064.	1.1	9
29	Human Infections Caused by Clonally Related African Clade (Clade III) Strains of <i>Candida auris</i> in the Greater Houston Region. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	1
30	Development and Evaluation of a Novel Protein-Based Assay for Specific Detection of KPC $\beta$ -Lactamases from <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>MSphere</i> , 2020, 5, .	1.3	3
31	Reduced <i>In Vitro</i> Susceptibility of <i>Streptococcus pyogenes</i> to $\beta$ -Lactam Antibiotics Associated with Mutations in the <i>pbp2x</i> Gene Is Geographically Widespread. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	55
32	<i>Streptococcus pyogenes</i> genes that promote pharyngitis in primates. <i>JCI Insight</i> , 2020, 5, .	2.3	8
33	Convalescent plasma anti-SARS-CoV-2 spike protein ectodomain and receptor-binding domain IgG correlate with virus neutralization. <i>Journal of Clinical Investigation</i> , 2020, 130, 6728-6738.	3.9	172
34	MOLECULAR MECHANISMS CONTRIBUTING TO FUZZY EPIDEMICS CAUSED BY GROUP A STREPTOCOCCUS, A FLESH-EATING HUMAN BACTERIAL PATHOGEN. <i>Transactions of the American Clinical and Climatological Association</i> , 2020, 131, 356-368.	0.9	3
35	Polymorphisms in Regulator of Cov Contribute to the Molecular Pathogenesis of Serotype M28 Group A <i>Streptococcus</i> . <i>American Journal of Pathology</i> , 2019, 189, 2002-2018.	1.9	7
36	Draft Genome Sequence of <i>Candida auris</i> Strain LOM, a Human Clinical Isolate from Greater Metropolitan Houston, Texas. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4

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37	Metal sensing and regulation of adaptive responses to manganese limitation by MtsR is critical for group A streptococcus virulence. <i>Nucleic Acids Research</i> , 2019, 47, 7476-7493.	6.5	18
38	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into <i>Streptococcus pyogenes</i> pathogenesis. <i>Nature Genetics</i> , 2019, 51, 548-559.	9.4	58
39	Gene fitness landscape of group A streptococcus during necrotizing myositis. <i>Journal of Clinical Investigation</i> , 2019, 129, 887-901.	3.9	34
40	Signaling by a Conserved Quorum Sensing Pathway Contributes to Growth <i>Ex Vivo</i> and Oropharyngeal Colonization of Human Pathogen Group A <i>Streptococcus</i> . <i>Infection and Immunity</i> , 2018, 86, .	1.0	13
41	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.	1.6	136
42	A Web-Based Respiratory Pathogen Laboratory Report for Summarizing Key Metrics to Stakeholders. <i>American Journal of Clinical Pathology</i> , 2018, 150, S153-S154.	0.4	0
43	2558. Predicting $\beta$ -Lactam Resistance Using Whole Genome Sequencing (WGS) in <i>Klebsiella pneumoniae</i> : The Challenge of $\beta$ -Lactam Inhibitors. <i>Open Forum Infectious Diseases</i> , 2018, 5, S70-S70.	0.4	1
44	Phenotypic Variation in the Group A <i>Streptococcus</i> Due to Natural Mutation of the Accessory Protein-Encoding Gene <i>rocA</i> . <i>MSphere</i> , 2018, 3, .	1.3	8
45	Postpartum Group A <i>Streptococcus</i> Case Series: Reach Out to Infection Prevention!. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy159.	0.4	4
46	RocA Has Serotype-Specific Gene Regulatory and Pathogenesis Activities in Serotype M28 Group A <i>Streptococcus</i> . <i>Infection and Immunity</i> , 2018, 86, .	1.0	14
47	Increased Pilus Production Conferred by a Naturally Occurring Mutation Alters Host-Pathogen Interaction in Favor of Carriage in <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , 2017, 85, .	1.0	21
48	Opacification Domain of Serum Opacity Factor Inhibits Beta-Hemolysis and Contributes to Virulence of <i>Streptococcus pyogenes</i> . <i>MSphere</i> , 2017, 2, .	1.3	6
49	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. <i>MBio</i> , 2017, 8, .	1.8	124
50	Contribution of Secreted NADase and Streptolysin O to the Pathogenesis of Epidemic Serotype M1 <i>Streptococcus pyogenes</i> Infections. <i>American Journal of Pathology</i> , 2017, 187, 605-613.	1.9	57
51	Leaderless secreted peptide signaling molecule alters global gene expression and increases virulence of a human bacterial pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8498-E8507.	3.3	46
52	Whole-Genome Sequencing of a Human Clinical Isolate of emm28 <i>Streptococcus pyogenes</i> Causing Necrotizing Fasciitis Acquired Contemporaneously with Hurricane Harvey. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
