Frank M Aarestrup

List of Publications by Year
in descending order

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Version: 2024-02-01

182 papers	30,904 citations	12330 69 h-index	5255 165 g-index
206 all docs	206 docs citations	206 times ranked	20684 citing authors

#	Article	IF	Citations
1	Emergence of methicillin resistance predates the clinical use of antibiotics. Nature, 2022, 602, 135-141.	27.8	138
2	ResFinder â€“ an open online resource for identification of antimicrobial resistance genes in next-generation sequencing data and prediction of phenotypes from genotypes. Microbial Genomics, 2022, 8, .	2.0	126
3	One Day in Denmark: Nationwide point-prevalence survey of human bacterial isolates and comparison of classical and whole-genome sequence-based species identification methods. PLoS ONE, 2022, 17, e0261999.	2.5	5
4	Global Distribution of mcr Gene Variants in 214K Metagenomic Samples. MSystems, 2022, 7, e0010522.	3.8	17
5	Library Preparation and Sequencing Platform Introduce Bias in Metagenomic-Based Characterizations of Microbiomes. Microbiology Spectrum, 2022, 10, e0009022.	3.0	12
6	PlasmidHostFinder: Prediction of Plasmid Hosts Using Random Forest. MSystems, 2022, 7, e0118021.	3.8	8
7	Metagenomic DNA sequencing for semi-quantitative pathogen detection from urine: a prospective, laboratory-based, proof-of-concept study. Lancet Microbe, The, 2022, , .	7.3	7
8	Detection of mobile genetic elements associated with antibiotic resistance in Salmonella enterica using a newly developed web tool: MobileElementFinder. Journal of Antimicrobial Chemotherapy, 2021, 76, 101-109.	3.0	274
9	Prevalence and genomic analysis of ESBL-producingEscherichia coliin retail raw meats in Singapore. Journal of Antimicrobial Chemotherapy, 2021, 76, 601-605.	3.0	25
10	Salmonella enterica serovar Typhi H58 clone has been endemic in Zimbabwe from 2012 to 2019. Journal of Antimicrobial Chemotherapy, 2021, 76, 1160-1167.	3.0	13
11	Metagenomics analysis of bacteriophages and antimicrobial resistance from global urban sewage. Scientific Reports, 2021, 11, 1600.	3.3	29
12	A Peek into the Plasmidome of Global Sewage. MSystems, 2021, 6, e0028321.	3.8	14
13	Microbiota long-term dynamics and prediction of acute graft-versus-host disease in pediatric allogeneic stem cell transplantation. Microbiome, 2021, 9, 148.	11.1	35
14	Risk Factors for Antimicrobial Resistance in Turkey Farms: A Cross-Sectional Study in Three European Countries. Antibiotics, 2021, 10, 820.	3.7	8
15	Genomic evolution of antimicrobial resistance in Escherichia coli. Scientific Reports, 2021, 11, 15108.	3.3	33
16	Arrangements of Mobile Genetic Elements among Virotype E Subpopulation of Escherichia coli Sequence Type 131 Strains with High Antimicrobial Resistance and Virulence Gene Content. MSphere, 2021, 6, e0055021.	2.9	10
17	Secrets of the Hospital Underbelly: Patterns of Abundance of Antimicrobial Resistance Genes in Hospital Wastewater Vary by Specific Antimicrobial and Bacterial Family. Frontiers in Microbiology, 2021, 12, 703560.	3.5	26
18	Pandemicsâ€“ One Health preparedness for the next. Lancet Regional Health - Europe, The, 2021, 9, 100210.	5.6	22

