

Stephen B Beres

List of Publications by Year in descending order

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64
papers

4,477
citations

126858

33
h-index

128225

60
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69
all docs

69
docs citations

69
times ranked

3390
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	Genetic Basis Underlying the Hyperhemolytic Phenotype of <i>Streptococcus agalactiae</i> Strain CNCTC10/84. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	10
6	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> β -Lactam Susceptibility. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	21
7	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
8	Genetic heterogeneity of the Spy1336/R28â€”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
9	Reduced <i>In Vitro</i> Susceptibility of <i>Streptococcus pyogenes</i> to β -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
10	<i>Streptococcus pyogenes</i> genes that promote pharyngitis in primates. <i>JCI Insight</i> , 2020, 5, .	2.3	8
11	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
12	Gene fitness landscape of group A streptococcus during necrotizing myositis. <i>Journal of Clinical Investigation</i> , 2019, 129, 887-901.	3.9	34
13	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
14	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
15	Case Series Description and Genomic Characterization of Invasive Group A Streptococcal Infections in Pediatric Patients. <i>Pediatric Infectious Disease Journal</i> , 2017, 36, 618-620.	1.1	2
16	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
17	Novel Genes Required for the Fitness of <i>Streptococcus pyogenes</i> in Human Saliva. <i>MSphere</i> , 2017, 2, .	1.3	30
18	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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19	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
20	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
21	Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2016, 7, .	1.8	47
22	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
23	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
24	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
25	Comparative Whole Genome Sequencing of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 8 from Primary Care Clinics in a Texas Community. <i>Pharmacotherapy</i> , 2015, 35, 220-228.	1.2	14
26	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
27	Group A <i>Streptococcus</i> and <i>Staphylococcus aureus</i> : Evolution, Reemergence, and Strain Diversification. , 2014, , 251-272.		0
28	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
29	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
30	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
31	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
32	Natural Disruption of Two Regulatory Networks in Serotype M3 Group A <i>Streptococcus</i> Isolates Contributes to the Virulence Factor Profile of This Hypervirulent Serotype. <i>Infection and Immunity</i> , 2014, 82, 1744-1754.	1.0	30
33	High-throughput <i>scRNA</i> sequencing of a formalin-fixed, paraffin-embedded autopsy lung tissue sample from the 1918 influenza pandemic. <i>Journal of Pathology</i> , 2013, 229, 535-545.	2.1	74
34	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
35	Polymorphisms in Regulator of Protease B (RopB) Alter Disease Phenotype and Strain Virulence of Serotype M3 Group A <i>Streptococcus</i> . <i>Journal of Infectious Diseases</i> , 2012, 205, 1719-1729.	1.9	25
36	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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37	Genomic Analysis of <i>emm59</i> Group A <i>Streptococcus</i> Invasive Strains, United States. <i>Emerging Infectious Diseases</i> , 2012, 18, 650-652.	2.0	23
38	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
39	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
40	Evolution of diversity in epidemics revealed by analysis of the human bacterial pathogen group A <i>Streptococcus</i> . <i>Epidemics</i> , 2011, 3, 159-170.	1.5	10
41	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
42	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
43	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
44	Virulence of serotype M3 Group A <i>Streptococcus</i> strains in wax worms (<i>Galleria</i>). <i>Trends in Microbiology</i> , 2011, 19, 462-467.	1.8	82
45	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
46	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
47	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
48	Contribution of AmyA, an extracellular α -glucan degrading enzyme, to group A streptococcal host-pathogen interaction. <i>Molecular Microbiology</i> , 2009, 74, 159-174.	1.2	16
49	Genome Sequence of a Lancefield Group C <i>Streptococcus zooepidemicus</i> Strain Causing Epidemic Nephritis: New Information about an Old Disease. <i>PLoS ONE</i> , 2008, 3, e3026.	1.1	115
50	A Naturally Occurring Single Nucleotide Mutation Significantly Impairs Necrotizing Fasciitis (‘Flesh’) in Waxworms (<i>Galleria mellonella</i>). <i>PLoS ONE</i> , 2008, 3, e3026.	0.2	1
51	Contribution of Exogenous Genetic Elements to the Group A <i>Streptococcus</i> Metagenome. <i>PLoS ONE</i> , 2007, 2, e800.	1.1	155
52	Molecular genetic anatomy of inter- and intraserotype variation in the human bacterial pathogen group A <i>Streptococcus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7059-7064.	3.3	203
53	Genetic Diversity among Type <i>emm28</i> Group A <i>Streptococcus</i> Strains Causing Invasive Infections and Pharyngitis. <i>Journal of Clinical Microbiology</i> , 2005, 43, 4083-4091.	1.8	52
54	Genome Sequence of a Serotype M28 Strain of Group A <i>Streptococcus</i> : Potential New Insights into Puerperal Sepsis and Bacterial Disease Specificity. <i>Journal of Infectious Diseases</i> , 2005, 192, 760-770.	1.9	214

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55	Genome-wide molecular dissection of serotype M3 group A Streptococcus strains causing two epidemics of invasive infections. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11833-11838.	3.3	121
56	Progress toward Characterization of the Group A Streptococcus Metagenome: Complete Genome Sequence of a Macrolide-Resistant Serotype M6 Strain. Journal of Infectious Diseases, 2004, 190, 727-738.	1.9	172
57	Analysis of a Novel Prophage-encoded Group A Streptococcus Extracellular Phospholipase A2. Journal of Biological Chemistry, 2004, 279, 45909-45918.	1.6	35
58	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
59	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
60	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
61	In Vitro Serial Passage of <i>Staphylococcus aureus</i> : Changes in Physiology, Virulence Factor Production, and <i>agr</i> Nucleotide Sequence. Journal of Bacteriology, 2002, 184, 1430-1437.	1.0	166
62	The fundamental contribution of phages to GAS evolution, genome diversification and strain emergence. Trends in Microbiology, 2002, 10, 515-521.	3.5	199
63	The Serotype of Type Ia and III Group B Streptococci Is Determined by the Polymerase Gene within the Polycistronic Capsule Operon. Journal of Bacteriology, 2000, 182, 4466-4477.	1.0	114
64	Contribution of Phages to Group A Streptococcus Genetic Diversity and Pathogenesis. , 0, , 319-P4.		3