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List of Publications by Year in descending order

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72
papers

4,716
citations

201385

27
h-index

106150

65
g-index

75
all docs

75
docs citations

75
times ranked

6277
citing authors

#	ARTICLE	IF	CITATIONS
1	Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. PLoS ONE, 2014, 9, e104984.	1.1	696
2	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	5.8	612
3	Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, mcr-1, mcr-2, mcr-3, mcr-4 and mcr-5 for surveillance purposes. Eurosurveillance, 2018, 23, .	3.9	431
4	The transcriptional landscape and small RNAs of <i>Salmonella enterica</i> serovar Typhimurium. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1277-86.	3.3	373
5	Detection of mcr-1 encoding plasmid-mediated colistin-resistant Escherichia coli isolates from human bloodstream infection and imported chicken meat, Denmark 2015. Eurosurveillance, 2015, 20, .	3.9	326
6	Evaluation of Whole Genome Sequencing for Outbreak Detection of Salmonella enterica. PLoS ONE, 2014, 9, e87991.	1.1	215
7	Emergence of a Clonal Lineage of Multidrug-Resistant ESBL-Producing Salmonella Infantis Transmitted from Broilers and Broiler Meat to Humans in Italy between 2011 and 2014. PLoS ONE, 2015, 10, e0144802.	1.1	171
8	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	1.4	105
9	Characterization and Genetic Variation of Vibrio cholerae Isolated from Clinical and Environmental Sources in Thailand. PLoS ONE, 2017, 12, e0169324.	1.1	88
10	snpTree - a web-server to identify and construct SNP trees from whole genome sequence data. BMC Genomics, 2012, 13, S6.	1.2	87
11	Genomic Signature of Multidrug-Resistant Salmonella enterica Serovar Typhi Isolates Related to a Massive Outbreak in Zambia between 2010 and 2012. Journal of Clinical Microbiology, 2015, 53, 262-272.	1.8	82
12	Genomic variation in Salmonella enterica core genes for epidemiological typing. BMC Genomics, 2012, 13, 88.	1.2	76
13	Is the Evolution of Salmonella enterica subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. MSystems, 2016, 1, .	1.7	74
14	Molecular Epidemiology of mcr-Encoded Colistin Resistance in Enterobacteriaceae From Food-Producing Animals in Italy Revealed Through the EU Harmonized Antimicrobial Resistance Monitoring. Frontiers in Microbiology, 2018, 9, 1217.	1.5	74
15	Population Genetic Structure of Listeria monocytogenes Strains as Determined by Pulsed-Field Gel Electrophoresis and Multilocus Sequence Typing. Applied and Environmental Microbiology, 2016, 82, 5720-5728.	1.4	69
16	Molecular epidemiology of Salmonella Infantis in Europe: insights into the success of the bacterial host and its parasitic pESI-like megaplasmid. Microbial Genomics, 2020, 6, .	1.0	68
17	An Assessment of Different Genomic Approaches for Inferring Phylogeny of Listeria monocytogenes. Frontiers in Microbiology, 2017, 8, 2351.	1.5	66
18	Occurrence and Characterization of mcr-1-Positive Escherichia coli Isolated From Food-Producing Animals in Poland, 2011–2016. Frontiers in Microbiology, 2019, 10, 1753.	1.5	65

