

# Marc Stegger

## List of Publications by Year in descending order

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143  
papers

7,875  
citations

53660

45  
h-index

64668

79  
g-index

164  
all docs

164  
docs citations

164  
times ranked

8790  
citing authors

#	ARTICLE	IF	CITATIONS
1	Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. MBio, 2012, 3, .	1.8	638
2	The Epidemic of Extended-Spectrum-β <sup>2</sup> -Lactamase-Producing Escherichia coli ST131 Is Driven by a Single Highly Pathogenic Subclone, <i>H</i> 30-Rx. MBio, 2013, 4, e00377-13.	1.8	380
3	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
4	Mapping the Evolution of Hypervirulent Klebsiella pneumoniae. MBio, 2015, 6, e00630.	1.8	270
5	SCC <i>mecA</i> Finder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome <i>mecA</i> in Staphylococcus aureus Using Whole-Genome Sequence Data. MSphere, 2018, 3, .	1.3	197
6	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . EMBO Molecular Medicine, 2013, 5, 509-515.	3.3	192
7	<i>Staphylococcus aureus</i> and the ecology of the nasal microbiome. Science Advances, 2015, 1, e1400216.	4.7	189
8	Escherichia coli ST131- <i>H</i> 22 as a Foodborne Uropathogen. MBio, 2018, 9, .	1.8	184
9	<i>Escherichia coli</i> Sequence Type 410 Is Causing New International High-Risk Clones. MSphere, 2018, 3, .	1.3	183
10	Epidemiological characterisation of the first 785 SARS-CoV-2 Omicron variant cases in Denmark, December 2021. Eurosurveillance, 2021, 26, .	3.9	163
11	Risk of hospitalisation associated with infection with SARS-CoV-2 omicron variant versus delta variant in Denmark: an observational cohort study. Lancet Infectious Diseases, The, 2022, 22, 967-976.	4.6	140
12	Emergence of methicillin resistance predates the clinical use of antibiotics. Nature, 2022, 602, 135-141.	13.7	138
13	Origin, evolution, and global transmission of community-acquired <i>Staphylococcus aureus</i> ST8. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10596-E10604.	3.3	136
14	Livestock-Associated Methicillin and Multidrug Resistant Staphylococcus aureus Is Present among Industrial, Not Antibiotic-Free Livestock Operation Workers in North Carolina. PLoS ONE, 2013, 8, e67641.	1.1	130
15	Methicillin-resistant Staphylococcus aureus CC398 is an increasing cause of disease in people with no livestock contact in Denmark, 1999 to 2011. Eurosurveillance, 2015, 20, .	3.9	130
16	spa typing of methicillin-resistant Staphylococcus aureus isolated from domestic animals and veterinary staff in the UK and Ireland. Journal of Antimicrobial Chemotherapy, 2006, 58, 1118-1123.	1.3	122
17	Origin and Evolution of European Community-Acquired Methicillin-Resistant Staphylococcus aureus. MBio, 2014, 5, e01044-14.	1.8	112
18	Rapid PCR Detection of Staphylococcus aureus Clonal Complex 398 by Targeting the Restriction-Modification System Carrying <i>sau1-hsdS1</i> . Journal of Clinical Microbiology, 2011, 49, 732-734.	1.8	104

