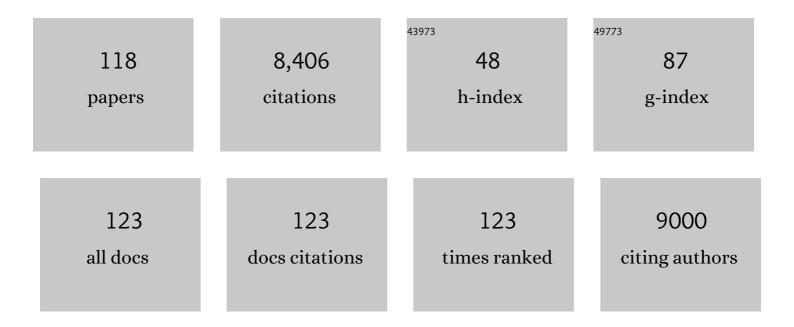
Rene SjÃ, gren Hendriksen

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Extended-Spectrum ß-Lactamase-Producing Escherichia coli Among Humans, Beef Cattle, and Abattoir Environments in Nigeria. Frontiers in Cellular and Infection Microbiology, 2022, 12, 869314.	1.8	6
2	Rapid risk assessment framework to assess public health risk of antimicrobial resistance found in foods. Food Control, 2022, 137, 108852.	2.8	1
3	Salmonella enterica serovar Typhi H58 clone has been endemic in Zimbabwe from 2012 to 2019. Journal of Antimicrobial Chemotherapy, 2021, 76, 1160-1167.	1.3	13
4	Genetic relatedness of multidrug resistant Escherichia coli isolated from humans, chickens and poultry environments. Antimicrobial Resistance and Infection Control, 2021, 10, 58.	1.5	61
5	New Brucella variant isolated from Croatian cattle. BMC Veterinary Research, 2021, 17, 126.	0.7	3
6	Phenotypic and genotypic characterization of mcr-1-positive multidrug-resistant Escherichia coli ST93, ST117, ST156, ST10, and ST744 isolated from poultry in Poland. Brazilian Journal of Microbiology, 2021, 52, 1597-1609.	0.8	13
7	Prevalence and risk factors for faecal carriage of multidrug resistant Escherichia coli among slaughterhouse workers. Scientific Reports, 2021, 11, 13362.	1.6	8
8	Emergence and Clonal Spread of CTX-M-65-Producing Escherichia coli From Retail Meat in Portugal. Frontiers in Microbiology, 2021, 12, 653595.	1.5	19
9	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. Journal of Antimicrobial Chemotherapy, 2021, 76, 3063-3065.	1.3	10
10	Mapping the coverage, availability and uptake of External Quality Assessment programmes across One Health sectors in Asia. Journal of Antimicrobial Chemotherapy, 2021, , .	1.3	4
11	Antimicrobial and Genomic Characterization of Salmonella Nigeria from Pigs and Poultry in Ilorin, North-central, Nigeria. Journal of Infection in Developing Countries, 2021, 15, 1899-1909.	O.5	1
12	Molecular Characteristics and Zoonotic Potential of Salmonella Weltevreden From Cultured Shrimp and Tilapia in Vietnam and China. Frontiers in Microbiology, 2020, 11, 1985.	1.5	15
13	Quantitative Microbial Risk Assessment Based on Whole Genome Sequencing Data: Case of Listeria monocytogenes. Microorganisms, 2020, 8, 1772.	1.6	13
14	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	1.6	4
15	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	1.5	7
16	Extended-spectrum ß-lactamase-producing Escherichia coli among humans, chickens and poultry environments in Abuja, Nigeria. One Health Outlook, 2020, 2, 8.	1.4	32
17	Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. Scientific Reports, 2020, 10, 3033.	1.6	7
18	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

