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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	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
2	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
3	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
4	<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
5	Metagenomics analysis of bacteriophages and antimicrobial resistance from global urban sewage. <i>Scientific Reports</i> , 2021, 11, 1600.	1.6	29
6	New <i>Brucella</i> variant isolated from Croatian cattle. <i>BMC Veterinary Research</i> , 2021, 17, 126.	0.7	3
7	<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
8	Genomic evolution of antimicrobial resistance in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2021, 11, 15108.	1.6	33
9	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
10	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
11	Evaluating the usefulness of next-generation sequencing for herb authentication. <i>Food Chemistry Molecular Sciences</i> , 2021, 3, 100044.	0.9	3
12	Danish Whole-Genome-Sequenced <i>Candida albicans</i> and <i>Candida glabrata</i> Samples Fit into Globally Prevalent Clades. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 962.	1.5	3
13	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
14	Molecular Characteristics and Zoonotic Potential of <i>Salmonella Weltevreden</i> From Cultured Shrimp and <i>Tilapia</i> in Vietnam and China. <i>Frontiers in Microbiology</i> , 2020, 11, 1985.	1.5	15
15	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
16	Long-Term Temporal Stability of the Resistome in Sewage from Copenhagen. <i>MSystems</i> , 2020, 5, .	1.7	6
17	Application of Whole-Genome Sequences and Machine Learning in Source Attribution of <i>Salmonella</i> Typhimurium. <i>Risk Analysis</i> , 2020, 40, 1693-1705.	1.5	36
18	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

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19	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. <i>Frontiers in Public Health</i> , 2020, 8, 38.	1.3	11
20	Molecular epidemiology of <i>Salmonella Infantis</i> in Europe: insights into the success of the bacterial host and its parasitic pESI-like megaplasmid. <i>Microbial Genomics</i> , 2020, 6, .	1.0	68
21	A metagenomic glimpse into the gut of wild and domestic animals: Quantification of antimicrobial resistance and more. <i>PLoS ONE</i> , 2020, 15, e0242987.	1.1	30
22	Machine Learning Methods as a Tool for Predicting Risk of Illness Applying Next-Generation Sequencing Data. <i>Risk Analysis</i> , 2019, 39, 1397-1413.	1.5	33
23	Occurrence and Characterization of mcr-1-Positive <i>Escherichia coli</i> Isolated From Food-Producing Animals in Poland, 2011-2016. <i>Frontiers in Microbiology</i> , 2019, 10, 1753.	1.5	65
24	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
25	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
26	Incl1 ST3 and Incl1 ST7 plasmids from CTX-M-1-producing <i>Escherichia coli</i> obtained from patients with bloodstream infections are closely related to plasmids from <i>E. coli</i> of animal origin. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2171-2175.	1.3	33
27	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
28	Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR <i>Acinetobacter baumannii</i> in Tanzania. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1484-1493.	1.3	46
29	Host Resistance, Genomics and Population Dynamics in a <i>Salmonella</i> Enteritidis and Phage System. <i>Viruses</i> , 2019, 11, 188.	1.5	16
30	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
31	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
32	ST131 <i>Escherichia coli</i> isolate with a bla _{CMY-2} /Incl1/ST12 plasmid obtained from a patient with bloodstream infection: highly similar to <i>E. coli</i> isolates of broiler origin. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 557-560.	1.3	34
33	Improving hazard characterization in microbial risk assessment using next generation sequencing data and machine learning: Predicting clinical outcomes in shigatoxigenic <i>Escherichia coli</i> . <i>International Journal of Food Microbiology</i> , 2019, 292, 72-82.	2.1	34
34	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
35	Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, mcr-1, mcr-2, mcr-3, mcr-4 and mcr-5 for surveillance purposes. <i>Eurosurveillance</i> , 2018, 23, .	3.9	431
36	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

