

Werner Ruppitsch

List of Publications by Year in descending order

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121
papers

2,591
citations

218381

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docs citations

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times ranked

2847
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#	ARTICLE	IF	CITATIONS
1	Defining and Evaluating a Core Genome Multilocus Sequence Typing Scheme for Whole-Genome Sequence-Based Typing of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 2869-2876.	1.8	266
2	Characterization of Antibiotic and Biocide Resistance Genes and Virulence Factors of <i>Staphylococcus</i> Species Associated with Bovine Mastitis in Rwanda. <i>Antibiotics</i> , 2020, 9, 1.	1.5	120
3	Classifying <i>spa</i> Types in Complexes Improves Interpretation of Typing Results for Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2006, 44, 2442-2448.	1.8	92
4	Update: Multinational listeriosis outbreak due to "Quargel"™, a sour milk curd cheese, caused by two different <i>L. monocytogenes</i> serotype 1/2a strains, 2009-2010. <i>Eurosurveillance</i> , 2010, 15, .	3.9	73
5	Outbreak of staphylococcal food intoxication after consumption of pasteurized milk products, June 2007, Austria. <i>Wiener Klinische Wochenschrift</i> , 2009, 121, 125-131.	1.0	68
6	Methicillin-resistant <i>Staphylococcus aureus</i> : a new zoonotic agent?. <i>Wiener Klinische Wochenschrift</i> , 2009, 121, 86-90.	1.0	67
7	Rapid identification of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates by <i>rpoB</i> gene scanning using high-resolution melting curve PCR analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 63, 1121-1127.	1.3	65
8	Overexpression of thioredoxin in Fanconi anemia fibroblasts prevents the cytotoxic and DNA damaging effect of mitomycin C and diepoxybutane. <i>FEBS Letters</i> , 1998, 422, 99-102.	1.3	63
9	Listeriosis outbreak caused by acid curd cheese "Quargel"™, Austria and Germany 2009. <i>Eurosurveillance</i> , 2010, 15, .	3.9	62
10	Retrospective validation of whole genome sequencing-enhanced surveillance of listeriosis in Europe, 2010 to 2015. <i>Eurosurveillance</i> , 2018, 23, .	3.9	61
11	Whole genome sequencing reveals resemblance between ESBL-producing and carbapenem resistant <i>Klebsiella pneumoniae</i> isolates from Austrian rivers and clinical isolates from hospitals. <i>Science of the Total Environment</i> , 2019, 662, 227-235.	3.9	60
12	An outbreak of febrile gastroenteritis associated with jellied pork contaminated with <i>Listeria monocytogenes</i> . <i>Wiener Klinische Wochenschrift</i> , 2009, 121, 149-156.	1.0	59
13	The role of oxygen metabolism for the pathological phenotype of Fanconi anemia. <i>Human Genetics</i> , 1997, 99, 710-719.	1.8	56
14	A Rapid and Sensitive Method for Direct Detection of <i>Erwinia amylovora</i> in Symptomatic and Asymptomatic Plant Tissues by Polymerase Chain Reaction. <i>Journal of Phytopathology</i> , 2006, 154, 469-473.	0.5	56
15	Whole Genome Sequencing Based Surveillance of <i>L. monocytogenes</i> for Early Detection and Investigations of Listeriosis Outbreaks. <i>Frontiers in Public Health</i> , 2019, 7, 139.	1.3	49
16	Multicenter Study of <i>Cronobacter sakazakii</i> Infections in Humans, Europe, 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 515-522.	2.0	47
17	Whole genome sequence-based serogrouping of <i>Listeria monocytogenes</i> isolates. <i>Journal of Biotechnology</i> , 2016, 235, 181-186.	1.9	45
18	Isolate-Based Surveillance of <i>Listeria monocytogenes</i> by Whole Genome Sequencing in Austria. <i>Frontiers in Microbiology</i> , 2019, 10, 2282.	1.5	44