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19	The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313. PLoS ONE, 2014, 9, e84566.	1.1	48
20	Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR Acinetobacter baumannii in Tanzania. Journal of Antimicrobial Chemotherapy, 2019, 74, 1484-1493.	1.3	46
21	The invasome of Salmonella Dublin as revealed by whole genome sequencing. BMC Infectious Diseases, 2017, 17, 544.	1.3	45
22	Colistin Resistance Mediated by mcr-1 in ESBL-Producing, Multidrug Resistant Salmonella Infantis in Broiler Chicken Industry, Italy (2016-2017). Frontiers in Microbiology, 2018, 9, 1880.	1.5	42
23	Application of Whole-Genome Sequences and Machine Learning in Source Attribution of Salmonella Typhimurium. Risk Analysis, 2020, 40, 1693-1705.	1.5	36
24	ST131 fimH22 Escherichia coli isolate with a blaCMY-2/Inc11/ST12 plasmid obtained from a patient with bloodstream infection: highly similar to E. coli isolates of broiler origin. Journal of Antimicrobial Chemotherapy, 2019, 74, 557-560.	1.3	34
25	Improving hazard characterization in microbial risk assessment using next generation sequencing data and machine learning: Predicting clinical outcomes in shigatoxigenic Escherichia coli. International Journal of Food Microbiology, 2019, 292, 72-82.	2.1	34
26	Machine Learning Methods as a Tool for Predicting Risk of Illness Applying Next-Generation Sequencing Data. Risk Analysis, 2019, 39, 1397-1413.	1.5	33
27	Inc11 ST3 and Inc11 ST7 plasmids from CTX-M-1-producing Escherichia coli obtained from patients with bloodstream infections are closely related to plasmids from E. coli of animal origin. Journal of Antimicrobial Chemotherapy, 2019, 74, 2171-2175.	1.3	33
28	Genomic evolution of antimicrobial resistance in Escherichia coli. Scientific Reports, 2021, 11, 15108.	1.6	33
29	Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds. Veterinary Microbiology, 2015, 176, 282-291.	0.8	32
30	Genomics of an emerging clone of Salmonella serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo. Journal of Infection in Developing Countries, 2013, 7, 696-706.	0.5	30
31	A metagenomic glimpse into the gut of wild and domestic animals: Quantification of antimicrobial resistance and more. PLoS ONE, 2020, 15, e0242987.	1.1	30
32	Metagenomics analysis of bacteriophages and antimicrobial resistance from global urban sewage. Scientific Reports, 2021, 11, 1600.	1.6	29
33	First detection of linezolid resistance due to the optrA gene in enterococci isolated from food products in Denmark. Journal of Global Antimicrobial Resistance, 2017, 9, 128-129.	0.9	28
34	Extremely Drug-Resistant Salmonella enterica Serovar Senftenberg Infections in Patients in Zambia. Journal of Clinical Microbiology, 2013, 51, 284-286.	1.8	26
35	Construction and Application of a Protein Interaction Map for White Spot Syndrome Virus (WSSV). Molecular and Cellular Proteomics, 2014, 13, 269-282.	2.5	26
36	Genomic Dissection of Travel-Associated Extended-Spectrum-Beta-Lactamase-Producing Salmonella enterica Serovar Typhi Isolates Originating from the Philippines: a One-Off Occurrence or a Threat to Effective Treatment of Typhoid Fever?. Journal of Clinical Microbiology, 2015, 53, 677-680.	1.8	25

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37	Prevalence and genomic analysis of ESBL-producing <i>Escherichia coli</i> in retail raw meats in Singapore. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 601-605.	1.3	25
38	Extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> and antimicrobial resistance in municipal and hospital wastewaters in Czech Republic: Culture-based and metagenomic approaches. <i>Environmental Research</i> , 2021, 193, 110487.	3.7	24
39	Genomic insights into <i>Vibrio cholerae</i> O1 responsible for cholera epidemics in Tanzania between 1993 and 2017. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007934.	1.3	21
40	Comparative genomics of <i>Vibrio cholerae</i> O1 isolated from cholera patients in Bangladesh. <i>Letters in Applied Microbiology</i> , 2018, 67, 329-336.	1.0	20
41	Surveillance and Genomics of Toxigenic <i>Vibrio cholerae</i> O1 From Fish, Phytoplankton and Water in Lake Victoria, Tanzania. <i>Frontiers in Microbiology</i> , 2019, 10, 901.	1.5	20
42	Cross-Border Transmission of <i>Salmonella Choleraesuis</i> var. Kunzendorf in European Pigs and Wild Boar: Infection, Genetics, and Evolution. <i>Frontiers in Microbiology</i> , 2019, 10, 179.	1.5	17
43	Investing in Food Safety for Developing Countries: Opportunities and Challenges in Applying Whole-Genome Sequencing for Food Safety Management. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 463-473.	0.8	16
44	Host Resistance, Genomics and Population Dynamics in a <i>Salmonella</i> Enteritidis and Phage System. <i>Viruses</i> , 2019, 11, 188.	1.5	16
45	Four European <i>Salmonella</i> Typhimurium datasets collected to develop WGS-based source attribution methods. <i>Scientific Data</i> , 2020, 7, 75.	2.4	16
46	Molecular Characteristics and Zoonotic Potential of <i>Salmonella</i> Weltevreden From Cultured Shrimp and <i>Tilapia</i> in Vietnam and China. <i>Frontiers in Microbiology</i> , 2020, 11, 1985.	1.5	15
47	Final report of ENGAGE – Establishing Next Generation sequencing Ability for Genomic analysis in Europe. <i>EFSA Supporting Publications</i> , 2018, 15, 1431E.	0.3	14
48	Hospital Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in a Tertiary Care Hospital in Moshi, Tanzania, as Determined by Whole Genome Sequencing. <i>BioMed Research International</i> , 2018, 1-12.	0.9	14
49	Quantitative Microbial Risk Assessment Based on Whole Genome Sequencing Data: Case of <i>Listeria monocytogenes</i> . <i>Microorganisms</i> , 2020, 8, 1772.	1.6	13
50	<i>Salmonella enterica</i> serovar Typhi H58 clone has been endemic in Zimbabwe from 2012 to 2019. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1160-1167.	1.3	13
51	Unique and conserved genome regions in <i>Vibrio harveyi</i> and related species in comparison with the shrimp pathogen <i>Vibrio harveyi</i> CAIM 1792. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1762-1779.	0.7	12
52	Epidemiology of Danish <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> in Fish Farms Using Whole Genome Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2411.	1.5	11
53	Comparative genomics of quinolone-resistant and susceptible <i>Campylobacter jejuni</i> of poultry origin from major poultry producing European countries (GENCAMP). <i>EFSA Supporting Publications</i> , 2018, 15, 1398E.	0.3	11
54	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. <i>Frontiers in Public Health</i> , 2020, 8, 38.	1.3	11