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19	Intermingled <i>Klebsiella pneumoniae</i> Populations Between Retail Meats and Human Urinary Tract Infections. <i>Clinical Infectious Diseases</i> , 2015, 61, 892-899.	2.9	104
20	Characteristics of <i>Escherichia coli</i> causing persistence or relapse of urinary tract infections: Phylogenetic groups, virulence factors and biofilm formation. <i>Virulence</i> , 2011, 2, 528-537.	1.8	102
21	Novel SCC mec type XIII (9A) identified in an ST152 methicillin-resistant <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , 2018, 61, 74-76.	1.0	97
22	Retrospective detection of methicillin resistant and susceptible <i>Staphylococcus aureus</i> ST398 in Danish slaughter pigs. <i>Veterinary Microbiology</i> , 2007, 122, 384-386.	0.8	93
23	Livestock-Associated Methicillin Resistant and Methicillin Susceptible <i>Staphylococcus aureus</i> Sequence Type (CC)1 in European Farmed Animals: High Genetic Relatedness of Isolates from Italian Cattle Herds and Humans. <i>PLoS ONE</i> , 2015, 10, e0137143.	1.1	89
24	Evidence for Human Adaptation and Foodborne Transmission of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> : Table 1.. <i>Clinical Infectious Diseases</i> , 2016, 63, 1349-1352.	2.9	89
25	Methicillin-Resistant <i>Staphylococcus aureus</i> CC398 in Humans and Pigs in Norway: A One Health Perspective on Introduction and Transmission. <i>Clinical Infectious Diseases</i> , 2016, 63, 1431-1438.	2.9	86
26	Resistance to critically important antimicrobials in Australian silver gulls ( <i>Chroicocephalus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 467 Td 2019, 74, 2566-2574.	1.3	82
27	Spread of avian pathogenic <i>Escherichia coli</i> ST117 O78:H4 in Nordic broiler production. <i>BMC Genomics</i> , 2017, 18, 13.	1.2	80
28	Molecular characterization of spa type t127, sequence type 1 methicillin-resistant <i>Staphylococcus aureus</i> from pigs. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1231-1235.	1.3	79
29	Rapid Differentiation between Livestock-Associated and Livestock-Independent <i>Staphylococcus aureus</i> CC398 Clades. <i>PLoS ONE</i> , 2013, 8, e79645.	1.1	78
30	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
31	Tandem repeat sequence analysis of staphylococcal protein A (spa) gene in methicillin-resistant <i>Staphylococcus pseudintermedius</i> . <i>Veterinary Microbiology</i> , 2009, 135, 320-326.	0.8	77
32	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
33	WGS-based surveillance of third-generation cephalosporin-resistant <i>Escherichia coli</i> from bloodstream infections in Denmark. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1922-1929.	1.3	73
34	Molecular epidemiology of the SARS-CoV-2 variant Omicron BA.2 sub-lineage in Denmark, 29 November 2021 to 2 January 2022. <i>Eurosurveillance</i> , 2022, 27, .	3.9	70
35	An accessory wall teichoic acid glycosyltransferase protects <i>Staphylococcus aureus</i> from the lytic activity of Podoviridae. <i>Scientific Reports</i> , 2015, 5, 17219.	1.6	68
36	Cross-Talk between <i>Staphylococcus aureus</i> and Other Staphylococcal Species via the agr Quorum Sensing System. <i>Frontiers in Microbiology</i> , 2016, 7, 1733.	1.5	67