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19	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
20	Accelerating surveillance and research of antimicrobial resistance – an online repository for sharing of antimicrobial susceptibility data associated with whole-genome sequences. Microbial Genomics, 2020, 6, .	1.0	5
21	Machine Learning Methods as a Tool for Predicting Risk of Illness Applying Nextâ€Generation Sequencing Data. Risk Analysis, 2019, 39, 1397-1413.	1.5	33
22	Using Genomics to Track Global Antimicrobial Resistance. Frontiers in Public Health, 2019, 7, 242.	1.3	263
23	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	5.9	184
24	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	1.1	24
25	Human skin bacterial flora differ with altitudes in different ethnic groups of Nepal. Asian Journal of Medical Sciences, 2019, 10, 11-17.	0.0	0
26	Application of different DNA extraction procedures, library preparation protocols and sequencing platforms: impact on sequencing results. Heliyon, 2019, 5, e02745.	1.4	12
27	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
28	Surveillance and Genomics of Toxigenic Vibrio cholerae O1 From Fish, Phytoplankton and Water in Lake Victoria, Tanzania. Frontiers in Microbiology, 2019, 10, 901.	1.5	20
29	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. Journal of Clinical Microbiology, 2019, 57, .	1.8	34
30	Whole-Genome Sequencing Analysis of Nontyphoidal Salmonella enterica of Chicken Meat and Human Origin Under Surveillance in Sri Lanka. Foodborne Pathogens and Disease, 2019, 16, 531-537.	0.8	16
31	Incl1 ST3 and Incl1 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
32	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	5.8	612
33	Cross-Border Transmission of Salmonella Choleraesuis var. Kunzendorf in European Pigs and Wild Boar: Infection, Genetics, and Evolution. Frontiers in Microbiology, 2019, 10, 179.	1.5	17
34	Genomic insights into Vibrio cholerae O1 responsible for cholera epidemics in Tanzania between 1993 and 2017. PLoS Neglected Tropical Diseases, 2019, 13, e0007934.	1.3	21
35	ST131 <i>fimH</i> 22 <i>Escherichia coli</i> isolate with a <i>bla</i> CMY-2/Incl1/ST12 plasmid obtained from a patient with bloodstream infection: highly similar to <i>E. coli</i> isolates of broiler origin. Journal of Antimicrobial Chemotherapy, 2019, 74, 557-560.	1.3	34
36	Evaluation of temocillin for phenotypic carbapenemase screening of Escherichia coli and Salmonella enterica isolates in relation to the presence of genes encoding ESBLs and carbapenemase production. Journal of Antimicrobial Chemotherapy, 2019, 74, 639-644.	1.3	5

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37	Global phylogenomics of multidrug-resistant Salmonella enterica serotype Kentucky ST198. Microbial Genomics, 2019, 5, .	1.0	69
38	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
39	Final report of ENGAGE ―Establishing Next Generation sequencing Ability for Genomic analysis in Europe. EFSA Supporting Publications, 2018, 15, 1431E.	0.3	14
40	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, .	1.8	17
41	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Typhimurium Sequence Type 313, Isolated from India. Microbiology Resource Announcements, 2018, 7, .	0.3	1
42	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
43	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.	0.3	11
44	Identification of a novel transposon-associated phosphoethanolamine transferase gene, mcr-5, conferring colistin resistance in d-tartrate fermenting Salmonella enterica subsp. enterica serovar Paratyphi B. Journal of Antimicrobial Chemotherapy, 2017, 72, 3317-3324.	1.3	450
45	Carbapenemase VCC-1–Producing <i>Vibrio cholerae</i> in Coastal Waters of Germany. Emerging Infectious Diseases, 2017, 23, 1735-1737.	2.0	52
46	An Assessment of Different Genomic Approaches for Inferring Phylogeny of Listeria monocytogenes. Frontiers in Microbiology, 2017, 8, 2351.	1.5	66
47	Characterization and Genetic Variation of Vibrio cholerae Isolated from Clinical and Environmental Sources in Thailand. PLoS ONE, 2017, 12, e0169324.	1.1	88
48	Global Microbial Identifier. , 2017, , 13-31.		13
49	CHROMagar COL-APSE: a selective bacterial culture medium for the isolation and differentiation of colistin-resistant Gram-negative pathogens. Journal of Medical Microbiology, 2017, 66, 1554-1561.	0.7	39
50	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.	1.1	25
51	Is the Evolution of Salmonella enterica subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. MSystems, 2016, 1, .	1.7	74
52	Apramycin treatment affects selection and spread of a multidrug-resistant Escherichia coli strain able to colonize the human gut in the intestinal microbiota of pigs. Veterinary Research, 2016, 47, 12.	1.1	18
53	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	1.4	105
54	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

