

Frank M Aarestrup

List of Publications by Year in descending order

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182
papers

30,904
citations

12303

69
h-index

5227

165
g-index

206
all docs

206
docs citations

206
times ranked

20684
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of acquired antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2640-2644.	1.3	4,515
2	<i>In Silico</i> Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3895-3903.	1.4	3,558
3	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	1.8	1,925
4	ResFinder 4.0 for predictions of phenotypes from genotypes. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3491-3500.	1.3	1,523
5	Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 1501-1510.	1.8	1,142
6	Rapid and Easy <i>In Silico</i> Serotyping of <i>Escherichia coli</i> Isolates by Use of Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2410-2426.	1.8	775
7	Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. <i>PLoS ONE</i> , 2014, 9, e104984.	1.1	696
8	<i>Staphylococcus aureus</i> CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. <i>MBio</i> , 2012, 3, .	1.8	638
9	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
10	Global Monitoring of <i>Salmonella</i> Serovar Distribution from the World Health Organization Global Foodborne Infections Network Country Data Bank: Results of Quality Assured Laboratories from 2001 to 2007. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 887-900.	0.8	543
11	PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2764-2768.	1.3	534
12	Effect of Abolishment of the Use of Antimicrobial Agents for Growth Promotion on Occurrence of Antimicrobial Resistance in Fecal Enterococci from Food Animals in Denmark. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 2054-2059.	1.4	533
13	Rapid and precise alignment of raw reads against redundant databases with KMA. <i>BMC Bioinformatics</i> , 2018, 19, 307.	1.2	433
14	Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2014, 52, 139-146.	1.8	424
15	PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data. <i>PLoS ONE</i> , 2013, 8, e77302.	1.1	365
16	β -Lactamases among extended-spectrum β -lactamase (ESBL)-resistant <i>Salmonella</i> from poultry, poultry products and human patients in The Netherlands. <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 56, 115-121.	1.3	335
17	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
18	Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 771-777.	1.3	307

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19	World Health Organization Ranking of Antimicrobials According to Their Importance in Human Medicine: A Critical Step for Developing Risk Management Strategies for the Use of Antimicrobials in Food Production Animals. <i>Clinical Infectious Diseases</i> , 2009, 49, 132-141.	2.9	306
20	Resistance in bacteria of the food chain: epidemiology and control strategies. <i>Expert Review of Anti-Infective Therapy</i> , 2008, 6, 733-750.	2.0	302
21	Veterinary Drug Usage and Antimicrobial Resistance in Bacteria of Animal Origin. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2005, 96, 271-281.	1.2	299
22	Detection of mobile genetic elements associated with antibiotic resistance in <i>Salmonella enterica</i> using a newly developed web tool: MobileElementFinder. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 101-109.	1.3	274
23	Population Genetics of <i>Vibrio cholerae</i> from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. <i>MBio</i> , 2011, 2, e00157-11.	1.8	268
24	Using Genomics to Track Global Antimicrobial Resistance. <i>Frontiers in Public Health</i> , 2019, 7, 242.	1.3	263
25	Occurrence of Glycopeptide Resistance among <i>Enterococcus faecium</i> Isolates from Conventional and Ecological Poultry Farms. <i>Microbial Drug Resistance</i> , 1995, 1, 255-257.	0.9	262
26	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
27	Pigs as Source of Methicillin-Resistant <i>Staphylococcus aureus</i> CC398 Infections in Humans, Denmark. <i>Emerging Infectious Diseases</i> , 2008, 14, 1383-1389.	2.0	234
28	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. <i>Nature Microbiology</i> , 2018, 3, 898-908.	5.9	230
29	Use of Antimicrobial Growth Promoters in Food Animals and <i>Enterococcus faecium</i> Resistance to Therapeutic Antimicrobial Drugs in Europe. <i>Emerging Infectious Diseases</i> , 1999, 5, 329-335.	2.0	226
30	Evaluation of Whole Genome Sequencing for Outbreak Detection of <i>Salmonella enterica</i> . <i>PLoS ONE</i> , 2014, 9, e87991.	1.1	215
31	The livestock reservoir for antimicrobial resistance: a personal view on changing patterns of risks, effects of interventions and the way forward. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140085.	1.8	205
32	SCC <i>mecA</i> Finder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome <i>mecA</i> in <i>Staphylococcus aureus</i> Using Whole-Genome Sequence Data. <i>MSphere</i> , 2018, 3, .	1.3	197
33	Surveillance of antimicrobial resistance in bacteria isolated from food animals to antimicrobial growth promoters and related therapeutic agents in Denmark. <i>Apmis</i> , 1998, 106, 606-622.	0.9	187
34	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
35	<i>tcrB</i> , a Gene Conferring Transferable Copper Resistance in <i>Enterococcus faecium</i> : Occurrence, Transferability, and Linkage to Macrolide and Glycopeptide Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 1410-1416.	1.4	183
36	Get pigs off antibiotics. <i>Nature</i> , 2012, 486, 465-466.	13.7	176

