

Jennifer L Gardy

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

7,368
citations

87888

38
h-index

69250

77
g-index

94
all docs

94
docs citations

94
times ranked

10452
citing authors

#	ARTICLE	IF	CITATIONS
1	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
2	A Web-Based and In-Person Risk Reframing Intervention to Influence Mothers'™ Tolerance for, and Parenting Practices Associated With, Children's™ Outdoor Risky Play: Randomized Controlled Trial. <i>Journal of Medical Internet Research</i> , 2021, 23, e24861.	4.3	14
3	Crowdsourcing virtual summer research opportunities to support minorities in microbiology. <i>Nature Microbiology</i> , 2020, 5, 1311-1313.	13.3	10
4	Using Whole-genome Sequencing to Determine the Timing of Secondary Tuberculosis in British Columbia, Canada. <i>Clinical Infectious Diseases</i> , 2020, 73, 535-537.	5.8	4
5	Ethical challenges in the treatment of non-refugee migrants with tuberculosis in Canada. <i>Journal of Public Health</i> , 2020, , .	1.8	0
6	Adjutant: an R-based tool to support topic discovery for systematic and literature reviews. <i>Bioinformatics</i> , 2019, 35, 1070-1072.	4.1	15
7	Beyond the SNP Threshold: Identifying Outbreak Clusters Using Inferred Transmissions. <i>Molecular Biology and Evolution</i> , 2019, 36, 587-603.	8.9	121
8	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	28.6	237
9	The problem with defining foreign birth as a risk factor in tuberculosis epidemiology studies. <i>PLoS ONE</i> , 2019, 14, e0216271.	2.5	4
10	Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing. <i>PLoS ONE</i> , 2019, 14, e0212193.	2.5	22
11	Building the Framework for Standardized Clinical Laboratory Reporting of Next-generation Sequencing Data for Resistance-associated Mutations in Mycobacterium tuberculosis Complex. <i>Clinical Infectious Diseases</i> , 2019, 69, 1631-1633.	5.8	10
12	Universal genotyping reveals province-level differences in the molecular epidemiology of tuberculosis. <i>PLoS ONE</i> , 2019, 14, e0214870.	2.5	3
13	Immunosignature Analysis of Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS). <i>Molecular Neurobiology</i> , 2019, 56, 4249-4257.	4.0	17
14	A systematic method for surveying data visualizations and a resulting genomic epidemiology visualization typology: GEViT. <i>Bioinformatics</i> , 2019, 35, 1668-1676.	4.1	13
15	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	1.8	103
16	Molecular Epidemiology of Tuberculosis in British Columbia, Canada: A 10-Year Retrospective Study. <i>Clinical Infectious Diseases</i> , 2018, 66, 849-856.	5.8	27
17	Universal Genotyping for Tuberculosis Prevention Programs: a 5-Year Comparison with On-Request Genotyping. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	6
18	Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , 2018, 19, 9-20.	16.3	505

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19	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
20	TB Transmission: Closing the Gaps. <i>EBioMedicine</i> , 2018, 34, 4-5.	6.1	1
21	Genotyping and Whole-Genome Sequencing to Identify Tuberculosis Transmission to Pediatric Patients in British Columbia, Canada, 2005–2014. <i>Journal of Infectious Diseases</i> , 2018, 218, 1155-1163.	4.0	23
22	Introducing the JMBE Themed Issue on Science Communication. <i>Journal of Microbiology and Biology Education</i> , 2018, 19, .	1.0	2
23	MentalIST – A fast MLST caller for large MLST schemes. <i>Microbial Genomics</i> , 2018, 4, .	2.0	55
24	Within-host <i>Mycobacterium tuberculosis</i> diversity and its utility for inferences of transmission. <i>Microbial Genomics</i> , 2018, 4, .	2.0	26
25	Evidence-based design and evaluation of a whole genome sequencing clinical report for the reference microbiology laboratory. <i>PeerJ</i> , 2018, 6, e4218.	2.0	43
26	Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. <i>Molecular Biology and Evolution</i> , 2017, 34, msw075.	8.9	181
27	A brief primer on genomic epidemiology: lessons learned from <i>Mycobacterium tuberculosis</i> . <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 59-77.	3.8	24
28	<i>Mycobacterium chimaera</i> : unraveling a mystery through genomics. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1004-1005.	9.1	1
29	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. <i>Clinical Infectious Diseases</i> , 2017, 64, 476-481.	5.8	21
30	Genome Sequences of the <i>Mycobacterium tuberculosis</i> H37Rv- <i>ptkA</i> Deletion Mutant and Its Parental Strain. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
31	Self-rated health and reasons for non-vaccination against seasonal influenza in Canadian adults with asthma. <i>PLoS ONE</i> , 2017, 12, e0172117.	2.5	13
32	Virus genomics and evolution: the transformative effect of new technologies and multidisciplinary collaboration on virus research and outbreak management. <i>Genome Biology</i> , 2016, 17, 159.	8.8	1
33	On Regulatory and Organizational Constraints in Visualization Design and Evaluation. , 2016, , .		7
34	Translating phylogeny into action for HIV surveillance. <i>Lancet HIV</i> , the, 2016, 3, e196-e197.	4.7	4
35	Declaring a tuberculosis outbreak over with genomic epidemiology. <i>Microbial Genomics</i> , 2016, 2, e000060.	2.0	27
36	Metagenomic Investigation of Plasma in Individuals with ME/CFS Highlights the Importance of Technical Controls to Elucidate Contamination and Batch Effects. <i>PLoS ONE</i> , 2016, 11, e0165691.	2.5	15