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55	Genomic Epidemiology: Whole-Genome-Sequencing–Powered Surveillance and Outbreak Investigation of Foodborne Bacterial Pathogens. Annual Review of Food Science and Technology, 2016, 7, 353-374.	5.1	152
56	Investigating Salmonella Eko from Various Sources in Nigeria by Whole Genome Sequencing to Identify the Source of Human Infections. PLoS ONE, 2016, 11, e0156212.	1.1	8
57	Audouin's gull, a potential vehicle of an extended spectrum β-lactamase producing Salmonella Agona. FEMS Microbiology Letters, 2015, 362, 1-4.	0.7	10
58	Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds. Veterinary Microbiology, 2015, 176, 282-291.	0.8	32
59	Proficiency testing for bacterial whole genome sequencing: an end-user survey of current capabilities, requirements and priorities. BMC Infectious Diseases, 2015, 15, 174.	1.3	62
60	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
61	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
62	Typhoid fever. Lancet, The, 2015, 385, 1136-1145.	6.3	265
63	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
64	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
65	Emergence and clonal dissemination of Salmonella enterica serovar Enteritidis causing salmonellosis in Mauritius. Journal of Infection in Developing Countries, 2014, 8, 454-460.	0.5	5
66	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	1.8	112
67	Genomic Epidemiology ofSalmonella entericaSerotype Enteritidis based on Population Structure of Prevalent Lineages. Emerging Infectious Diseases, 2014, 20, 1481-1489.	2.0	87
68	Persistence of fluoroquinolone-resistant Salmonella enterica serovar Kentucky from poultry and poultry sources in Nigeria. Journal of Infection in Developing Countries, 2014, 8, 384-388.	0.5	23
69	Diversity and antimicrobial susceptibility of Salmonella enterica serovars isolated from pig farms in Ibadan, Nigeria. Folia Microbiologica, 2014, 59, 69-77.	1.1	13
70	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.	0.8	144
71	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.	0.7	7
72	The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313. PLoS ONE, 2014, 9, e84566.	1.1	48

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73	Extended-Spectrum-Beta-Lactamases, AmpC Beta-Lactamases and Plasmid Mediated Quinolone Resistance in Klebsiella spp. from Companion Animals in Italy. PLoS ONE, 2014, 9, e90564.	1.1	86
74	Molecular clonality and antimicrobial resistance in Salmonella entericaserovars Enteritidis and Infantis from broilers in three Northern regions of Iran. BMC Veterinary Research, 2013, 9, 66.	0.7	53
75	Extremely Drug-Resistant Salmonella enterica Serovar Senftenberg Infections in Patients in Zambia. Journal of Clinical Microbiology, 2013, 51, 284-286.	1.8	26
76	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
77	Dissemination of Clonal <i>Salmonella enterica</i> Serovar Typhimurium Isolates Causing Salmonellosis in Mauritius. Foodborne Pathogens and Disease, 2013, 10, 618-623.	0.8	3
78	The global establishment of a highly-fluoroquinolone resistant Salmonella enterica serotype Kentucky ST198 strain. Frontiers in Microbiology, 2013, 4, 395.	1.5	114
79	Using next generation sequencing to tackle non-typhoidal Salmonella infections. Journal of Infection in Developing Countries, 2013, 7, 001-005.	0.5	25
80	Antimicrobial-resistant Shigella infections from Iran: an overlooked problem?. Journal of Antimicrobial Chemotherapy, 2012, 67, 1128-1133.	1.3	83
81	Characterization of Isolates of Salmonella enterica Serovar Stanley, a Serovar Endemic to Asia and Associated with Travel. Journal of Clinical Microbiology, 2012, 50, 709-720.	1.8	32
82	Characterization of Salmonella enterica serovar Enteritidis isolates recovered from blood and stool specimens in Thailand. BMC Microbiology, 2012, 12, 92.	1.3	17
83	Establishing Streptomycin Epidemiological Cut-Off Values for <i>Salmonella</i> and <i>Escherichia coli</i> . Microbial Drug Resistance, 2012, 18, 88-93.	0.9	27
84	SCCmec Type IX Element in Methicillin Resistant Staphylococcusaureusspa Type t337 (CC9) Isolated from Pigs and Pork in Thailand. Frontiers in Microbiology, 2012, 3, 103.	1.5	35
85	Antimicrobial resistance in Salmonella spp. recovered from patients admitted to six different hospitals in Tehran, Iran from 2007 to 2008. Folia Microbiologica, 2012, 57, 91-97.	1.1	26
86	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	2.0	64
87	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	2.0	61
88	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. Foodborne Pathogens and Disease, 2011, 8, 887-900.	0.8	543
89	Characterization of Salmonella Occurring at High Prevalence in a Population of the Land Iguana Conolophus subcristatus in Galápagos Islands, Ecuador. PLoS ONE, 2011, 6, e23147.	1.1	27
90	Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11.	1.8	268