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37	Susceptibility of different bacterial species isolated from food animals to copper sulphate, zinc chloride and antimicrobial substances used for disinfection. <i>Veterinary Microbiology</i> , 2004, 100, 83-89.	0.8	175
38	Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2484-2488.	1.3	166
39	A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance. <i>PLoS ONE</i> , 2016, 11, e0157718.	1.1	161
40	Characterization of Glycopeptide-Resistant <i>Enterococcus faecium</i> (GRE) from Broilers and Pigs in Denmark: Genetic Evidence that Persistence of GRE in Pig Herds Is Associated with Coselection by Resistance to Macrolides. <i>Journal of Clinical Microbiology</i> , 2000, 38, 2774-2777.	1.8	156
41	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. <i>MSystems</i> , 2016, 1, .	1.7	153
42	Prevalence of β -Lactamases among Ampicillin-Resistant <i>Escherichia coli</i> and <i>Salmonella</i> isolated from Food Animals in Denmark. <i>Microbial Drug Resistance</i> , 2004, 10, 334-340.	0.9	151
43	Characterization of extended-spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> obtained from Danish pigs, pig farmers and their families from farms with high or no consumption of third- or fourth-generation cephalosporins. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2650-2657.	1.3	149
44	Comparative Evaluation of the Antimicrobial Activity of Different Antimicrobial Peptides against a Range of Pathogenic Bacteria. <i>PLoS ONE</i> , 2015, 10, e0144611.	1.1	148
45	Antimicrobial resistance of zoonotic and commensal bacteria in Europe: The missing link between consumption and resistance in veterinary medicine. <i>Veterinary Microbiology</i> , 2014, 170, 1-9.	0.8	144
46	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
47	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	13.7	138
48	Changes in the use of antimicrobials and the effects on productivity of swine farms in Denmark. <i>American Journal of Veterinary Research</i> , 2010, 71, 726-733.	0.3	135
49	Zinc resistance of <i>Staphylococcus aureus</i> of animal origin is strongly associated with methicillin resistance. <i>Veterinary Microbiology</i> , 2011, 150, 344-348.	0.8	126
50	ResFinder – an open online resource for identification of antimicrobial resistance genes in next-generation sequencing data and prediction of phenotypes from genotypes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	126
51	Using sewage for surveillance of antimicrobial resistance. <i>Science</i> , 2020, 367, 630-632.	6.0	122
52	Antimicrobial resistance in swine production. <i>Animal Health Research Reviews</i> , 2008, 9, 135-148.	1.4	120
53	International Spread of Multidrug-resistant <i>Salmonella</i> Schwarzengrund in Food Products. <i>Emerging Infectious Diseases</i> , 2007, 13, 726-731.	2.0	117
54	Danish Integrated Antimicrobial Resistance Monitoring and Research Program. <i>Emerging Infectious Diseases</i> , 2007, 13, 1633-1639.	2.0	116

