

Evan S Snitkin

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

2,760
citations

331670

21
h-index

197818

49
g-index

73
all docs

73
docs citations

73
times ranked

4366
citing authors

#	ARTICLE	IF	CITATIONS
1	Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 148ra116.	12.4	781
2	Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae. <i>Science Translational Medicine</i> , 2014, 6, 254ra126.	12.4	307
3	Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14799-14804.	7.1	189
4	Genome-wide recombination drives diversification of epidemic strains of <i>Acinetobacter baumannii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13758-13763.	7.1	169
5	VisANT: an integrative framework for networks in systems biology. <i>Briefings in Bioinformatics</i> , 2008, 9, 317-325.	6.5	121
6	Genomic insights into the fate of colistin resistance and <i>Acinetobacter baumannii</i> during patient treatment. <i>Genome Research</i> , 2013, 23, 1155-1162.	5.5	101
7	Rapid Growth of Uropathogenic <i>Escherichia coli</i> during Human Urinary Tract Infection. <i>MBio</i> , 2018, 9, .	4.1	93
8	Phase-variable capsular polysaccharides and lipoproteins modify bacteriophage susceptibility in <i>Bacteroides thetaiotaomicron</i> . <i>Nature Microbiology</i> , 2020, 5, 1170-1181.	13.3	82
9	Metabolic Network Model of a Human Oral Pathogen. <i>Journal of Bacteriology</i> , 2009, 191, 74-90.	2.2	67
10	Genetically diverse uropathogenic <i>Escherichia coli</i> adopt a common transcriptional program in patients with UTIs. <i>ELife</i> , 2019, 8, .	6.0	56
11	Network of microbial and antibiotic interactions drive colonization and infection with multidrug-resistant organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10467-10472.	7.1	55
12	Epistatic Interaction Maps Relative to Multiple Metabolic Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1001294.	3.5	52
13	Integrated genomic and interfacility patient-transfer data reveal the transmission pathways of multidrug-resistant <i>Klebsiella pneumoniae</i> in a regional outbreak. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	47
14	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. <i>MSystems</i> , 2022, 7, e0094721.	3.8	40
15	Identification of Pathogenicity-Associated Loci in <i>Klebsiella pneumoniae</i> from Hospitalized Patients. <i>MSystems</i> , 2018, 3, .	3.8	38
16	Whole Genome Sequencing—Implications for Infection Prevention and Outbreak Investigations. <i>Current Infectious Disease Reports</i> , 2017, 19, 15.	3.0	37
17	TSG-6 Protein Binding to Glycosaminoglycans. <i>Journal of Biological Chemistry</i> , 2005, 280, 14476-14484.	3.4	34
18	Forest and Trees: Exploring Bacterial Virulence with Genome-wide Association Studies and Machine Learning. <i>Trends in Microbiology</i> , 2021, 29, 621-633.	7.7	34

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19	Genomic and Epidemiological Evidence for Community Origins of Hospital-Onset Methicillin-Resistant <i>Staphylococcus aureus</i> Bloodstream Infections. <i>Journal of Infectious Diseases</i> , 2017, 215, 1640-1647.	4.0	30
20	mikropml: User-Friendly R Package for Supervised Machine Learning Pipelines. <i>Journal of Open Source Software</i> , 2021, 6, 3073.	4.6	29
21	Genomic Epidemiology of USA300 Methicillin-Resistant <i>Staphylococcus aureus</i> in an Urban Community. <i>Clinical Infectious Diseases</i> , 2016, 62, 37-44.	5.8	28
22	MRSA Transmission in Intensive Care Units: Genomic Analysis of Patients, Their Environments, and Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 72, 1879-1887.	5.8	25
23	Whole-Genome Sequencing To Identify Drivers of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Transmission within and between Regional Long-Term Acute-Care Hospitals. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	24
24	Pan-PCR, a Computational Method for Designing Bacterium-Typing Assays Based on Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2013, 51, 752-758.	3.9	23
25	Regional Spread of <i>bla</i> _{NDM-1} -Containing <i>Klebsiella pneumoniae</i> ST147 in Post-Acute Care Facilities. <i>Clinical Infectious Diseases</i> , 2021, 73, 1431-1439.	5.8	23
26	Genetic Determinants of Trehalose Utilization Are Not Associated With Severe <i>Clostridium difficile</i> Infection Outcome. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofz548.	0.9	19
27	Genomic epidemiology of multidrug-resistant Gram-negative organisms. <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 39-56.	3.8	16
28	Frequent Methicillin-Resistant <i>Staphylococcus aureus</i> Introductions Into an Inner-city Jail: Indications of Community Transmission Networks. <i>Clinical Infectious Diseases</i> , 2020, 71, 323-331.	5.8	16
29	Epidemiology of Vancomycin-Resistant <i>Enterococcus faecium</i> and <i>Enterococcus faecalis</i> Colonization in Nursing Facilities. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofz553.	0.9	16
30	Patient and Microbial Genomic Factors Associated with Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Extraintestinal Colonization and Infection. <i>MSystems</i> , 2021, 6, .	3.8	16
31	<i>Pseudomonas aeruginosa</i> adaptation to human hosts. <i>Nature Genetics</i> , 2015, 47, 2-3.	21.4	15
32	Genomic Investigation of a Putative Endoscope-Associated Carbapenem-Resistant <i>Enterobacter cloacae</i> Outbreak Reveals a Wide Diversity of Circulating Strains and Resistance Mutations. <i>Clinical Infectious Diseases</i> , 2018, 66, 460-463.	5.8	14
33	Replication Dynamics for Six Gram-Negative Bacterial Species during Bloodstream Infection. <i>MBio</i> , 2021, 12, e0111421.	4.1	14
34	Contamination of Hospital Plumbing. <i>JAMA Network Open</i> , 2019, 2, e187660.	5.9	11
35	Gut Microbiota Features on Nursing Home Admission Are Associated With Subsequent Acquisition of Antibiotic-resistant Organism Colonization. <i>Clinical Infectious Diseases</i> , 2020, 71, 3244-3247.	5.8	10
36	Application of Combined Genomic and Transfer Analyses to Identify Factors Mediating Regional Spread of Antibiotic-resistant Bacterial Lineages. <i>Clinical Infectious Diseases</i> , 2020, 71, e642-e649.	5.8	10