53	Novel Genes Required for the Fitness of <i>Streptococcus pyogenes</i> in Human Saliva. <i>MSphere</i> , 2017, 2, .	1.3	30
54	Rapid Emergence of a New Clone Impacts the Population at Risk and Increases the Incidence of Type emm89 Group A <i>Streptococcus</i> Invasive Disease. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx042.	0.4	4

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55	Genome sequence analysis of emm89 <i>Streptococcus pyogenes</i> strains causing infections in Scotland, 2010–2016. <i>Journal of Medical Microbiology</i> , 2017, 66, 1765-1773.	0.7	18
56	Interacting networks of resistance, virulence and core machinery genes identified by genome-wide epistasis analysis. <i>PLoS Genetics</i> , 2017, 13, e1006508.	1.5	85
57	Deletion of <i>atoR</i> from <i>Streptococcus pyogenes</i> Results in Hypervirulence in a Mouse Model of Sepsis and is LuxS Independent. <i>Polish Journal of Microbiology</i> , 2017, 66, 17-24.	0.6	4
58	Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2016, 7, .	1.8	47
59	Intergenic Variable-Number Tandem-Repeat Polymorphism Upstream of <i>rocA</i> Alters Toxin Production and Enhances Virulence in <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , 2016, 84, 2086-2093.	1.0	20
60	Integrating Rapid Diagnostics and Antimicrobial Stewardship in Two Community Hospitals Improved Process Measures and Antibiotic Adjustment Time. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 425-432.	1.0	65
61	Genomic Landscape of Intrahost Variation in Group A <i>Streptococcus</i> : Repeated and Abundant Mutational Inactivation of the <i>fabT</i> Gene Encoding a Regulator of Fatty Acid Synthesis. <i>Infection and Immunity</i> , 2016, 84, 3268-3281.	1.0	24
62	Genomic Characteristics Behind the Spread of Bacteremic Group A <i>Streptococcus</i> Type emm89 in Finland, 2004–2014. <i>Journal of Infectious Diseases</i> , 2016, 214, 1987-1995.	1.9	22
63	Structural and functional analysis of RopB: a major virulence regulator in <i>Streptococcus pyogenes</i> . <i>Molecular Microbiology</i> , 2016, 99, 1119-1133.	1.2	24
64	Musser et al. Reply to “Emergence of the Same Successful Clade among Distinct Populations of emm89 <i>Streptococcus pyogenes</i> in Multiple Geographic Regions” <i>MBio</i> , 2015, 6, e01838-15.	1.8	3
65	The Majority of 9,729 Group A <i>Streptococcus</i> Strains Causing Disease Secrete SpeB Cysteine Protease: Pathogenesis Implications. <i>Infection and Immunity</i> , 2015, 83, 4750-4758.	1.0	33
66	Phosphorylation Events in the Multiple Gene Regulator of Group A <i>Streptococcus</i> Significantly Influence Global Gene Expression and Virulence. <i>Infection and Immunity</i> , 2015, 83, 2382-2395.	1.0	18
67	Molecular Pathogenesis Lessons from the World of Infectious Diseases Research. <i>American Journal of Pathology</i> , 2015, 185, 1502-1504.	1.9	0
68	Natural Variant of Collagen-Like Protein A in Serotype M3 Group A <i>Streptococcus</i> Increases Adherence and Decreases Invasive Potential. <i>Infection and Immunity</i> , 2015, 83, 1122-1129.	1.0	17
69	Adhesin competence repressor ( <i>AdcR</i> ) from <i>Streptococcus pyogenes</i> controls adaptive responses to zinc limitation and contributes to virulence. <i>Nucleic Acids Research</i> , 2015, 43, 418-432.	6.5	55
70	Trading Capsule for Increased Cytotoxin Production: Contribution to Virulence of a Newly Emerged Clade of emm89 <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2015, 6, e01378-15.	1.8	76
71	A Single Amino Acid Replacement in the Sensor Kinase <i>LiaS</i> Contributes to a Carrier Phenotype in Group A <i>Streptococcus</i> . <i>Infection and Immunity</i> , 2015, 83, 4237-4246.	1.0	17
72	A Naturally Occurring Single Amino Acid Replacement in Multiple Gene Regulator of Group A <i>Streptococcus</i> Significantly Increases Virulence. <i>American Journal of Pathology</i> , 2015, 185, 462-471.	1.9	19

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73	A molecular trigger for intercontinental epidemics of group A <i>Streptococcus</i> . <i>Journal of Clinical Investigation</i> , 2015, 125, 3545-3559.	3.9	119
74	Evolutionary pathway to increased virulence and epidemic group A <i>Streptococcus</i> disease derived from 3,615 genome sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1768-76.	3.3	215
75	Absence of Patient-to-Patient Intrahospital Transmission of <i>Staphylococcus aureus</i> as Determined by Whole-Genome Sequencing. <i>MBio</i> , 2014, 5, e01692-14.	1.8	78