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37	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
38	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, 2018, 1-12.	0.9	14
39	Colistin Resistance Mediated by <i>mcr-1</i> in ESBL-Producing, Multidrug Resistant <i>Salmonella</i> <i>Infantis</i> in Broiler Chicken Industry, Italy (2016–2017). <i>Frontiers in Microbiology</i> , 2018, 9, 1880.	1.5	42
40	Molecular Epidemiology of <i>mcr</i> -Encoded Colistin Resistance in Enterobacteriaceae From Food-Producing Animals in Italy Revealed Through the EU Harmonized Antimicrobial Resistance Monitoring. <i>Frontiers in Microbiology</i> , 2018, 9, 1217.	1.5	74
41	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
42	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
43	The CGE Tool Box. , 2017, , 65-90.		3
44	First detection of linezolid resistance due to the <i>optrA</i> gene in enterococci isolated from food products in Denmark. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 9, 128-129.	0.9	28
45	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
46	An Assessment of Different Genomic Approaches for Inferring Phylogeny of <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2351.	1.5	66
47	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
48	Characterization and Genetic Variation of <i>Vibrio cholerae</i> Isolated from Clinical and Environmental Sources in Thailand. <i>PLoS ONE</i> , 2017, 12, e0169324.	1.1	88
49	The invasome of <i>Salmonella</i> Dublin as revealed by whole genome sequencing. <i>BMC Infectious Diseases</i> , 2017, 17, 544.	1.3	45
50	Is the Evolution of <i>Salmonella enterica</i> subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. <i>MSystems</i> , 2016, 1, .	1.7	74
51	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
52	Population Genetic Structure of <i>Listeria monocytogenes</i> Strains as Determined by Pulsed-Field Gel Electrophoresis and Multilocus Sequence Typing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5720-5728.	1.4	69
53	Comparative genomics of toxigenic and non-toxigenic <i>Staphylococcus hyicus</i> . <i>Veterinary Microbiology</i> , 2016, 185, 34-40.	0.8	9
54	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

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55	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
56	Reappearance of <i>Salmonella</i> serovar Choleraesuis var. Kunzendorf in Danish pig herds. <i>Veterinary Microbiology</i> , 2015, 176, 282-291.	0.8	32
57	Genomic Signature of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhi Isolates Related to a Massive Outbreak in Zambia between 2010 and 2012. <i>Journal of Clinical Microbiology</i> , 2015, 53, 262-272.	1.8	82
58	Genomic Dissection of Travel-Associated Extended-Spectrum-Beta-Lactamase-Producing <i>Salmonella enterica</i> Serovar Typhi Isolates Originating from the Philippines: a One-Off Occurrence or a Threat to Effective Treatment of Typhoid Fever?. <i>Journal of Clinical Microbiology</i> , 2015, 53, 677-680.	1.8	25
59	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
60	Emergence of a Clonal Lineage of Multidrug-Resistant ESBL-Producing <i>Salmonella</i> Infantis Transmitted from Broilers and Broiler Meat to Humans in Italy between 2011 and 2014. <i>PLoS ONE</i> , 2015, 10, e0144802.	1.1	171
61	Detection of <i>mcr-1</i> encoding plasmid-mediated colistin-resistant <i>Escherichia coli</i> isolates from human bloodstream infection and imported chicken meat, Denmark 2015. <i>Eurosurveillance</i> , 2015, 20, .	3.9	326
62	Construction and Application of a Protein Interaction Map for White Spot Syndrome Virus (WSSV). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 269-282.	2.5	26
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	The Role of the <i>st313-td</i> Gene in Virulence of <i>Salmonella</i> Typhimurium ST313. <i>PLoS ONE</i> , 2014, 9, e84566.	1.1	48
65	Evaluation of Whole Genome Sequencing for Outbreak Detection of <i>Salmonella enterica</i> . <i>PLoS ONE</i> , 2014, 9, e87991.	1.1	215
66	Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. <i>PLoS ONE</i> , 2014, 9, e104984.	1.1	696
67	Extremely Drug-Resistant <i>Salmonella enterica</i> Serovar Senftenberg Infections in Patients in Zambia. <i>Journal of Clinical Microbiology</i> , 2013, 51, 284-286.	1.8	26
68	Genomics of an emerging clone of <i>Salmonella</i> serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo. <i>Journal of Infection in Developing Countries</i> , 2013, 7, 696-706.	0.5	30
69	The transcriptional landscape and small RNAs of <i>Salmonella enterica</i> serovar Typhimurium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1277-86.	3.3	373
70	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. <i>BMC Genomics</i> , 2012, 13, 88.	1.2	76
71	snpTree - a web-server to identify and construct SNP trees from whole genome sequence data. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	87
72	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