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37	Increased transmissibility of SARS-CoV-2 lineage B.1.1.7 by age and viral load. <i>Nature Communications</i> , 2021, 12, 7251.	5.8	67
38	Novel <i>mcr-3</i> variant, encoding mobile colistin resistance, in an ST131 <i>Escherichia coli</i> isolate from bloodstream infection, Denmark, 2014. <i>Eurosurveillance</i> , 2017, 22, .	3.9	61
39	A broad range quorum sensing inhibitor working through sRNA inhibition. <i>Scientific Reports</i> , 2017, 7, 9857.	1.6	60
40	Whole-genome comparison of urinary pathogenic <i>Escherichia coli</i> and faecal isolates of UTI patients and healthy controls. <i>International Journal of Medical Microbiology</i> , 2017, 307, 497-507.	1.5	57
41	Diversity and Population Overlap between Avian and Human <i>Escherichia coli</i> Belonging to Sequence Type 95. <i>MSphere</i> , 2019, 4, .	1.3	57
42	Investigation of a possible outbreak of carbapenem-resistant <i>Acinetobacter baumannii</i> in Odense, Denmark using PFGE, MLST and whole-genome-based SNPs. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1965-1968.	1.3	54
43	Genetic diversity in CC398 methicillin-resistant <i>Staphylococcus aureus</i> isolates of different geographical origin. <i>Clinical Microbiology and Infection</i> , 2010, 16, 1017-1019.	2.8	52
44	Microarray-based detection of extended virulence and antimicrobial resistance gene profiles in phylogroup B2 <i>Escherichia coli</i> of human, meat and animal origin. <i>Journal of Medical Microbiology</i> , 2011, 60, 1502-1511.	0.7	51
45	Genome investigations show host adaptation and transmission of LA-MRSA CC398 from pigs into Danish healthcare institutions. <i>Scientific Reports</i> , 2019, 9, 18655.	1.6	51
46	In Vivo Selection of a Unique Tandem Repeat Mediated Azole Resistance Mechanism (TR <sub>120</sub> ) in <i>Aspergillus fumigatus cyp51A</i> , Denmark. <i>Emerging Infectious Diseases</i> , 2019, 25, 577-580.	2.0	49
47	Emergence of <i>vanA</i> <i>Enterococcus faecium</i> in Denmark, 2005–15. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2184-2190.	1.3	47
48	Two Distinct Clones of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) with the Same USA300 Pulsed-Field Gel Electrophoresis Profile: a Potential Pitfall for Identification of USA300 Community-Associated MRSA. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3765-3768.	1.8	46
49	Use of WGS data for investigation of a long-term NDM-1-producing <i>Citrobacter freundii</i> outbreak and secondary in vivo spread of bla <sub>NDM-1</sub> to <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Klebsiella oxytoca</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3117-3124.	1.3	44
50	Extended-spectrum $\beta$ -lactamase (ESBL) in Danish clinical isolates of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> : Prevalence, $\beta$ -lactamase distribution, phylogroups, and co-resistance. <i>Scandinavian Journal of Infectious Diseases</i> , 2012, 44, 174-181.	1.5	43
51	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing <i>H30-Rx</i> Subclone of <i>Escherichia coli</i> ST131. <i>Genome Announcements</i> , 2013, 1, .	0.8	42
52	CHTyper, a Web Tool for Subtyping of Extraintestinal Pathogenic <i>Escherichia coli</i> Based on the <i>fimC</i> and <i>fimH</i> Alleles. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	42
53	Influence of Host Genetics and Environment on Nasal Carriage of <i>Staphylococcus aureus</i> in Danish Middle-Aged and Elderly Twins. <i>Journal of Infectious Diseases</i> , 2012, 206, 1178-1184.	1.9	41
54	Distinct clonal lineages and within-host diversification shape invasive <i>Staphylococcus epidermidis</i> populations. <i>PLoS Pathogens</i> , 2021, 17, e1009304.	2.1	41