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19	Large Nationwide Outbreak of Invasive Listeriosis Associated with Blood Sausage, Germany, 2018â€“2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 1456-1464.	2.0	40
20	Occurrence of <i>Vibrio cholerae</i> serogroups other than O1 and O139 in Austria. <i>Wiener Klinische Wochenschrift</i> , 2007, 119, 235-241.	1.0	39
21	Characterization of <i>mecC</i> gene-carrying coagulase-negative <i>Staphylococcus</i> spp. isolated from various animals. <i>Veterinary Microbiology</i> , 2019, 230, 138-144.	0.8	38
22	Fatal <i>Pseudomonas aeruginosa</i> pneumonia in a previously healthy woman was most likely associated with a contaminated hot tub. <i>Infection</i> , 2011, 39, 265-269.	2.3	35
23	Update: Multinational listeriosis outbreak due to 'Quargel', a sour milk curd cheese, caused by two different <i>L. monocytogenes</i> serotype 1/2a strains, 2009-2010. <i>Eurosurveillance</i> , 2010, 15, .	3.9	30
24	Overexpressed thioredoxin compensates Fanconi anemia related chromosomal instability. <i>Oncogene</i> , 2002, 21, 2406-2412.	2.6	29
25	Urban brown rats (<i>Rattus norvegicus</i>) as possible source of multidrug-resistant Enterobacteriaceae and methicillin-resistant <i>Staphylococcus</i> spp., Vienna, Austria, 2016 and 2017. <i>Eurosurveillance</i> , 2019, 24, .	3.9	29
26	Identification and prevalence of tetracycline resistance in enterococci isolated from poultry in Ilishan, Ogun State, Nigeria. <i>Journal of Pharmacy and Bioallied Sciences</i> , 2016, 8, 69.	0.2	29
27	An outbreak of listeriosis linked to turkey meat products in the Czech Republic, 2012â€“2016. <i>Epidemiology and Infection</i> , 2018, 146, 1407-1412.	1.0	28
28	Listeriosis outbreak caused by acid curd cheese Quargel , Austria and Germany 2009. <i>Eurosurveillance</i> , 2010, 15, .	3.9	28
29	Phenotypic and Genotypic Antimicrobial Resistance Traits of <i>Vibrio cholerae</i> Non-O1/Non-O139 Isolated From a Large Austrian Lake Frequently Associated With Cases of Human Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 2600.	1.5	27
30	Increased genetic diversity of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) isolated from companion animals. <i>Veterinary Microbiology</i> , 2019, 235, 118-126.	0.8	27
31	Characterization of <i>Erwinia amylovora</i> strains from different host plants using repetitive-sequences PCR analysis, and restriction fragment length polymorphism and short-sequence DNA repeats of plasmid pEA29. <i>Journal of Applied Microbiology</i> , 2006, 100, 1084-1094.	1.4	26
32	Stability of short sequence repeats and their application for the characterization of <i>Erwinia amylovora</i> strains. <i>FEMS Microbiology Letters</i> , 2004, 234, 1-8.	0.7	25
33	Outbreak of acute gastroenteritis in an Austrian boarding school, September 2006. <i>Eurosurveillance</i> , 2007, 12, 7-8.	3.9	24
34	Molecular characterization of <i>Listeria monocytogenes</i> isolates from a small-scale meat processor in Montenegro, 2011â€“2014. <i>Food Microbiology</i> , 2019, 79, 116-122.	2.1	23
35	Occurrence of the USA300 community-acquired <i>Staphylococcus aureus</i> clone in Austria. , 2007, 12, E071025.1.		23
36	Characterization of a community-acquired-MRSA USA300 isolate from a river sample in Austria and whole genome sequence based comparison to a diverse collection of USA300 isolates. <i>Scientific Reports</i> , 2018, 8, 9467.	1.6	22