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91	The Salmonella enterica Pan-genome. Microbial Ecology, 2011, 62, 487-504.	1.4	175
92	Association Between Antimicrobial Resistance in <i>Escherichia coli</i> Isolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study. Foodborne Pathogens and Disease, 2011, 8, 1295-1301.	0.8	107
93	International Spread of an Epidemic Population of Salmonella enterica Serotype Kentucky ST198 Resistant to Ciprofloxacin. Journal of Infectious Diseases, 2011, 204, 675-684.	1.9	226
94	Prevalence and Characterization of Human <i>Shigella</i> Infections in Henan Province, China, in 2006. Journal of Clinical Microbiology, 2011, 49, 232-242.	1.8	54
95	Reply to "South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strain― MBio, 2011, 2, e00245-11.	1.8	14
96	Epidemiological Investigation of <i>Salmonella enterica</i> Serovar Kedougou in Thailand. Foodborne Pathogens and Disease, 2011, 8, 203-211.	0.8	11
97	Microbiologic and Clinical Features of Salmonella Species Isolated From Bacteremic Children in Eastern Democratic Republic of Congo. Pediatric Infectious Disease Journal, 2010, 29, 504-510.	1.1	37
98	Molecular Characterization of Extended-Spectrum Cephalosporinase-Producing Salmonella enterica Serovar Choleraesuis Isolates from Patients in Thailand and Denmark. Journal of Clinical Microbiology, 2010, 48, 883-888.	1.8	52
99	Antimicrobial susceptibility and serovars of Salmonella from chickens and humans in Ibadan, Nigeria. Journal of Infection in Developing Countries, 2010, 4, 484-494.	0.5	89
100	Serotypes and antimicrobial resistance of Salmonella enterica ssp in central Thailand, 2001-2006. Southeast Asian Journal of Tropical Medicine and Public Health, 2010, 41, 1405-15.	1.0	34
101	Salmonella enterica Serovar Typhimurium in Mauritius Linked to Consumption of Marlin Mousse. Foodborne Pathogens and Disease, 2009, 6, 739-741.	0.8	10
102	Antimicrobial Susceptibilities, Phage Types, and Molecular Characterization ofSalmonella entericaSerovar Enteritidis from Chickens and Chicken Meat in Turkey. Foodborne Pathogens and Disease, 2009, 6, 265-271.	0.8	8
103	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
104	Risk Factors and Epidemiology of the Ten Most Common <i>Salmonella</i> Serovars from Patients in Thailand: 2002–2007. Foodborne Pathogens and Disease, 2009, 6, 1009-1019.	0.8	63
105	Occurrence and Characterization of <i>Salmonella</i> Hiduddify from Chickens and Poultry Meat in Nigeria. Foodborne Pathogens and Disease, 2009, 6, 425-430.	0.8	23
106	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. Journal of Clinical Microbiology, 2009, 47, 79-85.	1.8	26
107	Emergence of Multidrug-Resistant Salmonella Concord Infections in Europe and the United States in Children Adopted From Ethiopia, 2003–2007. Pediatric Infectious Disease Journal, 2009, 28, 814-818.	1.1	62
108	Molecular Characterization and Antimicrobial Susceptibility of <i>Salmonella</i> Isolates from Infections in Humans in Henan Province, China. Journal of Clinical Microbiology, 2009, 47, 401-409.	1.8	105

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109	Occurrence of antimicrobial resistance among bacterial pathogens and indicator bacteria in pigs in different European countries from year 2002 – 2004: the ARBAO-II study. Acta Veterinaria Scandinavica, 2008, 50, 19.	0.5	70
110	Prevalence of antimicrobial resistance among bacterial pathogens isolated from cattle in different European countries: 2002–2004. Acta Veterinaria Scandinavica, 2008, 50, 28.	0.5	125
111	<i>Shigella</i> from Humans in Thailand During 1993 to 2006: Spatial-Time Trends in Species and Serotype Distribution. Foodborne Pathogens and Disease, 2008, 5, 773-784.	0.8	39
112	Antimicrobial Resistance and Molecular Epidemiology of <i>Salmonella</i> Rissen from Animals, Food Products, and Patients in Thailand and Denmark. Foodborne Pathogens and Disease, 2008, 5, 605-619.	0.8	65
113	Prevalence and Antibiotic Resistance of <i>Salmonella</i> Isolated from a Poultry Farm and Processing Plant Environment in the State of Kuwait. Foodborne Pathogens and Disease, 2007, 4, 367-373.	0.8	29
114	International Spread of Multidrug-resistant <i>Salmonella</i> Schwarzengrund in Food Products. Emerging Infectious Diseases, 2007, 13, 726-731.	2.0	117
115	External quality assurance system for antibiotic resistance in bacteria of animal origin in Europe (ARBAO-II), 2003. Veterinary Microbiology, 2006, 115, 128-139.	0.8	8
116	Molecular Characterization and Occurrence of Extended-Spectrum β-Lactamase Resistance Genes among Salmonella enterica Serovar Corvallis from Thailand, Bulgaria, and Denmark. Microbial Drug Resistance, 2006, 12, 192-198.	0.9	99
117	<i>>Salmonella</i> >Serovars from Humans and Other Sources in Thailand, 1993–2002. Emerging Infectious Diseases, 2004, 10, 131-136.	2.0	169
118	Antimicrobial susceptibility and occurrence of resistance genes among Salmonella enterica serovar Weltevreden from different countries. Journal of Antimicrobial Chemotherapy, 2003, 52, 715-718.	1.3	111