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37	cognac: rapid generation of concatenated gene alignments for phylogenetic inference from large, bacterial whole genome sequencing datasets. BMC Bioinformatics, 2021, 22, 70.	2.6	10
38	Hogwash: three methods for genome-wide association studies in bacteria. Microbial Genomics, 2020, 6, .	2.0	10
39	Replication Study: Intestinal inflammation targets cancer-inducing activity of the microbiota. ELife, 2018, 7, .	6.0	10
40	Ferric Citrate Uptake Is a Virulence Factor in Uropathogenic Escherichia coli. MBio, 2022, 13, e0103522.	4.1	10
41	Interplay Between Patient Colonization and Environmental Contamination With Vancomycin-Resistant Enterococci and Their Association With Patient Health Outcomes in Postacute Care. Open Forum Infectious Diseases, 2020, 7, ofz519.	0.9	8
42	prewas: data pre-processing for more informative bacterial GWAS. Microbial Genomics, 2020, 6, .	2.0	8
43	A multisite genomic epidemiology study of Clostridioides difficile infections in the USA supports differential roles of healthcare versus community spread for two common strains. Microbial Genomics, 2021, 7, .	2.0	6
44	Genomic Epidemiology of MRSA During Incarceration at a Large Inner-City Jail. Clinical Infectious Diseases, 2021, 73, e3708-e3717.	5.8	5
45	Genomic Update of Phenotypic Prediction Rule for Methicillin-Resistant Staphylococcus aureus (MRSA) USA300 Discloses Jail Transmission Networks with Increased Resistance. Microbiology Spectrum, 2021, 9, e0037621.	3.0	5
46	Outbreak of Murine Infection with Clostridium difficile Associated with the Administration of a Pre- and Perinatal Methyl Donor Diet. MSphere, 2019, 4, .	2.9	4
47	A retrospective cohort study of antibiotic exposure and vancomycin-resistant <i>Enterococcus</i> recolonization. Infection Control and Hospital Epidemiology, 2019, 40, 414-419.	1.8	4
48	Homologous Recombination in Clostridioides difficile Mediates Diversification of Cell Surface Features and Transport Systems. MSphere, 2020, 5, .	2.9	4
49	Cohorting KPC+ <i>Klebsiella pneumoniae</i> (KPC-Kp) "positive patients: A genomic exposé of cross-colonization hazards in a long-term acute-care hospital (LTACH). Infection Control and Hospital Epidemiology, 2020, 41, 1162-1168.	1.8	3
50	Strain Variation in Clostridioides difficile Cytotoxicity Associated with Genomic Variation at Both Pathogenic and Nonpathogenic Loci. MSphere, 2022, 7, .	2.9	3
51	Threshold-free genomic cluster detection to track transmission pathways in health-care settings: a genomic epidemiology analysis. Lancet Microbe, The, 2022, , .	7.3	3
52	1247. Genomic Epidemiology of MRSA DURING Incarceration at a Large Inner-City Jail. Open Forum Infectious Diseases, 2018, 5, S379-S379.	0.9	2
53	Genomic Analysis of Community Transmission Networks for MRSA Among Females Entering a Large Inner-city Jail. Open Forum Infectious Diseases, 2022, 9, ofac049.	0.9	2
54	regentrans: a framework and R package for using genomics to study regional pathogen transmission. Microbial Genomics, 2022, 8, .	2.0	2

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55	159. Genomic Epidemiology of MRSA at Intake to a Large Inner-City Jail: Evidence for Community Transmission Networks?. <i>Open Forum Infectious Diseases</i> , 2018, 5, S13-S14.	0.9	1
56	Cohorting KPC+ <i>Klebsiella pneumoniae</i> (KPC-Kp)â€“Positive Patientsâ€”A Genomic ExposÃ© of Cross-Colonization Hazards. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, s172-s173.	1.8	0