Evan S Snitkin

List of Publications by Year
in descending order

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	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
2	regentrans: a framework and R package for using genomics to study regional pathogen transmission. Microbial Genomics, 2022, 8, .	2.0	2
3	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. MSystems, 2022, 7, e0094721.	3.8	40
4	Strain Variation in Clostridioides difficile Cytotoxicity Associated with Genomic Variation at Both Pathogenic and Nonpathogenic Loci. MSphere, 2022, 7, .	2.9	3
5	Ferric Citrate Uptake Is a Virulence Factor in Uropathogenic Escherichia coli. MBio, 2022, 13, e0103522.	4.1	10
6	Threshold-free genomic cluster detection to track transmission pathways in health-care settings: a genomic epidemiology analysis. Lancet Microbe, The, 2022, , .	7.3	3
7	MRSA Transmission in Intensive Care Units: Genomic Analysis of Patients, Their Environments, and Healthcare Workers. Clinical Infectious Diseases, 2021, 72, 1879-1887.	5.8	25
8	Genomic Epidemiology of MRSA During Incarceration at a Large Inner-City Jail. Clinical Infectious Diseases, 2021, 73, e3708-e3717.	5.8	5
9	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
10	Patient and Microbial Genomic Factors Associated with Carbapenem-Resistant Klebsiella pneumoniae Extraintestinal Colonization and Infection. MSystems, 2021, 6, .	3.8	16
11	mikropml: User-Friendly R Package for Supervised Machine Learning Pipelines. Journal of Open Source Software, 2021, 6, 3073.	4.6	29
12	Regional Spread of <i>bla</i>NDM-1-Containing <i>Klebsiella pneumoniae</i> ST147 in Post-Acute Care Facilities. Clinical Infectious Diseases, 2021, 73, 1431-1439.	5.8	23
13	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
14	Forest and Trees: Exploring Bacterial Virulence with Genome-wide Association Studies and Machine Learning. Trends in Microbiology, 2021, 29, 621-633.	7.7	34
15	Replication Dynamics for Six Gram-Negative Bacterial Species during Bloodstream Infection. MBio, 2021, 12, e0111421.	4.1	14
16	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
17	Frequent Methicillin-Resistant Staphylococcus aureus Introductions Into an Inner-city Jail: Indications of Community Transmission Networks. Clinical Infectious Diseases, 2020, 71, 323-331.	5.8	16
18	Gut Microbiota Features on Nursing Home Admission Are Associated With Subsequent Acquisition of Antibiotic-resistant Organism Colonization. Clinical Infectious Diseases, 2020, 71, 3244-3247.	5.8	10

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19	Phase-variable capsular polysaccharides and lipoproteins modify bacteriophage susceptibility in Bacteroides thetaiotaomicron. Nature Microbiology, 2020, 5, 1170-1181.	13.3	82
20	Cohorting KPC+ <i>Klebsiella pneumoniae</i> (KPC-Kp)â€"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
21	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
22	Epidemiology of Vancomycin-Resistant Enterococcus faecium and Enterococcus faecalis Colonization in Nursing Facilities. Open Forum Infectious Diseases, 2020, 7, ofz553.	0.9	16
23	Genetic Determinants of Trehalose Utilization Are Not Associated With Severe Clostridium difficile Infection Outcome. Open Forum Infectious Diseases, 2020, 7, ofz548.	0.9	19
24	Application of Combined Genomic and Transfer Analyses to Identify Factors Mediating Regional Spread of Antibiotic-resistant Bacterial Lineages. Clinical Infectious Diseases, 2020, 71, e642-e649.	5.8	10
25	prewas: data pre-processing for more informative bacterial GWAS. Microbial Genomics, 2020, 6, .	2.0	8
26	Hogwash: three methods for genome-wide association studies in bacteria. Microbial Genomics, 2020, 6, .	2.0	10
27	Homologous Recombination in Clostridioides difficile Mediates Diversification of Cell Surface Features and Transport Systems. MSphere, 2020, 5, .	2.9	4
28	Cohorting KPC+ <i>Klebsiella pneumoniae</i> (KPC-Kp)â€"Positive Patientsâ€"A Genomic Exposé of Cross-Colonization Hazards. Infection Control and Hospital Epidemiology, 2020, 41, s172-s173.	1.8	0
29	Whole-Genome Sequencing To Identify Drivers of Carbapenem-Resistant Klebsiella pneumoniae Transmission within and between Regional Long-Term Acute-Care Hospitals. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	24
30	Contamination of Hospital Plumbing. JAMA Network Open, 2019, 2, e187660.	5.9	11
31	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
32	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
33	Genomic epidemiology of multidrugâ€resistant Gramâ€negative organisms. Annals of the New York Academy of Sciences, 2019, 1435, 39-56.	3.8	16
34	Genetically diverse uropathogenic Escherichia coli adopt a common transcriptional program in patients with UTIs. ELife, 2019, 8, .	6.0	56
35	Rapid Growth of Uropathogenic <i>Escherichia coli</i> during Human Urinary Tract Infection. MBio, 2018, 9, .	4.1	93
36	Genomic Investigation of a Putative Endoscope-Associated Carbapenem-Resistant Enterobacter cloacae Outbreak Reveals a Wide Diversity of Circulating Strains and Resistance Mutations. Clinical Infectious Diseases, 2018, 66, 460-463.	5.8	14

