

Lucy A Weinert

List of Publications by Year in descending order

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48
papers

5,285
citations

159585

30
h-index

197818

49
g-index

54
all docs

54
docs citations

54
times ranked

8002
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Reduction Is Associated with Bacterial Pathogenicity across Different Scales of Temporal and Ecological Divergence. <i>Molecular Biology and Evolution</i> , 2021, 38, 1570-1579.	8.9	50
2	Evolutionary loss of inflammasomes in the Carnivora and implications for the carriage of zoonotic infections. <i>Cell Reports</i> , 2021, 36, 109614.	6.4	16
3	Large-scale genomic analysis of antimicrobial resistance in the zoonotic pathogen <i>Streptococcus suis</i> . <i>BMC Biology</i> , 2021, 19, 191.	3.8	26
4	Mutation rate dynamics reflect ecological change in an emerging zoonotic pathogen. <i>PLoS Genetics</i> , 2021, 17, e1009864.	3.5	5
5	Evaluation of the recombinant proteins RlpB and VacJ as a vaccine for protection against <i>Glaesserella parasuis</i> in pigs. <i>BMC Veterinary Research</i> , 2020, 16, 167.	1.9	5
6	Draft Genome Sequences of the Type Strains of <i>Actinobacillus indolicus</i> (46K2C) and <i>Actinobacillus porcinus</i> (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
7	The Evolutionary Genomics of Host Specificity in <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2020, 28, 465-477.	7.7	74
8	Generation and Evaluation of a <i>Glaesserella</i> (<i>Haemophilus</i>) <i>parasuis</i> Capsular Mutant. <i>Infection and Immunity</i> , 2020, 88, .	2.2	7
9	Understanding the emergence of bacterial pathogens in novel hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180328.	4.0	28
10	Pathotyping the Zoonotic Pathogen <i>Streptococcus suis</i> : Novel Genetic Markers To Differentiate Invasive Disease-Associated Isolates from Non-Disease-Associated Isolates from England and Wales. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	29
11	Effects of Environmental and Management-Associated Factors on Prevalence and Diversity of <i>Streptococcus suis</i> in Clinically Healthy Pig Herds in China and the United Kingdom. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	37
12	<i>Streptococcus suis</i> contains multiple phase-variable methyltransferases that show a discrete lineage distribution. <i>Nucleic Acids Research</i> , 2018, 46, 11466-11476.	14.5	31
13	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	7.8	156
14	Use of Proteins Identified through a Functional Genomic Screen To Develop a Protein Subunit Vaccine That Provides Significant Protection against Virulent <i>Streptococcus suis</i> in Pigs. <i>Infection and Immunity</i> , 2018, 86, .	2.2	16
15	Pathotyping Multiplex PCR Assay for <i>Haemophilus parasuis</i> : a Tool for Prediction of Virulence. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2617-2628.	3.9	18
16	Why Might Bacterial Pathogens Have Small Genomes?. <i>Trends in Ecology and Evolution</i> , 2017, 32, 936-947.	8.7	59
17	Patterns of antimicrobial resistance in <i>Streptococcus suis</i> isolates from pigs with or without streptococcal disease in England between 2009 and 2014. <i>Veterinary Microbiology</i> , 2017, 207, 117-124.	1.9	53
18	The Phylogeny of <i>Rickettsia</i> Using Different Evolutionary Signatures: How Tree-Like is Bacterial Evolution?. <i>Systematic Biology</i> , 2016, 65, 265-279.	5.6	64

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19	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1191.	3.5	27
20	Rates of Vaccine Evolution Show Strong Effects of Latency: Implications for Varicella Zoster Virus Epidemiology. <i>Molecular Biology and Evolution</i> , 2015, 32, 1020-1028.	8.9	32
21	The incidence of bacterial endosymbionts in terrestrial arthropods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150249.	2.6	414
22	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015, 178, 279-282.	1.9	34
23	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
24	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of <i>Haemophilus parasuis</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3812-3821.	3.9	80
25	Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2217-2222.	3.0	30
26	Comparative Analysis of Transcriptomes from Secondary Reproductives of Three Reticulitermes Termite Species. <i>PLoS ONE</i> , 2015, 10, e0145596.	2.5	14
27	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	4.1	95
28	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , 2014, 15, 1179.	2.8	34
29	Improved Calibration of the Human Mitochondrial Clock Using Ancient Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 2780-2792.	8.9	99
30	Multiplex PCR Assay for Unequivocal Differentiation of <i>Actinobacillus pleuropneumoniae</i> Serovars 1 to 3, 5 to 8, 10, and 12. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2380-2385.	3.9	36
31	Inferring Host Range Dynamics from Comparative Data: The Protozoan Parasites of New World Monkeys. <i>American Naturalist</i> , 2014, 184, 65-74.	2.1	16
32	Generation of a Tn5 transposon library in <i>Haemophilus parasuis</i> and analysis by transposon-directed insertion-site sequencing (TraDIS). <i>Veterinary Microbiology</i> , 2013, 166, 558-566.	1.9	15
33	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	5.5	412
34	Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013, 4, .	4.1	177
35	<i>Wolbachia</i> Variants Induce Differential Protection to Viruses in <i>Drosophila melanogaster</i> : A Phenotypic and Phylogenomic Analysis. <i>PLoS Genetics</i> , 2013, 9, e1003896.	3.5	277
36	Gene Content and Diversity of the Loci Encoding Biosynthesis of Capsular Polysaccharides of the 15 Serovar Reference Strains of <i>Haemophilus parasuis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 4264-4273.	2.2	37

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37	Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 577-582.	7.1	373
38	Population Genomics of the Wolbachia Endosymbiont in <i>Drosophila melanogaster</i> . PLoS Genetics, 2012, 8, e1003129.	3.5	178
39	Molecular dating of human-to-bovid host jumps by <i>Staphylococcus aureus</i> reveals an association with the spread of domestication. Biology Letters, 2012, 8, 829-832.	2.3	77
40	Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18732-18736.	7.1	375
41	Next-generation sequencing of transcriptomes: a guide to RNA isolation in nonmodel animals. Molecular Ecology Resources, 2011, 11, 650-661.	4.8	92
42	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	12.6	675
43	Transmission Network Parameters Estimated From HIV Sequences for a Nationwide Epidemic. Journal of Infectious Diseases, 2011, 204, 1463-1469.	4.0	184
44	Evolutionary Genomics of <i>Staphylococcus aureus</i> Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. Genome Biology and Evolution, 2010, 2, 454-466.	2.5	174
45	Conjugation genes are common throughout the genus <i>Rickettsia</i> and are transmitted horizontally. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 3619-3627.	2.6	37
46	Recent human-to-poultry host jump, adaptation, and pandemic spread of <i>Staphylococcus aureus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19545-19550.	7.1	363
47	Are we underestimating the diversity and incidence of insect bacterial symbionts? A case study in ladybird beetles. Biology Letters, 2007, 3, 678-681.	2.3	83
48	Stable antibiotic resistance and rapid human adaptation in livestock-associated MRSA. ELife, 0, 11, .	6.0	28