

Kimberly A Bishop-Lilly

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,201
citations

394421

19
h-index

276875

41
g-index

47
all docs

47
docs citations

47
times ranked

3749
citing authors

#	ARTICLE	IF	CITATIONS
1	Development and Use of Personalized Bacteriophage-Based Therapeutic Cocktails To Treat a Patient with a Disseminated Resistant <i>Acinetobacter baumannii</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	795
2	Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. <i>Nucleic Acids Research</i> , 2017, 45, 67-80.	14.5	147
3	Comparison of three next-generation sequencing platforms for metagenomic sequencing and identification of pathogens in blood. <i>BMC Genomics</i> , 2014, 15, 96.	2.8	143
4	Genomic Comparison of <i>Escherichia coli</i> O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage <i>stx2</i> . <i>PLoS ONE</i> , 2012, 7, e48228.	2.5	118
5	Characterizing Phage Genomes for Therapeutic Applications. <i>Viruses</i> , 2018, 10, 188.	3.3	118
6	A Case of Early Reinfection With Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). <i>Clinical Infectious Diseases</i> , 2021, 73, e2827-e2828.	5.8	75
7	Development of a high throughput assay for indirectly measuring phage growth using the OmniLog TM system. <i>Bacteriophage</i> , 2012, 2, 159-167.	1.9	71
8	Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. <i>Journal of Infectious Diseases</i> , 2020, 221, S292-S307.	4.0	64
9	Relatives of rubella virus in diverse mammals. <i>Nature</i> , 2020, 586, 424-428.	27.8	58
10	Arbovirus Detection in Insect Vectors by Rapid, High-Throughput Pyrosequencing. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e878.	3.0	53
11	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. <i>BMC Genomics</i> , 2010, 11, 242.	2.8	46
12	Genomic Signatures of Strain Selection and Enhancement in <i>Bacillus atrophaeus</i> var. <i>globigii</i> , a Historical Biowarfare Simulant. <i>PLoS ONE</i> , 2011, 6, e17836.	2.5	41
13	Reclassification of <i>Wolbachia persica</i> as <i>Francisella persica</i> comb. nov. and emended description of the family Francisellaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1200-1205.	1.7	41
14	Bioinformatic Characterization of Mosquito Viromes within the Eastern United States and Puerto Rico: Discovery of Novel Viruses. <i>Evolutionary Bioinformatics</i> , 2016, 12s2, EBO.S38518.	1.2	38
15	A <i>Yersinia pestis</i> -specific, lytic phage preparation significantly reduces viable <i>Y. pestis</i> on various hard surfaces experimentally contaminated with the bacterium. <i>Bacteriophage</i> , 2012, 2, 168-177.	1.9	34
16	Whole genome sequencing of phage resistant <i>Bacillus anthracis</i> mutants reveals an essential role for cell surface anchoring protein CsaB in phage AP50c adsorption. <i>Virology Journal</i> , 2012, 9, 246.	3.4	28
17	Genetic Evidence for the Involvement of the S-Layer Protein Gene <i>sap</i> and the Sporulation Genes <i>spo0A</i> , <i>spo0B</i> , and <i>spo0F</i> in Phage AP50c Infection of <i>Bacillus anthracis</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1143-1154.	2.2	28
18	Enrichment post-library preparation enhances the sensitivity of high-throughput sequencing-based detection and characterization of viruses from complex samples. <i>BMC Genomics</i> , 2019, 20, 155.	2.8	28

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19	Rapid Identification of Genetic Modifications in <i>Bacillus anthracis</i> Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e12397.	2.5	27
20	Scanning the Landscape of Genome Architecture of Non-O1 and Non-O139 <i>Vibrio cholerae</i> by Whole Genome Mapping Reveals Extensive Population Genetic Diversity. <i>PLoS ONE</i> , 2015, 10, e0120311.	2.5	19
21	Conjugative Transfer of a Novel Staphylococcal Plasmid Encoding the Biocide Resistance Gene, <i>qacA</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2664.	3.5	19
22	Fully Human Immunoglobulin G From Transchromosomal Bovines Treats Nonhuman Primates Infected With Ebola Virus Makona Isolate. <i>Journal of Infectious Diseases</i> , 2018, 218, S636-S648.	4.0	19
23	Genome Sequencing of Four Strains of <i>Rickettsia prowazekii</i> , the Causative Agent of Epidemic Typhus, Including One Flying Squirrel Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
24	Next-Generation Sequencing for Pathogen Detection and Identification. <i>Methods in Microbiology</i> , 2015, 42, 525-554.	0.8	17
25	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	12.8	17
26	Characterization of pPCP1 Plasmids in <i>Yersinia pestis</i> Strains Isolated from the Former Soviet Union. <i>International Journal of Microbiology</i> , 2010, 2010, 1-9.	2.3	15
27	Detection of Recombinant Roussettus Bat Coronavirus GCCDC1 in Lesser Dawn Bats (<i>Eonycteris Tj ETQq1 1 0.784314 rgBT /Overlock</i>	3.3	14
28	An Observational Study of Sepsis in Takeo Province Cambodia: An in-depth examination of pathogens causing severe infections. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008381.	3.0	12
29	Microbial Dysbiosis During Simian Immunodeficiency Virus Infection is Partially Reverted with Combination Anti-retroviral Therapy. <i>Scientific Reports</i> , 2020, 10, 6387.	3.3	11
30	The temporal RNA virome patterns of a lesser dawn bat (<i>Eonycteris spelaea</i>) colony revealed by deep sequencing. <i>Virus Evolution</i> , 2020, 6, veaa017.	4.9	10
31	Genomic epidemiology of MRSA infection and colonization isolates among military trainees with skin and soft tissue infection. <i>Infection</i> , 2019, 47, 729-737.	4.7	8
32	Brief Protocol for EDGE Bioinformatics: Analyzing Microbial and Metagenomic NGS Data. <i>Bio-protocol</i> , 2017, 7, e2622.	0.4	8
33	PheMaDB: A solution for storage, retrieval, and analysis of high throughput phenotype data. <i>BMC Bioinformatics</i> , 2011, 12, 109.	2.6	7
34	Direct-from-blood RNA sequencing identifies the cause of post-bronchoscopy fever. <i>BMC Infectious Diseases</i> , 2019, 19, 905.	2.9	6
35	Prospective Assessment of Symptoms to Evaluate Asymptomatic SARS-CoV-2 Infections in a Cohort of Health Care Workers. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofac030.	0.9	6
36	Differential MicroRNA Analyses of <i>Burkholderia pseudomallei</i> - and <i>Francisella tularensis</i> -Exposed hPBMCs Reveal Potential Biomarkers. <i>International Journal of Genomics</i> , 2017, 2017, 1-13.	1.6	4

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37	Genomic and Virological Characterization of SARS-CoV-2 Variants in a Subset of Unvaccinated and Vaccinated U.S. Military Personnel. <i>Frontiers in Medicine</i> , 2021, 8, 836658.	2.6	4
38	Manual Annotation Studio (MAS): a collaborative platform for manual functional annotation of viral and microbial genomes. <i>BMC Genomics</i> , 2021, 22, 733.	2.8	2
39	High-Quality Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> 268 Isolated from a Patient with a Left Ventricular Assist Device. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
40	Novel Insights for Biosurveillance of Bat-Borne Viruses. <i>Proceedings (mdpi)</i> , 2020, 50, .	0.2	0