76	Clinical Laboratory Response to a Mock Outbreak of Invasive Bacterial Infections: a Preparedness Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4210-4216.	1.8	22
77	Asymptomatic Carriage of Group A <i>Streptococcus</i> Is Associated with Elimination of Capsule Production. <i>Infection and Immunity</i> , 2014, 82, 3958-3967.	1.0	40
78	Molecular dissection of the evolution of carbapenem-resistant multilocus sequence type 258 <i>Klebsiella pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4988-4993.	3.3	325
79	PBP2a Mutations Causing High-Level Ceftaroline Resistance in Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6668-6674.	1.4	120
80	Integrating rapid diagnostics and antimicrobial stewardship improves outcomes in patients with antibiotic-resistant Gram-negative bacteremia. <i>Journal of Infection</i> , 2014, 69, 216-225.	1.7	252
81	S. Burt Wolbach, Rocky Mountain Spotted Fever, and Blood-Sucking Arthropods. <i>American Journal of Pathology</i> , 2013, 182, 291-293.	1.9	1
82	Evaluation of large genotypic <i>Mycobacterium tuberculosis</i> clusters: contributions from remote and recent transmission. <i>Tuberculosis</i> , 2013, 93, S38-S46.	0.8	10
83	Integrating Rapid Pathogen Identification and Antimicrobial Stewardship Significantly Decreases Hospital Costs. <i>Archives of Pathology and Laboratory Medicine</i> , 2013, 137, 1247-1254.	1.2	336
84	Natural Variation in the Promoter of the Gene Encoding the Mga Regulator Alters Host-Pathogen Interactions in Group A <i>Streptococcus</i> Carrier Strains. <i>Infection and Immunity</i> , 2013, 81, 4128-4138.	1.0	36
85	Integrated whole-genome sequencing and temporospatial analysis of a continuing Group A <i>Streptococcus</i> epidemic. <i>Emerging Microbes and Infections</i> , 2013, 2, 1-8.	3.0	16
86	Seasonal H3N2 influenza A virus fails to enhance <i>Staphylococcus aureus</i> co-infection in a non-human primate respiratory tract infection model. <i>Virulence</i> , 2013, 4, 707-715.	1.8	25
87	Bacterial Genomics in Infectious Disease and the Clinical Pathology Laboratory. <i>Archives of Pathology and Laboratory Medicine</i> , 2012, 136, 1414-1422.	1.2	34
88	Human Disease Isolates of Serotype M4 and M22 Group A <i>Streptococcus</i> Lack Genes Required for Hyaluronic Acid Capsule Biosynthesis. <i>MBio</i> , 2012, 3, e00413-12.	1.8	53
89	Multi High-Throughput Approach for Highly Selective Identification of Vaccine Candidates: the Group A <i>Streptococcus</i> Case. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015693.	2.5	115
90	Full-Genome Dissection of an Epidemic of Severe Invasive Disease Caused by a Hypervirulent, Recently Emerged Clone of Group A <i>Streptococcus</i> . <i>American Journal of Pathology</i> , 2012, 180, 1522-1534.	1.9	70

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91	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. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2452-2454.	1.8	64
92	Polymorphisms in regulator of protease B (RopB) alter disease phenotype and strain virulence of serotype M3 Group A <i>Streptococcus</i> . <i>FASEB Journal</i> , 2012, 26, 1034.3.	0.2	0
93	Whole Genome Sequence Analysis of a <i>B. cereus</i> Strain Causing a Fatal Anthrax-Like Pulmonary Infection. <i>FASEB Journal</i> , 2012, 26, 1034.5.	0.2	0
94	Molecular differentiation of historic phage-type 80/81 and contemporary epidemic <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18091-18096.	3.3	139
95	Group A <i>Streptococcus emm</i> Gene Types in Pharyngeal Isolates, Ontario, Canada, 2002–2010. <i>Emerging Infectious Diseases</i> , 2011, 17, 2010-7.	2.0	65
96	Lateral gene transfer of streptococcal ICE element RD2 (region of difference 2) encoding secreted proteins. <i>BMC Microbiology</i> , 2011, 11, 65.	1.3	51
97	Rapidly Progressive, Fatal, Inhalation Anthrax-like Infection in a Human: Case Report, Pathogen Genome Sequencing, Pathology, and Coordinated Response. <i>Archives of Pathology and Laboratory Medicine</i> , 2011, 135, 1447-1459.	1.2	64
98	Distinct signatures of diversifying selection revealed by genome analysis of respiratory tract and invasive bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5039-5044.	3.3	90
99	Distinct Single Amino Acid Replacements in the Control of Virulence Regulator Protein Differentially Impact Streptococcal Pathogenesis. <i>PLoS Pathogens</i> , 2011, 7, e1002311.	2.1	42
