

Jason T Ladner

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

5,205
citations

136950

32
h-index

98798

67
g-index

85
all docs

85
docs citations

85
times ranked

8627
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic basis for coral resilience to climate change. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1387-1392.	7.1	770
2	Molecular Evidence of Sexual Transmission of Ebola Virus. New England Journal of Medicine, 2015, 373, 2448-2454.	27.0	380
3	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	27.8	346
4	Tracking virus outbreaks in the twenty-first century. Nature Microbiology, 2019, 4, 10-19.	13.3	305
5	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	27.8	298
6	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	28.9	275
7	The simple fool's guide to population genomics via <i>scRNA-seq</i> : an introduction to high-throughput sequencing data analysis. Molecular Ecology Resources, 2012, 12, 1058-1067.	4.8	229
8	Epitope-resolved profiling of the SARS-CoV-2 antibody response identifies cross-reactivity with endemic human coronaviruses. Cell Reports Medicine, 2021, 2, 100189.	6.5	149
9	Extensive sympatry, cryptic diversity and introgression throughout the geographic distribution of two coral species complexes. Molecular Ecology, 2012, 21, 2224-2238.	3.9	139
10	Lineage-Specific Transcriptional Profiles of Symbiodinium spp. Unaltered by Heat Stress in a Coral Host. Molecular Biology and Evolution, 2014, 31, 1343-1352.	8.9	135
11	Possible sexual transmission of Ebola virus - Liberia, 2015. Morbidity and Mortality Weekly Report, 2015, 64, 479-81.	15.1	132
12	A Multicomponent Animal Virus Isolated from Mosquitoes. Cell Host and Microbe, 2016, 20, 357-367.	11.0	123
13	Protein evolution in two co-occurring types of Symbiodinium: an exploration into the genetic basis of thermal tolerance in Symbiodinium clade D. BMC Evolutionary Biology, 2012, 12, 217.	3.2	108
14	Precision epidemiology for infectious disease control. Nature Medicine, 2019, 25, 206-211.	30.7	94
15	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. MBio, 2014, 5, e01360-14.	4.1	89
16	Evolution and Spread of Ebola Virus in Liberia, 2014-2015. Cell Host and Microbe, 2015, 18, 659-669.	11.0	87
17	Complete Genome Sequences for 59 <i>Burkholderia</i> Isolates, Both Pathogenic and Near Neighbor. Genome Announcements, 2015, 3, .	0.8	82
18	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. Emerging Infectious Diseases, 2015, 21, 1135-1143.	4.3	79

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19	Emergence of Ebola Virus Escape Variants in Infected Nonhuman Primates Treated with the MB-003 Antibody Cocktail. <i>Cell Reports</i> , 2015, 12, 2111-2120.	6.4	68
20	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019, 178, 1057-1071.e11.	28.9	68
21	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016, 2, e1600378.	10.3	62
22	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 648-657.	9.1	62
23	First report of naturally infected <i>Aedes aegypti</i> with chikungunya virus genotype ECSA in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005630.	3.0	59
24	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). <i>Viruses</i> , 2016, 8, 164.	3.3	57
25	Complete Genome Sequences for 35 Biothreat Assay-Relevant <i>Bacillus</i> Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	52
26	Investigations of fine-scale phylogeography in <i>Tigriopus californicus</i> reveal historical patterns of population divergence. <i>BMC Evolutionary Biology</i> , 2009, 9, 139.	3.2	51
27	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	4.1	49
28	Persistence of Ebola virus after the end of widespread transmission in Liberia: an outbreak report. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1015-1024.	9.1	48
29	<i>Burkholderia humptydoensis</i> sp. nov., a New Species Related to <i>Burkholderia thailandensis</i> and the Fifth Member of the <i>Burkholderia pseudomallei</i> Complex. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	45
30	Genomic and phylogenetic characterization of viruses included in the Manzanilla and Oropouche species complexes of the genus <i>Orthobunyavirus</i> , family <i>Bunyaviridae</i> . <i>Journal of General Virology</i> , 2014, 95, 1055-1066.	2.9	43
31	Characterization of the Sandfly fever Naples species complex and description of a new Karimabad species complex (genus <i>Phlebovirus</i> , family <i>Bunyaviridae</i>). <i>Journal of General Virology</i> , 2014, 95, 292-300.	2.9	41
32	Complete Genome Sequences of Five Zika Virus Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	40
33	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018, 22, 1159-1168.	6.4	37
34	Thirty-Two Complete Genome Assemblies of Nine <i>Yersinia</i> Species, Including <i>Y. pestis</i> , <i>Y. pseudotuberculosis</i> , and <i>Y. enterocolitica</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	31
35	Complete Coding Genome Sequence for Mogiana Tick Virus, a Jingmenvirus Isolated from Ticks in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	30
36	Persistence and Intra-Host Genetic Evolution of Zika Virus Infection in Symptomatic Adults: A Special View in the Male Reproductive System. <i>Viruses</i> , 2018, 10, 615.	3.3	30