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37	Involvement of the Fanconi anemia protein FA-C in repair processes of oxidative DNA damages. FEBS Letters, 1998, 440, 103-106.	1.3	21
38	Molecular Characterization of a Prevalent Ribocluster of Methicillin-Sensitive Staphylococcus aureus from Orthopedic Implant Infections. Correspondence with MLST CC30. Frontiers in Cellular and Infection Microbiology, 2016, 6, 8.	1.8	21
39	A rapid and sensitive method for the detection of Xanthomonas fragariae, causal agent of angular leafspot disease in strawberry plants. Journal of Microbiological Methods, 2004, 58, 281-284.	0.7	20
40	Ongoing outbreak of invasive listeriosis, Germany, 2012 to 2015. Eurosurveillance, 2015, 20, .	3.9	20
41	Gene Scanning of an Internalin B Gene Fragment Using High-Resolution Melting Curve Analysis as a Tool for Rapid Typing of Listeria monocytogenes. Journal of Molecular Diagnostics, 2011, 13, 57-63.	1.2	19
42	One-Step Triplex High-Resolution Melting Analysis for Rapid Identification and Simultaneous Subtyping of Frequently Isolated Salmonella Serovars. Applied and Environmental Microbiology, 2012, 78, 3352-3360.	1.4	19
43	Carbapenemase-Producing Enterobacteriaceae Isolates from Edo State, Nigeria. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	19
44	Listeriosis outbreak likely due to contaminated liver pâté consumed in a tavern, Austria, December 2018. Eurosurveillance, 2019, 24, .	3.9	19
45	Profiling the Virulence and Antibiotic Resistance Genes of Cronobacter sakazakii Strains Isolated From Powdered and Dairy Formulas by Whole-Genome Sequencing. Frontiers in Microbiology, 2021, 12, 694922.	1.5	18
46	Suitability of partial 16S ribosomal RNA gene sequence analysis for the identification of dangerous bacterial pathogens. Journal of Applied Microbiology, 2007, 102, 852-859.	1.4	17
47	Virulence and Antibiotic Resistance Genes in Listeria monocytogenes Strains Isolated From Ready-to-Eat Foods in Chile. Frontiers in Microbiology, 2021, 12, 796040.	1.5	17
48	Antagonistic and quantitative assessment of indigenous lactic acid bacteria in different varieties of ogi against gastrointestinal pathogens. Pan African Medical Journal, 2017, 27, 22.	0.3	16
49	Whole genome sequencing of extended-spectrum β -lactamase genes in Enterobacteriaceae isolates from Nigeria. PLoS ONE, 2020, 15, e0231146.	1.1	16
50	Molecular Characterization of Cronobacter sakazakii Strains Isolated from Powdered Milk. Foods, 2021, 10, 20.	1.9	16
51	Accuracy of conventional identification methods used for Enterobacteriaceae isolates in three Nigerian hospitals. PeerJ, 2016, 4, e2511.	0.9	16
52	Broad-Spectrum Cephalosporin-Resistant Klebsiella spp. Isolated from Diseased Horses in Austria. Animals, 2020, 10, 332.	1.0	15
53	Characterization of selected Gram-negative non-fermenting bacteria isolated from honey bees (Apis mellifera). Journal of Microbiology and Biotechnology, 2014, 14, 107-114.	0.9	14
54	Improved Protocol for Rapid Identification of Certain Spa Types Using High Resolution Melting Curve Analysis. PLoS ONE, 2015, 10, e0116713.	1.1	14