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37	159. Genomic Epidemiology of MRSA at Intake to a Large Inner-City Jail: Evidence for Community Transmission Networks?. Open Forum Infectious Diseases, 2018, 5, S13-S14.	0.9	1
38	1247. Genomic Epidemiology of MRSA DURING Incarceration at a Large Inner-City Jail. Open Forum Infectious Diseases, 2018, 5, S379-S379.	0.9	2
39	Identification of Pathogenicity-Associated Loci in Klebsiella pneumoniae from Hospitalized Patients. MSystems, 2018, 3, .	3.8	38
40	Replication Study: Intestinal inflammation targets cancer-inducing activity of the microbiota. ELife, 2018, 7, .	6.0	10
41	Genomic and Epidemiological Evidence for Community Origins of Hospital-Onset Methicillin-Resistant Staphylococcus aureus Bloodstream Infections. Journal of Infectious Diseases, 2017, 215, 1640-1647.	4.0	30
42	Whole Genome Sequencingâ€"Implications for Infection Prevention and Outbreak Investigations. Current Infectious Disease Reports, 2017, 19, 15.	3.0	37
43	Network of microbial and antibiotic interactions drive colonization and infection with multidrug-resistant organisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10467-10472.	7.1	55
44	Integrated genomic and interfacility patient-transfer data reveal the transmission pathways of multidrug-resistant <i>Klebsiella pneumoniae</i> in a regional outbreak. Science Translational Medicine, 2017, 9, .	12.4	47
45	Genomic Epidemiology of USA300 Methicillin-ResistantStaphylococcus aureusin an Urban Community. Clinical Infectious Diseases, 2016, 62, 37-44.	5.8	28
46	Pseudomonas aeruginosa adaptation to human hosts. Nature Genetics, 2015, 47, 2-3.	21.4	15
47	Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae. Science Translational Medicine, 2014, 6, 254ra126.	12.4	307
48	Pan-PCR, a Computational Method for Designing Bacterium-Typing Assays Based on Whole-Genome Sequence Data. Journal of Clinical Microbiology, 2013, 51, 752-758.	3.9	23
49	Genomic insights into the fate of colistin resistance and <i>Acinetobacter baumannii</i> during patient treatment. Genome Research, 2013, 23, 1155-1162.	5.5	101
50	Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 148ra116.	12.4	781
51	Genome-wide recombination drives diversification of epidemic strains of <i>Acinetobacter baumannii</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13758-13763.	7.1	169
52	Epistatic Interaction Maps Relative to Multiple Metabolic Phenotypes. PLoS Genetics, 2011, 7, e1001294.	3.5	52
53	Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14799-14804.	7.1	189
54	Metabolic Network Model of a Human Oral Pathogen. Journal of Bacteriology, 2009, 191, 74-90.	2.2	67

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55	VisANT: an integrative framework for networks in systems biology. Briefings in Bioinformatics, 2008, 9, 317-325.	6.5	121
56	TSG-6 Protein Binding to Glycosaminoglycans. Journal of Biological Chemistry, 2005, 280, 14476-14484.	3.4	34