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55	Genome Sequence of <i>Staphylococcus aureus</i> Strain CA-347, a USA600 Methicillin-Resistant Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
56	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2015, 10, e0130955.	1.1	40
57	Genomic investigation of <i>Staphylococcus aureus</i> isolates from bulk tank milk and dairy cows with clinical mastitis. <i>Veterinary Microbiology</i> , 2018, 215, 35-42.	0.8	37
58	<i>Staphylococcus epidermidis</i> clones express <i>Staphylococcus aureus</i> -type wall teichoic acid to shift from a commensal to pathogen lifestyle. <i>Nature Microbiology</i> , 2021, 6, 757-768.	5.9	37
59	Turn Up the Heat—Food and Clinical <i>Escherichia coli</i> Isolates Feature Two Transferrable Loci of Heat Resistance. <i>Frontiers in Microbiology</i> , 2017, 8, 579.	1.5	36
60	Development of a Pefloxacin Disk Diffusion Method for Detection of Fluoroquinolone-Resistant <i>Salmonella enterica</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3411-3417.	1.8	35
61	<i>Staphylococcus lugdunensis</i> : antimicrobial susceptibility and optimal treatment options. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 1449-1455.	1.3	35
62	ST131 <i>fimH</i> 22 <i>Escherichia coli</i> isolate with a <i>bla</i> CMY-2/ <i>IncI1</i> /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
63	Mitochondrial DNA Levels in Fat and Blood Cells from Patients with Lipodystrophy or Peripheral Neuropathy and the Effect of 90 Days of High-Dose Coenzyme Q Treatment: A Randomized, Double-Blind, Placebo-Controlled Pilot Study. <i>Clinical Infectious Diseases</i> , 2004, 39, 1371-1379.	2.9	33
64	Antimicrobial Resistance and Virulence Gene Profiles of Methicillin-Resistant and -Susceptible <i>Staphylococcus aureus</i> From Food Products in Denmark. <i>Frontiers in Microbiology</i> , 2019, 10, 2681.	1.5	33
65	Genome Sequence of <i>Staphylococcus aureus</i> Strain 11819-97, an ST80-IV European Community-Acquired Methicillin-Resistant Isolate. <i>Journal of Bacteriology</i> , 2012, 194, 1625-1626.	1.0	31
66	Complete Nucleotide Sequence of an <i>Escherichia coli</i> Sequence Type 410 Strain Carrying <i>bla</i> NDM-5 on an <i>IncF</i> Multidrug Resistance Plasmid and <i>bla</i> OXA-181 on an <i>IncX3</i> Plasmid. <i>Genome Announcements</i> , 2018, 6, .	0.8	31
67	Description and characterization of a penicillin-resistant <i>Streptococcus dysgalactiae</i> subsp <i>equisimilis</i> clone isolated from blood in three epidemiologically linked patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3376-3380.	1.3	30
68	Livestock-Associated MRSA CC1 in Norway; Introduction to Pig Farms, Zoonotic Transmission, and Eradication. <i>Frontiers in Microbiology</i> , 2019, 10, 139.	1.5	30
69	LA-MRSA CC398 in Dairy Cattle and Veal Calf Farms Indicates Spillover From Pig Production. <i>Frontiers in Microbiology</i> , 2019, 10, 2733.	1.5	30
70	Effect of vaccination on household transmission of SARS-CoV-2 Delta variant of concern. <i>Nature Communications</i> , 2022, 13, .	5.8	28
71	Genomic analysis reveals different mechanisms of fusidic acid resistance in <i>Staphylococcus aureus</i> from Danish atopic dermatitis patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 856-861.	1.3	27
72	Characterization of antimicrobial-resistant <i>Staphylococcus aureus</i> from retail foods in Beijing, China. <i>Food Microbiology</i> , 2021, 93, 103603.	2.1	26

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73	Investigation of a possible outbreak of NDM-5-producing ST16 <i>Klebsiella pneumoniae</i> among patients in Denmark with no history of recent travel using whole-genome sequencing. <i>Journal of Global Antimicrobial Resistance</i> , 2015, 3, 219-221.	0.9	25
74	Staphylococcal Communities on Skin Are Associated with Atopic Dermatitis and Disease Severity. <i>Microorganisms</i> , 2021, 9, 432.	1.6	25
75	Dissemination and Characteristics of a Novel Plasmid-Encoded Carbapenem-Hydrolyzing Class D $\beta$ -Lactamase, OXA-436, Found in Isolates from Four Patients at Six Different Hospitals in Denmark. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	24
76	Implications of Foraging and Interspecies Interactions of Birds for Carriage of <i>Escherichia coli</i> Strains Resistant to Critically Important Antimicrobials. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	24
77	Emergence of Enteroaggregative <i>Escherichia coli</i> within the ST131 Lineage as a Cause of Extraintestinal Infections. <i>MBio</i> , 2020, 11, .	1.8	22
78	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	5.8	22
79	Phage-Mediated Immune Evasion and Transmission of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> in Humans. <i>Emerging Infectious Diseases</i> , 2020, 26, .	2.0	21
80	Whole-genome sequencing of bloodstream <i>Staphylococcus aureus</i> isolates does not distinguish bacteraemia from endocarditis. <i>Microbial Genomics</i> , 2017, 3, .	1.0	21
81	Selection of unique <i>Escherichia coli</i> clones by random amplified polymorphic DNA (RAPD): Evaluation by whole genome sequencing. <i>Journal of Microbiological Methods</i> , 2014, 103, 101-103.	0.7	20
82	<i>Escherichia coli</i> ST410 among humans and the environment in Southeast Asia. <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 228-232.	1.1	20
83	<i>mcr</i> -Positive <i>Escherichia coli</i> ST131-H22 from Poultry in Brazil. <i>Emerging Infectious Diseases</i> , 2020, 26, 1951-1954.	2.0	20
84	Fluoroquinolone Resistance Mechanisms in Urinary Tract Pathogenic <i>Escherichia coli</i> Isolated During Rapidly Increasing Fluoroquinolone Consumption in a Low-Use Country. <i>Microbial Drug Resistance</i> , 2011, 17, 395-406.	0.9	19
85	A universal primer-independent next-generation sequencing approach for investigations of norovirus outbreaks and novel variants. <i>Scientific Reports</i> , 2017, 7, 813.	1.6	19
86	Comparative genomics of <i>Staphylococcus epidermidis</i> from prosthetic-joint infections and nares highlights genetic traits associated with antimicrobial resistance, not virulence. <i>Microbial Genomics</i> , 2021, 7, .	1.0	19
87	Non-toxigenic <i>tox</i> gene-bearing <i>Corynebacterium ulcerans</i> in a traumatic ulcer from a human case and his asymptomatic dog. <i>Microbes and Infection</i> , 2015, 17, 717-719.	1.0	18
88	Bacterial content and characterization of antibiotic resistant <i>Staphylococcus aureus</i> in Danish sushi products and association with food inspector rankings. <i>International Journal of Food Microbiology</i> , 2019, 305, 108244.	2.1	18
89	Genome Analysis of <i>Staphylococcus aureus</i> ST291, a Double Locus Variant of ST398, Reveals a Distinct Genetic Lineage. <i>PLoS ONE</i> , 2013, 8, e63008.	1.1	18
90	Whole-Genome Analysis of Recurrent <i>Staphylococcus aureus</i> t571/ST398 Infection in Farmer, Iowa, USA. <i>Emerging Infectious Diseases</i> , 2018, 24, 153-154.	2.0	17