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37	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , 2019, 19, 1371-1378.	9.1	30
38	Ebola Virus Infections in Nonhuman Primates Are Temporally Influenced by Glycoprotein Poly-U Editing Site Populations in the Exposure Material. <i>Viruses</i> , 2015, 7, 6739-6754.	3.3	29
39	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	4.1	29
40	The role of genes in understanding the evolutionary ecology of reef building corals. <i>Evolutionary Ecology</i> , 2012, 26, 317-335.	1.2	28
41	Spontaneous Mutation at Amino Acid 544 of the Ebola Virus Glycoprotein Potentiates Virus Entry and Selection in Tissue Culture. <i>Journal of Virology</i> , 2017, 91, .	3.4	24
42	Characterization of the Punta Toro species complex (genus Phlebovirus, family Bunyaviridae). <i>Journal of General Virology</i> , 2015, 96, 2079-2085.	2.9	23
43	The population genetics of the causative agent of snake fungal disease indicate recent introductions to the USA. <i>PLoS Biology</i> , 2022, 20, e3001676.	5.6	23
44	An attenuated Machupo virus with a disrupted L-segment intergenic region protects guinea pigs against lethal Guanarito virus infection. <i>Scientific Reports</i> , 2017, 7, 4679.	3.3	21
45	Draft Genome Assembly of <i>Acinetobacter baumannii</i> ATCC 19606. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
46	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	4.0	19
47	Inference of Nipah virus evolution, 1999â€“2015. <i>Virus Evolution</i> , 2021, 7, veaa062.	4.9	18
48	A spontaneous mutation in <i>kdsD</i> , a biosynthesis gene for 3 Deoxy-D-manno-Octulosonic Acid, occurred in a ciprofloxacin resistant strain of <i>Francisella tularensis</i> and caused a high level of attenuation in murine models of tularemia. <i>PLoS ONE</i> , 2017, 12, e0174106.	2.5	17
49	Pathosphere.org: pathogen detection and characterization through a web-based, open-source informatics platform. <i>BMC Bioinformatics</i> , 2015, 16, 416.	2.6	16
50	Characterization of the murine macrophage response to infection with virulent and avirulent <i>Burkholderia</i> species. <i>BMC Microbiology</i> , 2015, 15, 259.	3.3	16
51	Genome Sequencing of 18 <i>Francisella</i> Strains To Aid in Assay Development and Testing. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
52	Evolution of Antibiotic Resistance in Surrogates of <i>Francisella tularensis</i> (LVS and <i>Francisella</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	3.5	16
53	Genome Sequence of <i>Weissella ceti</i> NC36, an Emerging Pathogen of Farmed Rainbow Trout in the United States. <i>Genome Announcements</i> , 2013, 1, .	0.8	15
54	Complete Coding Sequences of Eastern Equine Encephalitis Virus and Venezuelan Equine Encephalitis Virus Strains Isolated from Human Cases. <i>Genome Announcements</i> , 2015, 3, .	0.8	15

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55	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 2020, 9, 657.	1.6	14
56	Informing the Historical Record of Experimental Nonhuman Primate Infections with Ebola Virus: Genomic Characterization of USAMRIID Ebola Virus/H.sapiens-tc/COD/1995/Kikwit-9510621 Challenge Stock and Its Replacement. PLoS ONE, 2016, 11, e0150919.	2.5	14
57	Persistence of Brucella abortus lineages revealed by genomic characterization and phylodynamic analysis. PLoS Neglected Tropical Diseases, 2020, 14, e0008235.	3.0	13
58	A novel host-adapted strain of Salmonella Typhimurium causes renal disease in olive ridley turtles (Lepidochelys olivacea) in the Pacific. Scientific Reports, 2019, 9, 9313.	3.3	12
59	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 0, 9, 657.	1.6	8
60	COVID-19 vaccination elicits an evolving, cross-reactive antibody response to epitopes conserved with endemic coronavirus spike proteins. Cell Reports, 2022, 40, 111022.	6.4	8
61	Genomic signatures for predicting the zoonotic potential of novel viruses. PLoS Biology, 2021, 19, e3001403.	5.6	6
62	Genome Sequence of <i>Moraxella macacae</i> 0408225, a Novel Bacterial Species Isolated from a Cynomolgus Macaque with Epistaxis. Genome Announcements, 2013, 1, .	0.8	5
63	Development of real-time PCR assays for the detection of <i>Moraxella macacae</i> associated with bloody nose syndrome in rhesus (<i>Macaca mulatta</i>) and cynomolgus (<i>Macaca fascicularis</i>) macaques. Journal of Medical Primatology, 2015, 44, 364-372.	0.6	4
64	Comparative Genomics Analyses Support the Reclassification of Bisgaard Taxon 40 as <i>Mergibacter</i> gen. nov., With <i>Mergibacter septicus</i> sp. nov. as Type Species: Novel Insights Into the Phylogeny and Virulence Factors of a Pasteurellaceae Family Member Associated With Mortality Events in Seabirds. Frontiers in Microbiology, 2021, 12, 667356.	3.5	4
65	Countering Zika Virus: The USAMRIID Response. Advances in Experimental Medicine and Biology, 2018, 1062, 303-318.	1.6	3
66	Cross-Border Transmission of Ebola Virus as the Cause of a Resurgent Outbreak in Liberia in April 2016. Clinical Infectious Diseases, 2018, 67, 1147-1149.	5.8	3
67	Phylodynamic Analysis of Ebola Virus Disease Transmission in Sierra Leone. Viruses, 2019, 11, 71.	3.3	3
68	Molecular characterization of plasmid pMoma1 of <i>Moraxella macacae</i> , a newly described bacterial pathogen of macaques. Folia Microbiologica, 2015, 60, 235-239.	2.3	2
69	Reply to "Expanding the Conversation on High-Throughput Virome Sequencing Standards To Include Consideration of Microbial Contamination Sources". MBio, 2014, 5, e02084.	4.1	0
70	Complete Genome Sequence of Pigmentation-Negative <i>Yersinia pestis</i> Strain Cadman. Genome Announcements, 2016, 4, .	0.8	0
71	Title is missing!. , 2020, 14, e0008235.		0
72	Title is missing!. , 2020, 14, e0008235.		0

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73	Title is missing!. , 2020, 14, e0008235.		0
74	Title is missing!. , 2020, 14, e0008235.		0
75	Title is missing!.. , 2020, 14, e0008235.		0