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55	Tracking the Origin of Austrian Human Brucellosis Cases Using Whole Genome Sequencing. <i>Frontiers in Medicine</i> , 2021, 8, 635547.	1.2	14
56	The Pheno- and Genotypic Characterization of Porcine <i>Escherichia coli</i> Isolates. <i>Microorganisms</i> , 2021, 9, 1676.	1.6	14
57	Genome Sequences of <i>Lactococcus garvieae</i> and <i>Lactococcus petauri</i> Strains Isolated from Traditional Montenegrin Brine Cheeses. <i>Microbiology Resource Announcements</i> , 2021, 10, e0054621.	0.3	14
58	Detection of virulence-associated and regulatory protein genes in association with phage typing of human <i>Vibrio cholerae</i> from several geographical regions of the world. <i>Journal of Medical Microbiology</i> , 2009, 58, 1160-1167.	0.7	13
59	Limited value of routine spa typing: A cross-sectional study of methicillin-resistant <i>Staphylococcus aureus</i> -positive patients in an Austrian hospital. <i>American Journal of Infection Control</i> , 2013, 41, 617-624.	1.1	13
60	Petting zoos as sources of Shiga toxin-producing <i>Escherichia coli</i> (STEC) infections. <i>International Journal of Medical Microbiology</i> , 2018, 308, 927-932.	1.5	13
61	Hospital outbreak caused by linezolid resistant <i>Enterococcus faecium</i> in Upper Austria. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 150.	1.5	13
62	Meticillin-resistant <i>Staphylococcus aureus</i> : occurrence of a new spa type in two acute care hospitals in Austria. <i>Journal of Hospital Infection</i> , 2007, 67, 316-322.	1.4	12
63	Detection of the mcr-1 Gene in a Multidrug-Resistant <i>Escherichia coli</i> Isolate from an Austrian Patient. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	12
64	Draft Genome Sequence of Carbapenemase-Producing <i>Serratia marcescens</i> Isolated from a Patient with Chronic Obstructive Pulmonary Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
65	Genetic Diversity of <i>Leuconostoc mesenteroides</i> Isolates from Traditional Montenegrin Brine Cheese. <i>Microorganisms</i> , 2021, 9, 1612.	1.6	12
66	Werner Syndrome: Characterization of Mutations in the WRN Gene in an Affected Family. <i>European Journal of Human Genetics</i> , 1997, 5, 364-370.	1.4	12
67	An outbreak of multidrug-resistant tuberculosis among refugees in Austria, 2005-2006. <i>International Journal of Tuberculosis and Lung Disease</i> , 2008, 12, 1190-5.	0.6	12
68	Draft Genome Sequence of a Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Isolate from a River Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
69	Presence of β -Lactamase-producing Enterobacteriales and <i>Salmonella</i> Isolates in Marine Mammals. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5905.	1.8	10
70	Molecular characterization of clonal lineage and staphylococcal toxin genes from <i>S. aureus</i> in Southern Nigeria. <i>PeerJ</i> , 2018, 6, e5204.	0.9	10
71	Chromosomal Instability of Fanconi Anemia Cells Is Not the Consequence of a Defective Repair Activity of the Ribosomal Protein S3. <i>Biochemical and Biophysical Research Communications</i> , 1999, 264, 518-524.	1.0	9
72	Fecal <i>Klebsiella pneumoniae</i> Carriage Is Intermittent and of High Clonal Diversity. <i>Frontiers in Microbiology</i> , 2020, 11, 581081.	1.5	9