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37	Brain-derived neurotrophic factor concentration may not be depressed in chronic fatigue syndrome. <i>Fatigue: Biomedicine, Health and Behavior</i> , 2015, 3, 122-125.	1.9	1
38	Real-time digital pathogen surveillance "the time is now. <i>Genome Biology</i> , 2015, 16, 155.	8.8	123
39	On the Mark? Responses to a Sting. <i>Journal of Librarianship and Scholarly Communication</i> , 2015, 2, 1116.	0.5	7
40	Whole-Genome Sequencing of Measles Virus Genotypes H1 and D8 During Outbreaks of Infection Following the 2010 Olympic Winter Games Reveals Viral Transmission Routes. <i>Journal of Infectious Diseases</i> , 2015, 212, 1574-1578.	4.0	59
41	Lyme Disease Diagnosed by Alternative Methods: A Phenotype Similar to That of Chronic Fatigue Syndrome. <i>Clinical Infectious Diseases</i> , 2015, 61, 1084-1091.	5.8	38
42	A Microbiological Revolution Meets an Ancient Disease: Improving the Management of Tuberculosis with Genomics. <i>Clinical Microbiology Reviews</i> , 2015, 28, 523-539.	13.6	32
43	Genetic determinants of cocaine-associated agranulocytosis. <i>BMC Research Notes</i> , 2015, 8, 240.	1.4	12
44	Towards genomic prediction of drug resistance in tuberculosis. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1124-1125.	9.1	9
45	Accelerating tuberculosis elimination in low-incidence settings: the role of genomics. <i>European Respiratory Journal</i> , 2015, 46, 1840-1841.	6.7	1
46	Stopping outbreaks with real-time genomic epidemiology. <i>Genome Medicine</i> , 2014, 6, 104.	8.2	25
47	Phylogenetic tree shapes resolve disease transmission patterns. <i>Evolution, Medicine and Public Health</i> , 2014, 2014, 96-108.	2.5	72
48	Bayesian Inference of Infectious Disease Transmission from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 1869-1879.	8.9	191
49	Genomic analysis identifies targets of convergent positive selection in drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 1183-1189.	21.4	393
50	Metagenomics for pathogen detection in public health. <i>Genome Medicine</i> , 2013, 5, 81.	8.2	202
51	Investigation of disease outbreaks with genome sequencing. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 101-102.	9.1	10
52	<i>Mycobacterium tuberculosis</i> mutation rate estimates from different lineages predict substantial differences in the emergence of drug-resistant tuberculosis. <i>Nature Genetics</i> , 2013, 45, 784-790.	21.4	405
53	A metagenomic approach to investigate the microbial causes of myalgic encephalomyelitis/chronic fatigue syndrome: moving beyond XMRV. <i>Fatigue: Biomedicine, Health and Behavior</i> , 2013, 1, 185-189.	1.9	3
54	Characterization of the Upper Respiratory Tract Microbiomes of Patients with Pandemic H1N1 Influenza. <i>PLoS ONE</i> , 2013, 8, e69559.	2.5	67