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91	Human $\beta$ -defensin 3 (DEFB103) and its influence on <i>Staphylococcus aureus</i> nasal carriage. <i>International Journal of Infectious Diseases</i> , 2011, 15, e388-e394.	1.5	16
92	Adaptation of <i>Escherichia coli</i> traversing from the faecal environment to the urinary tract. <i>International Journal of Medical Microbiology</i> , 2016, 306, 595-603.	1.5	16
93	Whole-genome sequence profiling of antibiotic-resistant <i>Staphylococcus aureus</i> isolates from livestock and farm attendants in Ghana. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 527-532.	0.9	16
94	Evolution and Population Dynamics of Clonal Complex 152 Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MSphere</i> , 2020, 5, .	1.3	16
95	Presence of the neonatal <i>Staphylococcus capitis</i> outbreak clone (NRCS-A) in prosthetic joint infections. <i>Scientific Reports</i> , 2020, 10, 22389.	1.6	16
96	Identification of a PVL-negative SCC <i>mec-IVa</i> sublineage of the methicillin-resistant <i>Staphylococcus aureus</i> CC80 lineage: understanding the clonal origin of CA-MRSA. <i>Clinical Microbiology and Infection</i> , 2018, 24, 273-278.	2.8	15
97	Genomic characterization, phylogenetic analysis, and identification of virulence factors in <i>Aerococcus sanguinicola</i> and <i>Aerococcus urinae</i> strains isolated from infection episodes. <i>Microbial Pathogenesis</i> , 2017, 112, 327-340.	1.3	14
98	Global Epidemiology and Evolutionary History of <i>Staphylococcus aureus</i> ST45. <i>Journal of Clinical Microbiology</i> , 2020, 59, .	1.8	14
99	A three-year whole genome sequencing perspective of <i>Enterococcus faecium</i> sepsis in Australia. <i>PLoS ONE</i> , 2020, 15, e0228781.	1.1	14
100	<i>Escherichia coli</i> Causing Recurrent Urinary Tract Infections: Comparison to Non-Recurrent Isolates and Genomic Adaptation in Recurrent Infections. <i>Microorganisms</i> , 2021, 9, 1416.	1.6	14
101	Reduced Risk of Hospitalisation Associated With Infection With SARS-CoV-2 Omicron Relative to Delta: A Danish Cohort Study. <i>SSRN Electronic Journal</i> , 0, , .	0.4	14
102	<i>Staphylococcus aureus</i> mutants lacking cell wall-bound protein A found in isolates from bacteraemia, MRSA infection and a healthy nasal carrier. <i>Pathogens and Disease</i> , 2013, 67, 19-24.	0.8	13
103	Spread of LA-MRSA CC398 in Danish mink ( <i>Neovison vison</i> ) and mink farm workers. <i>Veterinary Microbiology</i> , 2020, 245, 108705.	0.8	12
104	Characterisation of an IMP-7-producing ST357 <i>Pseudomonas aeruginosa</i> isolate detected in Denmark using whole genome sequencing. <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 200-201.	1.1	11
105	Molecular characterisation of the clonal emergence of high-level ciprofloxacin-mono-resistant <i>Haemophilus influenzae</i> in the Region of Southern Denmark. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 5, 67-70.	0.9	11
106	Demographic fluctuation of community-acquired antibiotic-resistant <i>Staphylococcus aureus</i> lineages: potential role of flimsy antibiotic exposure. <i>ISME Journal</i> , 2018, 12, 1879-1894.	4.4	11
107	High Prevalence of USA300 Among Clinical Isolates of Methicillin-Resistant <i>Staphylococcus aureus</i> on St. Kitts and Nevis, West Indies. <i>Frontiers in Microbiology</i> , 2019, 10, 1123.	1.5	11
108	Antimicrobial resistance and genomic insights into bovine mastitis-associated <i>Staphylococcus aureus</i> in Australia. <i>Veterinary Microbiology</i> , 2020, 250, 108850.	0.8	11