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19	Standard Sample Storage Conditions Have an Impact on Inferred Microbiome Composition and Antimicrobial Resistance Patterns. Microbiology Spectrum, 2021, 9, e0138721.	3.0	24
20	Evaluating the usefulness of next-generation sequencing for herb authentication. Food Chemistry Molecular Sciences, 2021, 3, 100044.	2.1	3
21	Danish Whole-Genome-Sequenced Candida albicans and Candida glabrata Samples Fit into Globally Prevalent Clades. Journal of Fungi (Basel, Switzerland), 2021, 7, 962.	3.5	3
22	Expansion of a Subset Within the C2 Subclade of Escherichia coli Sequence Type 131 (ST131) Is Driving the Increasing Rates of Aminoglycoside Resistance. Open Forum Infectious Diseases, 2020, 7, ofaa410.	0.9	3
23	Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers: A metagenome-wide cross-sectional study. Environment International, 2020, 143, 105939.	10.0	33
24	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	3.6	4
25	Long-Term Temporal Stability of the Resistome in Sewage from Copenhagen. MSystems, 2020, 5, .	3.8	6
26	Farm dust resistomes and bacterial microbiomes in European poultry and pig farms. Environment International, 2020, 143, 105971.	10.0	66
27	ResFinder 4.0 for predictions of phenotypes from genotypes. Journal of Antimicrobial Chemotherapy, 2020, 75, 3491-3500.	3.0	1,523
28	Setting a baseline for global urban virome surveillance in sewage. Scientific Reports, 2020, 10, 13748.	3.3	39
29	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. Communications Biology, 2020, 3, 155.	4.4	33
30	Large scale automated phylogenomic analysis of bacterial isolates and the Evergreen Online platform. Communications Biology, 2020, 3, 137.	4.4	7
31	Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. Scientific Reports, 2020, 10, 3033.	3.3	7
32	Comment on: Gross national income and antibiotic resistance in invasive isolates: analysis of the top-ranked antibiotic-resistant bacteria on the 2017 WHO priority list. Journal of Antimicrobial Chemotherapy, 2020, 75, 2017-2018.	3.0	2
33	Using sewage for surveillance of antimicrobial resistance. Science, 2020, 367, 630-632.	12.6	122
34	Prediction of Acquired Antimicrobial Resistance for Multiple Bacterial Species Using Neural Networks. MSystems, 2020, 5, .	3.8	36
35	Metagenomics-Based Approach to Source-Attribution of Antimicrobial Resistance Determinants â€“ Identification of Reservoir Resistome Signatures. Frontiers in Microbiology, 2020, 11, 601407.	3.5	29
36	A metagenomic glimpse into the gut of wild and domestic animals: Quantification of antimicrobial resistance and more. PLoS ONE, 2020, 15, e0242987.	2.5	30

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37	Using Genomics to Track Global Antimicrobial Resistance. Frontiers in Public Health, 2019, 7, 242.	2.7	263
38	Ceftriaxone use in a tertiary care hospital in Kilimanjaro, Tanzania: A need for a hospital antibiotic stewardship programme. PLoS ONE, 2019, 14, e0220261.	2.5	27
39	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€"2017. Malaria Journal, 2019, 18, 252.	2.3	17
40	Worldwide human mitochondrial haplogroup distribution from urban sewage. Scientific Reports, 2019, 9, 11624.	3.3	12
41	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
42	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	2.5	24
43	Comparison of Gene Expression Profiles of Uropathogenic Escherichia Coli CFT073 after Prolonged Exposure to Subinhibitory Concentrations of Different Biocides. Antibiotics, 2019, 8, 167.	3.7	7
44	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131.	11.1	65
45	Megaphages infect Prevotella and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700.	13.3	141
46	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated In Silico High-Throughput Sequencing Data Sets. Journal of Clinical Microbiology, 2019, 57, .	3.9	34
47	Associations between antimicrobial use and the faecal resistome on broiler farms from nine European countries. Journal of Antimicrobial Chemotherapy, 2019, 74, 2596-2604.	3.0	49
48	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	12.8	612
49	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.	3.0	46
50	Host Resistance, Genomics and Population Dynamics in a Salmonella Enteritidis and Phage System. Viruses, 2019, 11, 188.	3.3	16
51	The COMPARE Data Hubs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	28
52	Improved Resistance Prediction in Mycobacterium tuberculosis by Better Handling of Insertions and Deletions, Premature Stop Codons, and Filtering of Non-informative Sites. Frontiers in Microbiology, 2019, 10, 2464.	3.5	7
53	Metagenomic analysis of viruses in toilet waste from long distance flightsâ€"A new procedure for global infectious disease surveillance. PLoS ONE, 2019, 14, e0210368.	2.5	26
54	The antimicrobial resistome in relation to antimicrobial use and biosecurity in pig farming, a metagenome-wide association study in nine European countries. Journal of Antimicrobial Chemotherapy, 2019, 74, 865-876.	3.0	63