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55	Cross-reactive and Vaccine-Induced Antibody to an Emerging Swine-Origin Variant of Influenza A Virus Subtype H3N2 (H3N2v). <i>Journal of Infectious Diseases</i> , 2012, 206, 1852-1861.	4.0	82
56	Estimates of Influenza Vaccine Effectiveness for 2007â€“2008 From Canada's Sentinel Surveillance System: Cross-Protection Against Major and Minor Variants. <i>Journal of Infectious Diseases</i> , 2012, 205, 1858-1868.	4.0	52
57	A Sentinel Platform to Evaluate Influenza Vaccine Effectiveness and New Variant Circulation, Canada 2010â€“2011 Season. <i>Clinical Infectious Diseases</i> , 2012, 55, 332-342.	5.8	106
58	Modern contact investigation methods for enhancing tuberculosis control in Aboriginal communities. <i>International Journal of Circumpolar Health</i> , 2012, 71, 18643.	1.2	19
59	Cross-Lineage Influenza B and Heterologous Influenza A Antibody Responses in Vaccinated Mice: Immunologic Interactions and B/Yamagata Dominance. <i>PLoS ONE</i> , 2012, 7, e38929.	2.5	40
60	Diagnostic Testing for Vaccinomics: Is the Regulatory Approval Framework Adequate? A Comparison of Canada, the United States, and Europe. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 597-605.	2.0	3
61	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	27.0	665
62	Immuno-epidemiologic Correlates of Pandemic H1N1 Surveillance Observations: Higher Antibody and Lower Cell-Mediated Immune Responses with Advanced Age. <i>Journal of Infectious Diseases</i> , 2011, 203, 158-167.	4.0	86
63	Navigating transmission networks with genomics and phylogenetic trees. <i>Future Virology</i> , 2010, 5, 251-253.	1.8	1
64	Association between the 2008â€“09 Seasonal Influenza Vaccine and Pandemic H1N1 Illness during Springâ€“Summer 2009: Four Observational Studies from Canada. <i>PLoS Medicine</i> , 2010, 7, e1000258.	8.4	266
65	Robust TLR4-induced gene expression patterns are not an accurate indicator of human immunity. <i>Journal of Translational Medicine</i> , 2010, 8, 6.	4.4	4
66	Intracellular Receptor for Human Host Defense Peptide LL-37 in Monocytes. <i>Journal of Immunology</i> , 2009, 183, 2688-2696.	0.8	139
67	Systems-Level Comparison of Host-Responses Elicited by Avian H5N1 and Seasonal H1N1 Influenza Viruses in Primary Human Macrophages. <i>PLoS ONE</i> , 2009, 4, e8072.	2.5	109
68	Enabling a systems biology approach to immunology: focus on innate immunity. <i>Trends in Immunology</i> , 2009, 30, 249-262.	6.8	122
69	Systems biology evaluation of immune responses induced by human host defence peptide LL-37 in mononuclear cells. <i>Molecular BioSystems</i> , 2009, 5, 483.	2.9	92
70	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. <i>Trends in Biotechnology</i> , 2008, 26, 190-200.	9.3	101
71	Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2008, 14, 1253-1260.	4.4	89
72	The Commensal <i>Streptococcus salivarius</i> K12 Downregulates the Innate Immune Responses of Human Epithelial Cells and Promotes Host-Microbe Homeostasis. <i>Infection and Immunity</i> , 2008, 76, 4163-4175.	2.2	230

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73	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. <i>Molecular Systems Biology</i> , 2008, 4, 218.	7.2	330
74	Cerebral: a Cytoscape plugin for layout of and interaction with biological networks using subcellular localization annotation. <i>Bioinformatics</i> , 2007, 23, 1040-1042.	4.1	163
75	Complexities of targeting innate immunity to treat infection. <i>Trends in Immunology</i> , 2007, 28, 260-266.	6.8	91
76	Methods for predicting bacterial protein subcellular localization. <i>Nature Reviews Microbiology</i> , 2006, 4, 741-751.	28.6	154
77	Assessing the precision of high-throughput computational and laboratory approaches for the genome-wide identification of protein subcellular localization in bacteria. <i>BMC Genomics</i> , 2005, 6, 162.	2.8	40
78	Genome-wide identification of <i>Pseudomonas aeruginosa</i> exported proteins using a consensus computational strategy combined with a laboratory-based PhoA fusion screen. <i>Genome Research</i> , 2005, 15, 321-329.	5.5	103
79	PSORTdb: a protein subcellular localization database for bacteria. <i>Nucleic Acids Research</i> , 2004, 33, D164-D168.	14.5	117
80	PSORT-B: improving protein subcellular localization prediction for Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 3613-3617.	14.5	383
81	Methods for the Computational Prediction of Periplasmic Proteins. , 0, , 389-405.		0