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73	Assessing the Genetic Diversity of Austrian <i>Corynebacterium diphtheriae</i> Clinical Isolates, 2011 to 2019. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	9
74	A European-wide dataset to uncover adaptive traits of <i>Listeria monocytogenes</i> to diverse ecological niches. <i>Scientific Data</i> , 2022, 9, 190.	2.4	9
75	Activity of Ternary Gelatinase A-TIMP-2- Matrix Metallo-Proteinase Complexes. <i>Biological Chemistry Hoppe-Seyler</i> , 1994, 375, 589-596.	1.4	8
76	Analysis of the genetic stability of event NK603 in stacked corn varieties using high-resolution melting (HRM) analysis and Sanger sequencing. <i>European Food Research and Technology</i> , 2017, 243, 353-365.	1.6	8
77	Whole-Genome Analysis of a Human <i>Enterobacter mori</i> Isolate Carrying a bla _{IMI-2} Carbapenemase in Austria. <i>Microbial Drug Resistance</i> , 2019, 25, 94-96.	0.9	8
78	Draft Genome Sequence of a 94-Year-Old <i>Listeria monocytogenes</i> Isolate, SLCC208. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
79	Molecular typing of bacteria for epidemiological surveillance and outbreak investigation / Molekulare Typisierung von Bakterien für die epidemiologische Überwachung und Ausbruchsabklärung. <i>Bodenkultur</i> , 2016, 67, 199-224.	0.1	7
80	The First Report of mcr-1-Carrying <i>Escherichia coli</i> Originating from Animals in Serbia. <i>Antibiotics</i> , 2021, 10, 1063.	1.5	7
81	Multilocus Sequence Typing (MLST) and Whole Genome Sequencing (WGS) of <i>Listeria monocytogenes</i> and <i>Listeria innocua</i> . <i>Methods in Molecular Biology</i> , 2021, 2220, 89-103.	0.4	7
82	Prevalence and Antimicrobial Properties of Lactic Acid Bacteria in Nigerian Women During the Menstrual Cycle. <i>Polish Journal of Microbiology</i> , 2019, 68, 203-209.	0.6	7
83	Outbreak of acute gastroenteritis in an Austrian boarding school, September 2006. <i>Eurosurveillance</i> , 2007, 12, 224.	3.9	7
84	Genomic Characterization of <i>Cronobacter</i> spp. and <i>Salmonella</i> spp. Strains Isolated From Powdered Infant Formula in Chile. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	7
85	Nosocomial outbreak of <i>Streptococcus pyogenes</i> puerperal sepsis. <i>Clinical Microbiology and Infection</i> , 2019, 25, 521-523.	2.8	6
86	Oxazolidinone Resistance Mediated by <i>optrA</i> in Clinical <i>Enterococcus faecalis</i> Isolates in Upper Austria: First Report and Characterization by Whole Genome Sequencing. <i>Microbial Drug Resistance</i> , 2021, 27, 685-690.	0.9	6
87	Stability of short sequence repeats and their application for the characterization of <i>Erwinia amylovora</i> strains. <i>FEMS Microbiology Letters</i> , 2004, 234, 1-8.	0.7	6
88	Draft Genome Sequences of Seven <i>Cronobacter sakazakii</i> Strains Carrying the <i>mcr</i> 9.1 Gene Isolated in Chile. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050621.	0.3	5
89	Evaluation of <i>Adh1</i> alleles and transgenic soybean seeds using Scorpion PCR and HRM analysis. <i>European Food Research and Technology</i> , 2013, 237, 125-135.	1.6	4
90	Draft Genome Sequence of <i>Legionella jamestowniensis</i> Isolated from a Patient with Chronic Respiratory Disease. <i>Genome Announcements</i> , 2016, 4, .	0.8	4

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91	Characterization of Bacteria in Nigerian Yogurt as Promising Alternative to Antibiotics in Gastrointestinal Infections. <i>Journal of Dietary Supplements</i> , 2019, 16, 141-151.	1.4	4
92	Draft Genome Sequences of Five <i>Enterococcus faecium</i> Isolates from Traditional Montenegrin Brine Cheese. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
93	Draft Genome Sequences of Interpatient and Inpatient Epidemiologically Linked <i>Neisseria gonorrhoeae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
94	Draft Genome Sequence of the First Documented Clinical <i>Siccibacter turicensis</i> Isolate in Austria. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
95	Isolate-Based Surveillance of <i>Bordetella pertussis</i> , Austria, 2018–2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 862-871.	2.0	3
96	Draft Genome Sequences of Six <i>Corynebacterium ulcerans</i> Strains Isolated from Humans and Animals in Austria, 2013 to 2019. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
97	Werner syndrome: characterization of mutations in the WRN gene in an affected family. <i>European Journal of Human Genetics</i> , 1997, 5, 364-70.	1.4	3
98	Genetic Characterization of Antibiotic Resistant Enterobacteriaceae Isolates From Bovine Animals and the Environment in Nigeria. <i>Frontiers in Microbiology</i> , 2022, 13, 793541.	1.5	3
99	Rifampicin Resistance Associated with <i>rpoB</i> Mutations in <i>Neisseria gonorrhoeae</i> Clinical Strains Isolated in Austria, 2016 to 2020. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
100	TEN YEARS OF FIRE BLIGHT IN AUSTRIA: SURVEY AND CONTROL MEASURES. <i>Acta Horticulturae</i> , 2006, , 43-50.	0.1	2
101	Genetic characterization of the origin of off-type plants in maize inbred lines. <i>Seed Science and Technology</i> , 2009, 37, 423-435.	0.6	2
102	Plasmid-mediated colistin-resistance in <i>Escherichia coli</i> isolated from poultry and broiler meat in Austria in 2016. <i>International Journal of Infectious Diseases</i> , 2016, 53, 36-37.	1.5	2
103	Genetic diversity of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> isolates from Austria. <i>International Journal of Infectious Diseases</i> , 2016, 53, 68.	1.5	2
104	Use of genome wide gene-by-gene comparison for <i>Salmonella enterica</i> outbreak investigation in Austria. <i>International Journal of Infectious Diseases</i> , 2016, 53, 118.	1.5	2
105	Draft Genome Sequence of a Vancomycin-Resistant and Vancomycin-Dependent <i>Enterococcus faecium</i> Isolate. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
106	Advances in foodborne outbreak investigation and source tracking using whole genome sequencing. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 333, 012010.	0.2	2
107	Outbreak of infestation with body lice in a home for assisted living, Austria, 2018. <i>International Journal of Infectious Diseases</i> , 2019, 79, 126-127.	1.5	2
108	Draft Genome Sequences of <i>Legionella taurinensis</i> Recovered from a Hot Water System in Austria, 2018. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