100	Naturally occurring single amino acid replacements in a regulatory protein alter streptococcal gene expression and virulence in mice. <i>Journal of Clinical Investigation</i> , 2011, 121, 1956-1968.	3.9	63
101	Decreased necrotizing fasciitis capacity caused by a single nucleotide mutation that alters a multiple gene virulence axis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 888-893.	3.3	99
102	Molecular complexity of successive bacterial epidemics deconvoluted by comparative pathogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4371-4376.	3.3	153
103	A Combination of Independent Transcriptional Regulators Shapes Bacterial Virulence Gene Expression during Infection. <i>PLoS Pathogens</i> , 2010, 6, e1000817.	2.1	57
104	Molecular Pathogenesis of Necrotizing Fasciitis. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2010, 5, 1-31.	9.6	117
105	CovS Simultaneously Activates and Inhibits the CovR-Mediated Repression of Distinct Subsets of Group A <i>Streptococcus</i> Virulence Factor-Encoding Genes. <i>Infection and Immunity</i> , 2009, 77, 3141-3149.	1.0	106
106	Contribution of AmyA, an extracellular $\alpha$ -glucan degrading enzyme, to group A streptococcal host-pathogen interaction. <i>Molecular Microbiology</i> , 2009, 74, 159-174.	1.2	16
107	Molecular mechanisms underlying group A streptococcal pathogenesis. <i>Cellular Microbiology</i> , 2009, 11, 1-12.	1.1	99
108	A decade of molecular pathogenomic analysis of group A <i>Streptococcus</i> . <i>Journal of Clinical Investigation</i> , 2009, 119, 2455-2463.	3.9	80

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109	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
110	The role of complex carbohydrate catabolism in the pathogenesis of invasive streptococci. Trends in Microbiology, 2008, 16, 318-325.	3.5	109
111	A Non-Human Primate Model of Acute Group A Streptococcus Pharyngitis. , 2008, 431, 255-267.		21
112	A Naturally Occurring Single Nucleotide Mutation Significantly Impairs Necrotizing Fasciitis (â€œFlesh) Tj ETQq0 0 0 rgBT /Overlock 10	0.2	1
113	Contribution of Exogenous Genetic Elements to the Group A Streptococcus Metagenome. PLoS ONE, 2007, 2, e800.	1.1	155
114	Analysis of the Transcriptome of Group A Streptococcus in Mouse Soft Tissue Infection. American Journal of Pathology, 2006, 169, 927-942.	1.9	86
115	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
116	emm typing of invasive T28 group A streptococci, 1995â€“2004, Finland. Journal of Medical Microbiology, 2006, 55, 1701-1706.	0.7	19
117	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
118	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
119	Evolutionary Origin and Emergence of a Highly Successful Clone of Serotype M1 Group A Streptococcus Involved Multiple Horizontal Gene Transfer Events. Journal of Infectious Diseases, 2005, 192, 771-782.	1.9	312
120	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
121	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
122	Genome Sequence of a Serotype M28 Strain of Group A Streptococcus: Potential New Insights into Puerperal Sepsis and Bacterial Disease Specificity. Journal of Infectious Diseases, 2005, 192, 760-770.	1.9	214
123	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
124	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
125	Progress toward Characterization of the Group A Streptococcus Metagenome: Complete Genome Sequence of a Macrolideâ€“Resistant Serotype M6 Strain. Journal of Infectious Diseases, 2004, 190, 727-738.	1.9	172
126	Identification of New Candidate Vaccine Antigens Made by Streptococcus pyogenes: Purification and Characterization of 16 Putative Extracellular Lipoproteins. Journal of Infectious Diseases, 2004, 189, 79-89.	1.9	75



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127	Engagement of the Pathogen Survival Response Used by Group A <i>Streptococcus</i> to Avert Destruction by Innate Host Defense. <i>Journal of Immunology</i> , 2004, 173, 1194-1201.	0.4	77
128	Characterization of an Extracellular Virulence Factor Made by Group A <i>Streptococcus</i> with Homology to the <i>Listeria monocytogenes</i> Internalin Family of Proteins. <i>Infection and Immunity</i> , 2003, 71, 7043-7052.	1.0	47
129	Genome-wide protective response used by group A <i>Streptococcus</i> to evade destruction by human polymorphonuclear leukocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1996-2001.	3.3	148
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