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55	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.	2.9	17
56	Genomics-Based Identification of Microorganisms in Human Ocular Body Fluid. Scientific Reports, 2018, 8, 4126.	3.3	69
57	SCC mec Finder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome mec in Staphylococcus aureus Using Whole-Genome Sequence Data. MSphere, 2018, 3, .	2.9	197
58	Drivers and Dynamics of Methicillin-Resistant Livestock-Associated Staphylococcus aureus CC398 in Pigs and Humans in Denmark. MBio, 2018, 9, .	4.1	74
59	Proficiency of WHO Global Foodborne Infections Network External Quality Assurance System Participants in Identification and Susceptibility Testing of Thermotolerant Campylobacter spp. from 2003 to 2012. Journal of Clinical Microbiology, 2018, 56, .	3.9	17
60	Rapid and precise alignment of raw reads against redundant databases with KMA. BMC Bioinformatics, 2018, 19, 307.	2.6	433
61	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908.	13.3	230
62	Whole genome sequencing reveals high clonal diversity of Escherichia coli isolated from patients in a tertiary care hospital in Moshi, Tanzania. Antimicrobial Resistance and Infection Control, 2018, 7, 72.	4.1	22
63	Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 1901-1914.	2.9	19
64	Direct whole-genome sequencing of Plasmodium falciparum specimens from dried erythrocyte spots. Malaria Journal, 2018, 17, 91.	2.3	12
65	Comparative genomics of quinoloneâ€resistant and susceptible Campylobacter jejuni of poultry origin from major poultry producing European countries (GENCAMP). EFSA Supporting Publications, 2018, 15, 1398E.	0.7	11
66	Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods. BMC Genomics, 2017, 18, 19.	2.8	40
67	The CGE Tool Box. , 2017, , 65-90.		3
68	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.	2.3	43
69	High throughput resistance profiling of Plasmodium falciparum infections based on custom dual indexing and Illumina next generation sequencing-technology. Scientific Reports, 2017, 7, 2398.	3.3	57
70	PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2017, 72, 2764-2768.	3.0	534
71	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. Journal of Antimicrobial Chemotherapy, 2017, 72, 385-392.	3.0	89
72	Commentary: Benefits and risks of antimicrobial use in food-producing animals. Frontiers in Microbiology, 2017, 8, 181.	3.5	4

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73	An Assessment of Different Genomic Approaches for Inferring Phylogeny of Listeria monocytogenes. Frontiers in Microbiology, 2017, 8, 2351.	3.5	66
74	Epidemiology of Danish Aeromonas salmonicida subsp. salmonicida in Fish Farms Using Whole Genome Sequencing. Frontiers in Microbiology, 2017, 8, 2411.	3.5	11
75	MGmapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. PLoS ONE, 2017, 12, e0176469.	2.5	66
76	Characterization and Genetic Variation of Vibrio cholerae Isolated from Clinical and Environmental Sources in Thailand. PLoS ONE, 2017, 12, e0169324.	2.5	88
77	Emergence of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Bloodstream Infections in Denmark. Clinical Infectious Diseases, 2017, 65, 1072-1076.	5.8	78
78	Evaluation of Methods for the Concentration and Extraction of Viruses from Sewage in the Context of Metagenomic Sequencing. PLoS ONE, 2017, 12, e0170199.	2.5	107
79	The Lake Chad Basin, an Isolated and Persistent Reservoir of Vibrio cholerae O1: A Genomic Insight into the Outbreak in Cameroon, 2010. PLoS ONE, 2016, 11, e0155691.	2.5	25
80	A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance. PLoS ONE, 2016, 11, e0157718.	2.5	161
81	Is the Evolution of Salmonella enterica subsp.entericaLinked to Restriction-Modification Systems?. MSystems, 2016, 1, .	3.8	74
82	Benchtop Whole-Genome Sequencing for Identification of Nosocomial Outbreaks in Tanzania. Infection Control and Hospital Epidemiology, 2016, 37, 622-623.	1.8	2
83	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	3.1	105
84	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.	3.1	69
85	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. MSystems, 2016, 1, .	3.8	153
86	Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals. Antimicrobial Resistance and Infection Control, 2016, 5, 18.	4.1	70
87	Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. Journal of Antimicrobial Chemotherapy, 2016, 71, 2484-2488.	3.0	166
88	Consolidating and Exploring Antibiotic Resistance Gene Data Resources. Journal of Clinical Microbiology, 2016, 54, 851-859.	3.9	94
89	Sharing Data for Global Infectious Disease Surveillance and Outbreak Detection. Trends in Microbiology, 2016, 24, 241-245.	7.7	45
90	Comparative genomics of toxigenic and non-toxigenic Staphylococcus hyicus. Veterinary Microbiology, 2016, 185, 34-40.	1.9	9