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109	Alteration of Bacterial Communities in Anterior Nares and Skin Sites of Patients Undergoing Arthroplasty Surgery: Analysis by 16S rRNA and Staphylococcal-Specific <i>tuf</i> Gene Sequencing. <i>Microorganisms</i> , 2020, 8, 1977.	1.6	10
110	Genomic relatedness of <i>Staphylococcus pettenkoferi</i> isolates of different origins. <i>Journal of Medical Microbiology</i> , 2017, 66, 601-608.	0.7	10
111	Diversity detected in commensals at host and farm level reveals implications for national antimicrobial resistance surveillance programmes. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 400-408.	1.3	10
112	Local and Transboundary Transmissions of Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 through Pig Trading. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
113	Heterogeneity of <i>Staphylococcus epidermidis</i> in prosthetic joint infections: time to reevaluate microbiological criteria?. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 87-97.	1.3	9
114	Genetic Variability in Beta-Defensins Is Not Associated with Susceptibility to <i>Staphylococcus aureus</i> Bacteremia. <i>PLoS ONE</i> , 2012, 7, e32315.	1.1	8
115	The Epidome - a species-specific approach to assess the population structure and heterogeneity of <i>Staphylococcus epidermidis</i> colonization and infection. <i>BMC Microbiology</i> , 2020, 20, 362.	1.3	8
116	Evaluating coverage bias in next-generation sequencing of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2021, 16, e0253440.	1.1	8
117	Dynamics of the Human Nasal Microbiota and <i>Staphylococcus aureus</i> CC398 Carriage in Pig Truck Drivers across One Workweek. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0122521.	1.4	8
118	<i>Staphylococcus argenteus</i> as an etiological agent of prosthetic hip joint infection: a case presentation. <i>Journal of Bone and Joint Infection</i> , 2020, 5, 172-175.	0.6	8
119	Real-Time Relative qPCR without Reference to Control Samples and Estimation of Run-Specific PCR Parameters from Run-Internal Mini-Standard Curves. <i>PLoS ONE</i> , 2010, 5, e11723.	1.1	7
120	Draft Genome Sequences of Two Avian Pathogenic <i>Escherichia coli</i> Strains of Clinical Importance, E44 and E51. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
121	Polyclonal spread of <i>vanA</i> <i>Enterococcus faecium</i> in Central Denmark Region, 2009-2013, investigated using PFGE, MLST and WGS. <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 767-768.	1.1	7
122	A snapshot of diversity: Intraclonal variation of <i>Escherichia coli</i> clones as commensals and pathogens. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151401.	1.5	7
123	Methicillin-Resistant <i>Staphylococcus epidermidis</i> Lineages in the Nasal and Skin Microbiota of Patients Planned for Arthroplasty Surgery. <i>Microorganisms</i> , 2021, 9, 265.	1.6	7
124	Genomic analysis of the zoonotic ST73 lineage containing avian and human extraintestinal pathogenic <i>Escherichia coli</i> (ExPEC). <i>Veterinary Microbiology</i> , 2022, 267, 109372.	0.8	7
125	Characterization and transfer studies of macrolide resistance genes in <i>Streptococcus pneumoniae</i> from Denmark. <i>Scandinavian Journal of Infectious Diseases</i> , 2010, 42, 586-593.	1.5	6
126	Draft Genome Sequence of a Sequence Type 398 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate from a Danish Dairy Cow with Mastitis. <i>Genome Announcements</i> , 2017, 5, .	0.8	6