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109	Draft Genome Sequences of Two <i>Listeria monocytogenes</i> Strains Isolated from Invasive Snails (<i>Arion</i>) Tj ETQq1 1 0,784314 rgBT /Overl	0,3	2
110	Draft Genome Sequence of a Multidrug-Resistant <i>Escherichia coli</i> Sequence Type 1193 Pandemic Clone Isolated from Wastewater in Austria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0076221.	0.3	2
111	A core genome multilocus sequence typing scheme for <i>Mycoplasma hyorhinis</i> . <i>Veterinary Microbiology</i> , 2021, 262, 109249.	0.8	2
112	Comparison of Automated Ribotyping, <i>spa</i> Typing, and MLST in 108 Clinical Isolates of <i>Staphylococcus aureus</i> from Orthopedic Infections. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1660.	1.8	2
113	P1301 Comparative molecular analysis of veterinary, dairy, and clinical <i>Staphylococcus aureus</i> isolates by <i>spa</i> typing and amplification of the <i>mecA</i> and the PVL genes. <i>International Journal of Antimicrobial Agents</i> , 2007, 29, S359-S360.	1.1	1
114	STABILITY OF SHORT SEQUENCE REPEATS AND SUITABILITY OF SSR, AFLP AND RAPD FOR THE CHARACTERIZATION OF <i>ERWINIA AMYLOVORA</i> STRAINS. <i>Acta Horticulturae</i> , 2006, , 75-86.	0.1	1
115	Letter to the editor: Livestock-associated meticillin-resistant <i>Staphylococcus aureus</i> (LA-MRSA), Austria, 2013. <i>Eurosurveillance</i> , 2017, 22, .	3.9	1
116	The First Bacterial Endocarditis Due to <i>Achromobacter xylosoxidans</i> in a Dog. <i>Pathogens</i> , 2021, 10, 1580.	1.2	1
117	Genome Sequence of OXA-726-Encoding <i>Aeromonas dhakensis</i> Igbk (Sequence Type 1171) from an Edible Snail Traded in Nigeria. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	1
118	Rapid identification of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates by <i>rpoB</i> gene scanning using high-resolution melting curve PCR analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 436-436.	1.3	0
119	Austria-wide survey on resistant, potentially pathogenic bacteria at Austrian bathing sites, 2017. <i>Bodenkultur</i> , 2019, 70, 81-88.	0.1	0
120	Stress survival islets contribute to clonal and serotype-specific differences in <i>L. monocytogenes</i> . IOP Conference Series: Earth and Environmental Science, 2021, 854, 012050.	0.2	0
121	Outbreak of <i>Cronobacter turicensis</i> in European brown hares (<i>Lepus europaeus</i>). <i>Letters in Applied Microbiology</i> , 2022, , .	1.0	0