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91	Investigating Salmonella Eko from Various Sources in Nigeria by Whole Genome Sequencing to Identify the Source of Human Infections. PLoS ONE, 2016, 11, e0156212.	2.5	8
92	Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. Scientific Reports, 2015, 5, 11444.	3.3	74
93	Reads2Type: a web application for rapid microbial taxonomy identification. BMC Bioinformatics, 2015, 16, 398.	2.6	5
94	Audouin's gull, a potential vehicle of an extended spectrum Î²-lactamase producing Salmonella Agona. FEMS Microbiology Letters, 2015, 362, 1-4.	1.8	10
95	Rapid and EasyIn SilicoSerotyping of Escherichia coli Isolates by Use of Whole-Genome Sequencing Data. Journal of Clinical Microbiology, 2015, 53, 2410-2426.	3.9	775
96	The livestock reservoir for antimicrobial resistance: a personal view on changing patterns of risks, effects of interventions and the way forward. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140085.	4.0	205
97	Biocide Susceptibility ofStaphylococcus aureusCC398 and CC30 Isolates from Pigs and Identification of the Biocide Resistance Genes,qacGandqacC. Microbial Drug Resistance, 2015, 21, 527-536.	2.0	21
98	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.	3.9	82
99	Identification of a Pseudomonas aeruginosa co-producing NDM-1, VIM-5 and VIM-6 metallo-Î²-lactamases in Denmark using whole-genome sequencing. International Journal of Antimicrobial Agents, 2015, 45, 324-325.	2.5	12
100	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.	3.9	25
101	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.	2.2	42
102	Identification and Antimicrobial Resistance of Bacteria Isolated from Probiotic Products Used in Shrimp Culture. PLoS ONE, 2015, 10, e0132338.	2.5	42
103	Comparative Evaluation of the Antimicrobial Activity of Different Antimicrobial Peptides against a Range of Pathogenic Bacteria. PLoS ONE, 2015, 10, e0144611.	2.5	148
104	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, .	7.0	326
105	Characterization of extended-spectrum Î²-lactamase (ESBL)-producing Escherichia coli obtained from Danish pigs, pig farmers and their families from farms with high or no consumption of third- or fourth-generation cephalosporins. Journal of Antimicrobial Chemotherapy, 2014, 69, 2650-2657.	3.0	149
106	In Silico Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing. Antimicrobial Agents and Chemotherapy, 2014, 58, 3895-3903.	3.2	3,558
107	Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples. Journal of Clinical Microbiology, 2014, 52, 139-146.	3.9	424
108	Antimicrobial resistance of zoonotic and commensal bacteria in Europe: The missing link between consumption and resistance in veterinary medicine. Veterinary Microbiology, 2014, 170, 1-9.	1.9	144