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55	Antimicrobial susceptibility and occurrence of resistance genes among <i>Salmonella enterica</i> serovar Weltevreden from different countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2003, 52, 715-718.	1.3	111
56	Association Between Antimicrobial Resistance in <i>Escherichia coli</i> Isolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 1295-1301.	0.8	107
57	Evaluation of Methods for the Concentration and Extraction of Viruses from Sewage in the Context of Metagenomic Sequencing. <i>PLoS ONE</i> , 2017, 12, e0170199.	1.1	107
58	Copper Resistance in <i>Enterococcus faecium</i> , Mediated by the <i>tcrB</i> Gene, Is Selected by Supplementation of Pig Feed with Copper Sulfate. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5784-5789.	1.4	106
59	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
60	Voluntary ban on cephalosporin use in Danish pig production has effectively reduced extended-spectrum cephalosporinase-producing <i>Escherichia coli</i> in slaughter pigs. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 569-572.	1.3	104
61	Molecular Characterization and Occurrence of Extended-Spectrum β -Lactamase Resistance Genes among <i>Salmonella enterica</i> Serovar Corvallis from Thailand, Bulgaria, and Denmark. <i>Microbial Drug Resistance</i> , 2006, 12, 192-198.	0.9	99
62	Prevalence of extended-spectrum cephalosporinase (ESC)-producing <i>Escherichia coli</i> in Danish slaughter pigs and retail meat identified by selective enrichment and association with cephalosporin usage. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 582-588.	1.3	94
63	Consolidating and Exploring Antibiotic Resistance Gene Data Resources. <i>Journal of Clinical Microbiology</i> , 2016, 54, 851-859.	1.8	94
64	Occurrence of <i>satA</i> and <i>vgb</i> Genes in Streptogramin-Resistant <i>Enterococcus faecium</i> Isolates of Animal and Human Origins in The Netherlands. <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 3330-3331.	1.4	90
65	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 385-392.	1.3	89
66	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
67	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
68	Emergence of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Bloodstream Infections in Denmark. <i>Clinical Infectious Diseases</i> , 2017, 65, 1072-1076.	2.9	78
69	Study of methicillin resistant <i>Staphylococcus aureus</i> (MRSA) in Danish pigs at slaughter and in imported retail meat reveals a novel MRSA type in slaughter pigs. <i>Veterinary Microbiology</i> , 2012, 157, 246-250.	0.8	76
70	Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. <i>Scientific Reports</i> , 2015, 5, 11444.	1.6	74
71	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
72	Drivers and Dynamics of Methicillin-Resistant Livestock-Associated <i>Staphylococcus aureus</i> CC398 in Pigs and Humans in Denmark. <i>MBio</i> , 2018, 9, .	1.8	74

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73	Occurrence of antimicrobial resistance among bacterial pathogens and indicator bacteria in pigs in different European countries from year 2002 to 2004: the ARBAO-II study. <i>Acta Veterinaria Scandinavica</i> , 2008, 50, 19.	0.5	70
74	Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals. <i>Antimicrobial Resistance and Infection Control</i> , 2016, 5, 18.	1.5	70
75	Diversity of the tetracycline resistance gene tet(M) and identification of Tn916- and Tn5801-like (Tn6014) transposons in <i>Staphylococcus aureus</i> from humans and animals. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 490-500.	1.3	69
76	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
77	Genomics-Based Identification of Microorganisms in Human Ocular Body Fluid. <i>Scientific Reports</i> , 2018, 8, 4126.	1.6	69
78	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
79	MGMapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. <i>PLoS ONE</i> , 2017, 12, e0176469.	1.1	66
80	Farm dust resistomes and bacterial microbiomes in European poultry and pig farms. <i>Environment International</i> , 2020, 143, 105971.	4.8	66
81	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. <i>Microbiome</i> , 2019, 7, 131.	4.9	65
82	Occurrence of integrons and antimicrobial resistance genes among <i>Salmonella enterica</i> from Brazil. <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 58, 305-309.	1.3	64
83	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1.	2.0	64
84	Characterisation of streptomycin resistance determinants in Danish isolates of <i>Salmonella</i> Typhimurium. <i>Veterinary Microbiology</i> , 2000, 75, 73-82.	0.8	63
85	Clonal diversity of <i>Staphylococcus aureus</i> originating from the small ruminants goats and sheep. <i>Veterinary Microbiology</i> , 2012, 156, 157-161.	0.8	63
86	The antimicrobial resistome in relation to antimicrobial use and biosecurity in pig farming, a metagenome-wide association study in nine European countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 865-876.	1.3	63
87	Antimicrobial susceptibility of <i>Haemophilus parasuis</i> and <i>Histophilus somni</i> from pigs and cattle in Denmark. <i>Veterinary Microbiology</i> , 2004, 101, 143-146.	0.8	62
88	Decreased susceptibility to zinc chloride is associated with methicillin resistant <i>Staphylococcus aureus</i> CC398 in Danish swine. <i>Veterinary Microbiology</i> , 2010, 142, 455-457.	0.8	61
89	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1.	2.0	61
90	Effect of Tylosin Used as a Growth Promoter on the Occurrence of Macrolide-Resistant Enterococci and Staphylococci in Pigs. <i>Microbial Drug Resistance</i> , 1998, 4, 307-312.	0.9	60

