

# 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	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
2	COVID-19 vaccination elicits an evolving, cross-reactive antibody response to epitopes conserved with endemic coronavirus spike proteins. <i>Cell Reports</i> , 2022, 40, 111022.	6.4	8
3	Inference of Nipah virus evolution, 1999–2015. <i>Virus Evolution</i> , 2021, 7, veaa062.	4.9	18
4	Epitope-resolved profiling of the SARS-CoV-2 antibody response identifies cross-reactivity with endemic human coronaviruses. <i>Cell Reports Medicine</i> , 2021, 2, 100189.	6.5	149
5	Genomic signatures for predicting the zoonotic potential of novel viruses. <i>PLoS Biology</i> , 2021, 19, e3001403.	5.6	6
6	Comparative Genomics Analyses Support the Reclassification of <i>Bisgaardia</i> 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. <i>Frontiers in Microbiology</i> , 2021, 12, 667356.	3.5	4
7	Evolution of Antibiotic Resistance in Surrogates of <i>Francisella tularensis</i> (LVS and <i>Francisella</i> ) Tj ETQq1 1 0.784314, rgBT /Overlock 10	3.3	16
8	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	4.1	29
9	Persistence of <i>Brucella abortus</i> lineages revealed by genomic characterization and phylodynamic analysis. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008235.	3.0	13
10	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	1.6	14
11	Title is missing!. , 2020, 14, e0008235.		0
12	Title is missing!. , 2020, 14, e0008235.		0
13	Title is missing!. , 2020, 14, e0008235.		0
14	Title is missing!. , 2020, 14, e0008235.		0
15	Title is missing!. , 2020, 14, e0008235.		0
16	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1371-1378.	9.1	30
17	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019, 178, 1057-1071.e11.	28.9	68
18	Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. <i>Viruses</i> , 2019, 11, 71.	3.3	3

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19	A novel host-adapted strain of Salmonella Typhimurium causes renal disease in olive ridley turtles ( <i>Lepidochelys olivacea</i> ) in the Pacific. <i>Scientific Reports</i> , 2019, 9, 9313.	3.3	12
20	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
21	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211.	30.7	94
22	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
23	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018, 22, 1159-1168.	6.4	37
24	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
25	Countering Zika Virus: The USAMRIID Response. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1062, 303-318.	1.6	3
26	Cross-Border Transmission of Ebola Virus as the Cause of a Resurgent Outbreak in Liberia in April 2016. <i>Clinical Infectious Diseases</i> , 2018, 67, 1147-1149.	5.8	3
27	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
28	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
29	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
30	Complete Coding Genome Sequence for Mogiana Tick Virus, a Jingmenvirus Isolated from Ticks in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	30
31	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
32	<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
33	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
34	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
35	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
36	Genomic Characterization of the Genus <i>Nairovirus</i> (Family <i>Bunyaviridae</i> ). <i>Viruses</i> , 2016, 8, 164.	3.3	57

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37	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	4.0	19
38	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016, 2, e1600378.	10.3	62
39	Complete Genome Sequences of Five Zika Virus Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	40
40	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016, 20, 357-367.	11.0	123
41	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	4.1	49
42	Complete Genome Sequence of Pigmentation-Negative <i>Yersinia pestis</i> Strain Cadman. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
43	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 R4368 and Its Replacement R4415. <i>PLoS ONE</i> , 2016, 11, e0150919.	2.5	14
44	Pathosphere.org: pathogen detection and characterization through a web-based, open-source informatics platform. <i>BMC Bioinformatics</i> , 2015, 16, 416.	2.6	16
45	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
46	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. <i>Journal of Medical Primatology</i> , 2015, 44, 364-372.	0.6	4
47	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
48	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. <i>Emerging Infectious Diseases</i> , 2015, 21, 1135-1143.	4.3	79
49	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
50	Evolution and Spread of Ebola Virus in Liberia, 2014–2015. <i>Cell Host and Microbe</i> , 2015, 18, 659-669.	11.0	87
51	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
52	Genome Sequencing of 18 <i>Francisella</i> Strains To Aid in Assay Development and Testing. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
53	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
54	Complete Genome Sequences for 59 <i>Burkholderia</i> Isolates, Both Pathogenic and Near Neighbor. <i>Genome Announcements</i> , 2015, 3, .	0.8	82

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55	Molecular characterization of plasmid pMoma1 of <i>Moraxella macacae</i> , a newly described bacterial pathogen of macaques. <i>Folia Microbiologica</i> , 2015, 60, 235-239.	2.3	2
56	Characterization of the Punta Toro species complex (genus <i>Phlebovirus</i> , family <i>Bunyaviridae</i> ). <i>Journal of General Virology</i> , 2015, 96, 2079-2085.	2.9	23
57	Complete Genome Sequences for 35 Biothreat Assay-Relevant <i>Bacillus</i> Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	52
58	Molecular Evidence of Sexual Transmission of Ebola Virus. <i>New England Journal of Medicine</i> , 2015, 373, 2448-2454.	27.0	380
59	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
60	Possible sexual transmission of Ebola virus - Liberia, 2015. <i>Morbidity and Mortality Weekly Report</i> , 2015, 64, 479-81.	15.1	132
61	Draft Genome Assembly of <i>Acinetobacter baumannii</i> ATCC 19606. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
62	Reply to "Expanding the Conversation on High-Throughput Virome Sequencing Standards To Include Consideration of Microbial Contamination Sources". <i>MBio</i> , 2014, 5, e02084.	4.1	0
63	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
64	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
65	Lineage-Specific Transcriptional Profiles of <i>Symbiodinium</i> spp. Unaltered by Heat Stress in a Coral Host. <i>Molecular Biology and Evolution</i> , 2014, 31, 1343-1352.	8.9	135
66	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	4.1	89
67	Genomic basis for coral resilience to climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1387-1392.	7.1	770
68	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
69	Genome Sequence of <i>Moraxella macacae</i> O408225, a Novel Bacterial Species Isolated from a <i>Cynomolgus</i> Macaque with Epistaxis. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
70	The simple fool's guide to population genomics via <i>RNA-Seq</i> : an introduction to high-throughput sequencing data analysis. <i>Molecular Ecology Resources</i> , 2012, 12, 1058-1067.	4.8	229
71	Protein evolution in two co-occurring types of <i>Symbiodinium</i> : an exploration into the genetic basis of thermal tolerance in <i>Symbiodinium</i> clade D. <i>BMC Evolutionary Biology</i> , 2012, 12, 217.	3.2	108
72	Extensive sympatry, cryptic diversity and introgression throughout the geographic distribution of two coral species complexes. <i>Molecular Ecology</i> , 2012, 21, 2224-2238.	3.9	139

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73	The role of genes in understanding the evolutionary ecology of reef building corals. <i>Evolutionary Ecology</i> , 2012, 26, 317-335.	1.2	28
74	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
75	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 0, 9, 657.	1.6	8