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109	Benchmarking of Methods for Genomic Taxonomy. Journal of Clinical Microbiology, 2014, 52, 1529-1539.	3.9	241
110	Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic Escherichia coli. Journal of Clinical Microbiology, 2014, 52, 1501-1510.	3.9	1,142
111	Analysis of the contribution of bacteriophage ST64B to in vitro virulence traits of Salmonella enterica serovar Typhimurium. Journal of Medical Microbiology, 2014, 63, 331-342.	1.8	7
112	Evidence-based policy for controlling antimicrobial resistance in the food chain in Denmark. Food Control, 2014, 40, 185-192.	5.5	37
113	The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313. PLoS ONE, 2014, 9, e84566.	2.5	48
114	Evaluation of Whole Genome Sequencing for Outbreak Detection of Salmonella enterica. PLoS ONE, 2014, 9, e87991.	2.5	215
115	Genome-Wide High-Throughput Screening to Investigate Essential Genes Involved in Methicillin-Resistant Staphylococcus aureus Sequence Type 398 Survival. PLoS ONE, 2014, 9, e89018.	2.5	23
116	Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. PLoS ONE, 2014, 9, e104984.	2.5	696
117	Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing. Journal of Antimicrobial Chemotherapy, 2013, 68, 771-777.	3.0	307
118	Human Deaths and Third-Generation Cephalosporin use in Poultry, Europe. Emerging Infectious Diseases, 2013, 19, 1339-1340.	4.3	43
119	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.	1.2	30
120	Voluntary ban on cephalosporin use in Danish pig production has effectively reduced extended-spectrum cephalosporinase-producing Escherichia coli in slaughter pigs. Journal of Antimicrobial Chemotherapy, 2013, 68, 569-572.	3.0	104
121	PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data. PLoS ONE, 2013, 8, e77302.	2.5	365
122	Human Deaths and Third-Generation Cephalosporin use in Poultry, Europe. Emerging Infectious Diseases, 2013, 19, 1339-1340.	4.3	21
123	Prevalence of extended-spectrum cephalosporinase (ESC)-producing Escherichia coli in Danish slaughter pigs and retail meat identified by selective enrichment and association with cephalosporin usage. Journal of Antimicrobial Chemotherapy, 2012, 67, 582-588.	3.0	94
124	Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. MBio, 2012, 3, .	4.1	638
125	Identification of acquired antimicrobial resistance genes. Journal of Antimicrobial Chemotherapy, 2012, 67, 2640-2644.	3.0	4,515
126	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.	3.1	51

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127	Establishing Streptomycin Epidemiological Cut-Off Values forSalmonellaandEscherichia coli. Microbial Drug Resistance, 2012, 18, 88-93.	2.0	27
128	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. Journal of Clinical Microbiology, 2012, 50, 1355-1361.	3.9	1,925
129	Get pigs off antibiotics. Nature, 2012, 486, 465-466.	27.8	176
130	Clonal diversity of Staphylococcus aureus originating from the small ruminants goats and sheep. Veterinary Microbiology, 2012, 156, 157-161.	1.9	63
131	Study of methicillin resistant Staphylococcus aureus (MRSA) in Danish pigs at slaughter and in imported retail meat reveals a novel MRSA type in slaughter pigs. Veterinary Microbiology, 2012, 157, 246-250.	1.9	76
132	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	4.3	64
133	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	4.3	61
134	Global Monitoring of Salmonella Serovar Distribution from the World Health Organization Global Foodborne Infections Network Country Data Bank: Results of Quality Assured Laboratories from 2001 to 2007. Foodborne Pathogens and Disease, 2011, 8, 887-900.	1.8	543
135	Zinc resistance of Staphylococcus aureus of animal origin is strongly associated with methicillin resistance. Veterinary Microbiology, 2011, 150, 344-348.	1.9	126
136	Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11.	4.1	268
137	Association Between Antimicrobial Resistance inEscherichia coliIsolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study. Foodborne Pathogens and Disease, 2011, 8, 1295-1301.	1.8	107
138	Susceptibility of Clostridium difficile Toward Antimicrobial Agents Used as Feed Additives for Food Animals. Microbial Drug Resistance, 2011, 17, 125-127.	2.0	1
139	Evaluation of ceftiofur and cefquinome for phenotypic detection of methicillin resistance in Staphylococcus aureus using disk diffusion testing and MIC-determinations. Veterinary Microbiology, 2010, 140, 176-179.	1.9	8
140	Decreased susceptibility to zinc chloride is associated with methicillin resistant Staphylococcus aureus CC398 in Danish swine. Veterinary Microbiology, 2010, 142, 455-457.	1.9	61
141	Evaluation of Eight Different Cephalosporins for Detection of Cephalosporin Resistance in Salmonella enterica and Escherichia coli. Microbial Drug Resistance, 2010, 16, 253-261.	2.0	31
142	Changes in the use of antimicrobials and the effects on productivity of swine farms in Denmark. American Journal of Veterinary Research, 2010, 71, 726-733.	0.6	135
143	WHO Global Salm-Surv External Quality Assurance System for Serotyping of Salmonella Isolates from 2000 to 2007. Journal of Clinical Microbiology, 2009, 47, 2729-2736.	3.9	49
144	Diversity of the tetracycline resistance gene tet(M) and identification of Tn916- and Tn5801-like (Tn6014) transposons in Staphylococcus aureus from humans and animals. Journal of Antimicrobial Chemotherapy, 2009, 64, 490-500.	3.0	69