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91	High throughput resistance profiling of Plasmodium falciparum infections based on custom dual indexing and Illumina next generation sequencing-technology. Scientific Reports, 2017, 7, 2398.	1.6	57
92	Association between phage types and antimicrobial resistance among bovine Staphylococcus aureus from 10 countries. Veterinary Microbiology, 2003, 95, 133-147.	0.8	55
93	EmtA, a rRNA methyltransferase conferring high-level evernimicin resistance. Molecular Microbiology, 2001, 41, 1349-1356.	1.2	51
94	Expansion of a Plasmid Classification System for Gram-Positive Bacteria and Determination of the Diversity of Plasmids in Staphylococcus aureus Strains of Human, Animal, and Food Origins. Applied and Environmental Microbiology, 2012, 78, 5948-5955.	1.4	51
95	Association Between the Use of Avilamycin for Growth Promotion and the Occurrence of Resistance among <i>Enterococcus faecium</i> from Broilers: Epidemiological Study and Changes Over Time. Microbial Drug Resistance, 2000, 6, 71-75.	0.9	50
96	WHO Global Salm-Surv External Quality Assurance System for Serotyping of <i>Salmonella</i> Isolates from 2000 to 2007. Journal of Clinical Microbiology, 2009, 47, 2729-2736.	1.8	49
97	Associations between antimicrobial use and the faecal resistome on broiler farms from nine European countries. Journal of Antimicrobial Chemotherapy, 2019, 74, 2596-2604.	1.3	49
98	The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313. PLoS ONE, 2014, 9, e84566.	1.1	48
99	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
100	Presence of Variations in Ribosomal Protein L16 Corresponding to Susceptibility of Enterococci to Oligosaccharides (Avilamycin and Evernimicin). Antimicrobial Agents and Chemotherapy, 2000, 44, 3425-3427.	1.4	45
101	Sharing Data for Global Infectious Disease Surveillance and Outbreak Detection. Trends in Microbiology, 2016, 24, 241-245.	3.5	45
102	Human Deaths and Third-Generation Cephalosporin use in Poultry, Europe. Emerging Infectious Diseases, 2013, 19, 1339-1340.	2.0	43
103	Patterns of infections, aetiological agents and antimicrobial resistance at a tertiary care hospital in northern Tanzania. Tropical Medicine and International Health, 2017, 22, 454-464.	1.0	43
104	The EcoKI Type I Restriction-Modification System in Escherichia coli Affects but Is Not an Absolute Barrier for Conjugation. Journal of Bacteriology, 2015, 197, 337-342.	1.0	42
105	Identification and Antimicrobial Resistance of Bacteria Isolated from Probiotic Products Used in Shrimp Culture. PLoS ONE, 2015, 10, e0132338.	1.1	42
106	Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods. BMC Genomics, 2017, 18, 19.	1.2	40
107	Setting a baseline for global urban virome surveillance in sewage. Scientific Reports, 2020, 10, 13748.	1.6	39
108	Evidence-based policy for controlling antimicrobial resistance in the food chain in Denmark. Food Control, 2014, 40, 185-192.	2.8	37