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55	Predicted sub-populations in a marine shrimp proteome as revealed by combined EST and cDNA data from multiple <i>Penaeus</i> species. <i>BMC Research Notes</i> , 2010, 3, 295.	0.6	10
56	Audouin's gull, a potential vehicle of an extended spectrum β -lactamase producing <i>Salmonella</i> Agona. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-4.	0.7	10
57	Phenotypic and genotypic comparison of salmonellae from diarrhoeic and healthy humans and cattle, Nigeria. <i>Zoonoses and Public Health</i> , 2018, 65, e185-e195.	0.9	10
58	Arrangements of Mobile Genetic Elements among Virotype E Subpopulation of <i>Escherichia coli</i> Sequence Type 131 Strains with High Antimicrobial Resistance and Virulence Gene Content. <i>MSphere</i> , 2021, 6, e0055021.	1.3	10
59	Co-localization of carbapenem (<i>bla</i> OXA-162) and colistin (<i>mcr-1</i>) resistance genes on a transferable IncHI2 plasmid in <i>Escherichia coli</i> of chicken origin. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 3063-3065.	1.3	10
60	Comparative genomics of toxigenic and non-toxigenic <i>Staphylococcus hyicus</i> . <i>Veterinary Microbiology</i> , 2016, 185, 34-40.	0.8	9
61	<i>Campylobacter jejuni</i> ST50, a pathogen of global importance: A comparative genomic analysis of isolates from Australia, Europe and North America. <i>Zoonoses and Public Health</i> , 2021, 68, 638-649.	0.9	9
62	Investigating <i>Salmonella</i> Eko from Various Sources in Nigeria by Whole Genome Sequencing to Identify the Source of Human Infections. <i>PLoS ONE</i> , 2016, 11, e0156212.	1.1	8
63	Analysis of the contribution of bacteriophage ST64B to in vitro virulence traits of <i>Salmonella enterica</i> serovar Typhimurium. <i>Journal of Medical Microbiology</i> , 2014, 63, 331-342.	0.7	7
64	Draft Genome Sequence of <i>Acinetobacter johnsonii</i> C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
65	Long-Term Temporal Stability of the Resistome in Sewage from Copenhagen. <i>MSystems</i> , 2020, 5, .	1.7	6
66	The CGE Tool Box. , 2017, , 65-90.		3
67	Expansion of a Subset Within the C2 Subclade of <i>Escherichia coli</i> Sequence Type 131 (ST131) Is Driving the Increasing Rates of Aminoglycoside Resistance. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa410.	0.4	3
68	New <i>Brucella</i> variant isolated from Croatian cattle. <i>BMC Veterinary Research</i> , 2021, 17, 126.	0.7	3
69	Evaluating the usefulness of next-generation sequencing for herb authentication. <i>Food Chemistry Molecular Sciences</i> , 2021, 3, 100044.	0.9	3
70	Danish Whole-Genome-Sequenced <i>Candida albicans</i> and <i>Candida glabrata</i> Samples Fit into Globally Prevalent Clades. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 962.	1.5	3
71	Clonal and plasmid-mediated flow of ESBL/AmpC genes in <i>Escherichia coli</i> in a commercial laying hen farm. <i>Veterinary Microbiology</i> , 2022, 270, 109453.	0.8	3
72	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Typhimurium Sequence Type 313, Isolated from India. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1