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145	Comment on: Causal regulations vs. political will: Why human zoonotic infections increase despite precautionary bans on animal antibiotics. Environment International, 2009, 35, 760-761.	10.0	5
146	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. Clinical Infectious Diseases, 2009, 49, 132-141.	5.8	306
147	Results of Use of WHO Global Salm-Surv External Quality Assurance System for Antimicrobial Susceptibility Testing of Salmonella Isolates from 2000 to 2007. Journal of Clinical Microbiology, 2009, 47, 79-85.	3.9	26
148	Occurrence of antimicrobial resistance among bacterial pathogens and indicator bacteria in pigs in different European countries from year 2002 â€“ 2004: the ARBAO-II study. Acta Veterinaria Scandinavica, 2008, 50, 19.	1.6	70
149	Resistance in bacteria of the food chain: epidemiology and control strategies. Expert Review of Anti-Infective Therapy, 2008, 6, 733-750.	4.4	302
150	Antimicrobial resistance in swine production. Animal Health Research Reviews, 2008, 9, 135-148.	3.1	120
151	Pigs as Source of Methicillin-ResistantStaphylococcus aureusCC398 Infections in Humans, Denmark. Emerging Infectious Diseases, 2008, 14, 1383-1389.	4.3	234
152	Danish Integrated Antimicrobial Resistance Monitoring and Research Program. Emerging Infectious Diseases, 2007, 13, 1633-1639.	4.3	116
153	International Spread of Multidrug-resistantSalmonellaSchwarzengrund in Food Products. Emerging Infectious Diseases, 2007, 13, 726-731.	4.3	117
154	External quality assurance system for antibiotic resistance in bacteria of animal origin in Europe (ARBAO-II), 2003. Veterinary Microbiology, 2006, 115, 128-139.	1.9	8
155	Copper Resistance in Enterococcus faecium, Mediated by the tcrB Gene, Is Selected by Supplementation of Pig Feed with Copper Sulfate. Applied and Environmental Microbiology, 2006, 72, 5784-5789.	3.1	106
156	Occurrence of integrons and antimicrobial resistance genes among Salmonella enterica from Brazil. Journal of Antimicrobial Chemotherapy, 2006, 58, 305-309.	3.0	64
157	Molecular Characterization and Occurrence of Extended-Spectrum Î²-Lactamase Resistance Genes among Salmonella enterica Serovar Corvallis from Thailand, Bulgaria, and Denmark. Microbial Drug Resistance, 2006, 12, 192-198.	2.0	99
158	Veterinary Drug Usage and Antimicrobial Resistance in Bacteria of Animal Origin. Basic and Clinical Pharmacology and Toxicology, 2005, 96, 271-281.	2.5	299
159	ResistantSalmonellaVirchow in Quail Products. Emerging Infectious Diseases, 2005, 11, 1984-1985.	4.3	12
160	Î²-Lactamases among extended-spectrum Î²-lactamase (ESBL)-resistant Salmonella from poultry, poultry products and human patients in The Netherlands. Journal of Antimicrobial Chemotherapy, 2005, 56, 115-121.	3.0	335
161	Susceptibility of different bacterial species isolated from food animals to copper sulphate, zinc chloride and antimicrobial substances used for disinfection. Veterinary Microbiology, 2004, 100, 83-89.	1.9	175
162	Antimicrobial susceptibility of Haemophilus parasuis and Histophilus somni from pigs and cattle in Denmark. Veterinary Microbiology, 2004, 101, 143-146.	1.9	62

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163	Prevalence of Î²-Lactamases among Ampicillin-ResistantEscherichia coliandSalmonellaIsolated from Food Animals in Denmark. Microbial Drug Resistance, 2004, 10, 334-340.	2.0	151
164	Association between phage types and antimicrobial resistance among bovine Staphylococcus aureus from 10 countries. Veterinary Microbiology, 2003, 95, 133-147.	1.9	55
165	Antimicrobial susceptibility and occurrence of resistance genes among Salmonella enterica serovar Weltevreden from different countries. Journal of Antimicrobial Chemotherapy, 2003, 52, 715-718.	3.0	111
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167	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. Antimicrobial Agents and Chemotherapy, 2001, 45, 2054-2059.	3.2	533
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