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109	Prediction of Acquired Antimicrobial Resistance for Multiple Bacterial Species Using Neural Networks. <i>MSystems</i> , 2020, 5, .	1.7	36
110	Microbiota long-term dynamics and prediction of acute graft-versus-host disease in pediatric allogeneic stem cell transplantation. <i>Microbiome</i> , 2021, 9, 148.	4.9	35
111	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	34
112	Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers: A metagenome-wide cross-sectional study. <i>Environment International</i> , 2020, 143, 105939.	4.8	33
113	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. <i>Communications Biology</i> , 2020, 3, 155.	2.0	33
114	Genomic evolution of antimicrobial resistance in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2021, 11, 15108.	1.6	33
115	Evaluation of Eight Different Cephalosporins for Detection of Cephalosporin Resistance in <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>Microbial Drug Resistance</i> , 2010, 16, 253-261.	0.9	31
116	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
117	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
118	Metagenomics analysis of bacteriophages and antimicrobial resistance from global urban sewage. <i>Scientific Reports</i> , 2021, 11, 1600.	1.6	29
119	Metagenomics-Based Approach to Source-Attribution of Antimicrobial Resistance Determinants – Identification of Reservoir Resistome Signatures. <i>Frontiers in Microbiology</i> , 2020, 11, 601407.	1.5	29
120	The COMPARE Data Hubs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	28
121	Establishing Streptomycin Epidemiological Cut-Off Values for <i>Salmonella</i> and <i>Escherichia coli</i> . <i>Microbial Drug Resistance</i> , 2012, 18, 88-93.	0.9	27
122	Ceftriaxone use in a tertiary care hospital in Kilimanjaro, Tanzania: A need for a hospital antibiotic stewardship programme. <i>PLoS ONE</i> , 2019, 14, e0220261.	1.1	27
123	Results of Use of WHO Global Salm-Surv External Quality Assurance System for Antimicrobial Susceptibility Testing of <i>Salmonella</i> Isolates from 2000 to 2007. <i>Journal of Clinical Microbiology</i> , 2009, 47, 79-85.	1.8	26
124	Metagenomic analysis of viruses in toilet waste from long distance flights – A new procedure for global infectious disease surveillance. <i>PLoS ONE</i> , 2019, 14, e0210368.	1.1	26
125	Secrets of the Hospital Underbelly: Patterns of Abundance of Antimicrobial Resistance Genes in Hospital Wastewater Vary by Specific Antimicrobial and Bacterial Family. <i>Frontiers in Microbiology</i> , 2021, 12, 703560.	1.5	26
126	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

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127	The Lake Chad Basin, an Isolated and Persistent Reservoir of <i>Vibrio cholerae</i> O1: A Genomic Insight into the Outbreak in Cameroon, 2010. PLoS ONE, 2016, 11, e0155691.	1.1	25
128	Prevalence and genomic analysis of ESBL-producing <i>Escherichia coli</i> in retail raw meats in Singapore. Journal of Antimicrobial Chemotherapy, 2021, 76, 601-605.	1.3	25
129	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	1.1	24
130	Mechanisms and Spread of Bacterial Resistance to Antimicrobial Agents. , 0, , 73-98.		24
131	Standard Sample Storage Conditions Have an Impact on Inferred Microbiome Composition and Antimicrobial Resistance Patterns. Microbiology Spectrum, 2021, 9, e0138721.	1.2	24
132	Genome-Wide High-Throughput Screening to Investigate Essential Genes Involved in Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Survival. PLoS ONE, 2014, 9, e89018.	1.1	23
133	Whole genome sequencing reveals high clonal diversity of <i>Escherichia coli</i> isolated from patients in a tertiary care hospital in Moshi, Tanzania. Antimicrobial Resistance and Infection Control, 2018, 7, 72.	1.5	22
134	Pandemicsâ€œ One Health preparedness for the next. Lancet Regional Health - Europe, The, 2021, 9, 100210.	3.0	22
135	Biocide Susceptibility of <i>Staphylococcus aureus</i> CC398 and CC30 Isolates from Pigs and Identification of the Biocide Resistance Genes, <i>qacG</i> and <i>qacC</i> . Microbial Drug Resistance, 2015, 21, 527-536.	0.9	21
136	Antimicrobial Resistance in Staphylococci and Streptococci of Animal Origin. , 0, , 187-212.		21
137	Human Deaths and Third-Generation Cephalosporin use in Poultry, Europe. Emerging Infectious Diseases, 2013, 19, 1339-1340.	2.0	21
138	Molecular epidemiology of virulence and antimicrobial resistance determinants in <i>Klebsiella pneumoniae</i> from hospitalised patients in Kilimanjaro, Tanzania. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 1901-1914.	1.3	19
139	Prevalence and risk factors for CTX-M gram-negative bacteria in hospitalized patients at a tertiary care hospital in Kilimanjaro, Tanzania. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 897-906.	1.3	17
140	Proficiency of WHO Global Foodborne Infections Network External Quality Assurance System Participants in Identification and Susceptibility Testing of Thermotolerant <i>Campylobacter</i> spp. from 2003 to 2012. Journal of Clinical Microbiology, 2018, 56, .	1.8	17
141	Proof of concept: used malaria rapid diagnostic tests applied for parallel sequencing for surveillance of molecular markers of anti-malarial resistance in Bissau, Guinea-Bissau during 2014â€œ2017. Malaria Journal, 2019, 18, 252.	0.8	17
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