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127	Sepsis, Endocarditis, and Purulent Arthritis due to a Rare Zoonotic Infection with <i>Streptococcus equi</i> Subspecies <i>zooepidemicus</i> . <i>Case Reports in Infectious Diseases</i> , 2018, 2018, 1-8.	0.2	6
128	Genomic analyses of <i>Staphylococcus aureus</i> clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
129	Same Organism, Different Phenotype - Are Phenotypic Criteria Adequate In Coagulase-Negative Staphylococcal Orthopaedic Implant-Associated Infections?. <i>Journal of Bone and Joint Infection</i> , 2019, 4, 16-19.	0.6	5
130	One Health Genomic Study of Human and Animal <i>Klebsiella pneumoniae</i> Isolated at Diagnostic Laboratories on a Small Caribbean Island. <i>Antibiotics</i> , 2022, 11, 42.	1.5	5
131	Staphylococcal Phages Adapt to New Hosts by Extensive Attachment Site Variability. <i>MBio</i> , 2021, 12, e0225921.	1.8	5
132	Molecular characteristics of <i>Staphylococcus aureus</i> associated prosthetic joint infections after hip fractures treated with hemiarthroplasty: a retrospective genome-wide association study. <i>Scientific Reports</i> , 2020, 10, 16553.	1.6	4
133	<i>Salmonella</i> Newport outbreak in Brazilian parrots: confiscated birds from the illegal pet trade as possible zoonotic sources. <i>Environmental Microbiology Reports</i> , 2021, 13, 702-707.	1.0	4
134	Long-Term Sinonasal Carriage of <i>Staphylococcus aureus</i> and Anti-Staphylococcal Humoral Immune Response in Patients with Chronic Rhinosinusitis. <i>Microorganisms</i> , 2021, 9, 256.	1.6	3
135	Spontaneous Phage Resistance in Avian Pathogenic <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 782757.	1.5	3
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137	Comparative Genome Sequence Analysis of <i>Actinobacillus pleuropneumoniae</i> Serovar 8 Isolates From Norway, Denmark, and the United Kingdom Indicates Distinct Phylogenetic Lineages and Differences in Distribution of Antimicrobial Resistance Genes. <i>Frontiers in Microbiology</i> , 2021, 12, 729637.	1.5	2
138	Complete genome for <i>Actinobacillus pleuropneumoniae</i> serovar 8 reference strain 405: comparative analysis with draft genomes for different laboratory stock cultures indicates little genetic variation. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
139	Increased transmission of SARS-CoV-2 in Denmark during UEFA European championships.. <i>Epidemiology and Infection</i> , 2022, , 1-27.	1.0	1
140	<i>Staphylococcus aureus</i> isolates from nares of orthopaedic patients in Sweden are mupirocin susceptible. <i>Infectious Diseases</i> , 2019, 51, 475-478.	1.4	0
141	Complete genome of a methicillin-resistant <i>Staphylococcus vitulinus</i> from Danish ground beef meat carrying a <i>mecA2</i> resistance gene and a novel <i>ccr</i> allotype. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 221-223.	0.9	0
142	Genome-wide association studies reveal candidate genes associated to bacteraemia caused by ST93-IV CA-MRSA. <i>BMC Genomics</i> , 2021, 22, 418.	1.2	0
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