

# Werner Ruppitsch

## List of Publications by Year in descending order

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121  
papers

2,591  
citations

218381

26  
h-index

243296

44  
g-index

123  
all docs

123  
docs citations

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times ranked

2847  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of Automated Ribotyping, spa 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
2	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
3	Outbreak of <i>Cronobacter turicensis</i> in European brown hares ( <i>Lepus europaeus</i> ). <i>Letters in Applied Microbiology</i> , 2022, , .	1.0	0
4	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
5	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
6	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
7	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
8	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
9	Tracking the Origin of Austrian Human Brucellosis Cases Using Whole Genome Sequencing. <i>Frontiers in Medicine</i> , 2021, 8, 635547.	1.2	14
10	Isolate-Based Surveillance of <i>Bordetella pertussis</i> , Austria, 2018–2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 862-871.	2.0	3
11	Draft Genome Sequences of Two <i>Listeria monocytogenes</i> Strains Isolated from Invasive Snails ( <i>Arion</i> ) Tj ETQq1 1 0,784314 rgBT /Ovele	0.3	2
12	Presence of $\beta$ -Lactamase-producing Enterobacterales and <i>Salmonella</i> Isolates in Marine Mammals. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5905.	1.8	10
13	Profiling the Virulence and Antibiotic Resistance Genes of <i>Cronobacter sakazakii</i> Strains Isolated From Powdered and Dairy Formulas by Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 694922.	1.5	18
14	Draft Genome Sequences of Seven <i>Cronobacter sakazakii</i> Strains Carrying the <i>mcr-1</i> 9.1 Gene Isolated in Chile. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050621.	0.3	5
15	Genetic Diversity of <i>Leuconostoc mesenteroides</i> Isolates from Traditional Montenegrin Brine Cheese. <i>Microorganisms</i> , 2021, 9, 1612.	1.6	12
16	The Pheno- and Genotypic Characterization of Porcine <i>Escherichia coli</i> Isolates. <i>Microorganisms</i> , 2021, 9, 1676.	1.6	14
17	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
18	The First Report of <i>mcr-1</i> -Carrying <i>Escherichia coli</i> Originating from Animals in Serbia. <i>Antibiotics</i> , 2021, 10, 1063.	1.5	7

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19	Draft Genome Sequence of a Multidrug-Resistant Escherichia coli Sequence Type 1193 Pandemic Clone Isolated from Wastewater in Austria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0076221.	0.3	2
20	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
21	Molecular Characterization of <i>Cronobacter sakazakii</i> Strains Isolated from Powdered Milk. <i>Foods</i> , 2021, 10, 20.	1.9	16
22	A core genome multilocus sequence typing scheme for <i>Mycoplasma hyorhinis</i> . <i>Veterinary Microbiology</i> , 2021, 262, 109249.	0.8	2
23	Stress survival islets contribute to clonal and serotype-specific differences in <i>L. monocytogenes</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 854, 012050.	0.2	0
24	Virulence and Antibiotic Resistance Genes in <i>Listeria monocytogenes</i> Strains Isolated From Ready-to-Eat Foods in Chile. <i>Frontiers in Microbiology</i> , 2021, 12, 796040.	1.5	17
25	The First Bacterial Endocarditis Due to <i>Achromobacter xylosoxidans</i> in a Dog. <i>Pathogens</i> , 2021, 10, 1580.	1.2	1
26	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
27	Fecal <i>Klebsiella pneumoniae</i> Carriage Is Intermittent and of High Clonal Diversity. <i>Frontiers in Microbiology</i> , 2020, 11, 581081.	1.5	9
28	Large Nationwide Outbreak of Invasive Listeriosis Associated with Blood Sausage, Germany, 2018–2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 1456-1464.	2.0	40
29	Broad-Spectrum Cephalosporin-Resistant <i>Klebsiella</i> spp. Isolated from Diseased Horses in Austria. <i>Animals</i> , 2020, 10, 332.	1.0	15
30	Whole genome sequencing of extended-spectrum $\beta$ -lactamase genes in <i>Enterobacteriaceae</i> isolates from Nigeria. <i>PLoS ONE</i> , 2020, 15, e0231146.	1.1	16
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	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
39	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
40	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
41	Multicenter Study of <i>Cronobacter sakazakii</i> Infections in Humans, Europe, 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 515-522.	2.0	47
42	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
43	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
44	Molecular characterization of <i>Listeria monocytogenes</i> isolates from a small-scale meat processor in Montenegro, 2011–2014. <i>Food Microbiology</i> , 2019, 79, 116-122.	2.1	23
45	Nosocomial outbreak of <i>Streptococcus pyogenes</i> puerperal sepsis. <i>Clinical Microbiology and Infection</i> , 2019, 25, 521-523.	2.8	6
46	Whole-Genome Analysis of a Human <i>Enterobacter mori</i> Isolate Carrying a <i>bla</i> IMI-2 Carbapenemase in Austria. <i>Microbial Drug Resistance</i> , 2019, 25, 94-96.	0.9	8
47	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
48	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
49	Listeriosis outbreak likely due to contaminated liver pâté consumed in a tavern, Austria, December 2018. <i>Eurosurveillance</i> , 2019, 24, .	3.9	19
50	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
51	Austria-wide survey on resistant, potentially pathogenic bacteria at Austrian bathing sites, 2017. <i>Bodenkultur</i> , 2019, 70, 81-88.	0.1	0
52	Draft Genome Sequences of Interpatient and Inpatient Epidemiologically Linked <i>Neisseria gonorrhoeae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
53	Draft Genome Sequence of the First Documented Clinical <i>Siccibacter turicensis</i> Isolate in Austria. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
54	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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55	An outbreak of listeriosis linked to turkey meat products in the Czech Republic, 2012–2016. <i>Epidemiology and Infection</i> , 2018, 146, 1407-1412.	1.0	28
56	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
57	Retrospective validation of whole genome sequencing-enhanced surveillance of listeriosis in Europe, 2010 to 2015. <i>Eurosurveillance</i> , 2018, 23, .	3.9	61
58	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
59	Detection of the <i>mcr-1</i> 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
60	Carbapenemase-Producing Enterobacteriaceae Isolates from Edo State, Nigeria. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	19
61	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
62	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
63	Antagonistic and quantitative assessment of indigenous lactic acid bacteria in different varieties of ogi against gastrointestinal pathogens. <i>Pan African Medical Journal</i> , 2017, 27, 22.	0.3	16
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	Letter to the editor: Livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> (LA-MRSA), Austria, 2013. <i>Eurosurveillance</i> , 2017, 22, .	3.9	1
66	Molecular Characterization of a Prevalent Ribocluster of Methicillin-Sensitive <i>Staphylococcus aureus</i> from Orthopedic Implant Infections. Correspondence with MLST CC30. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 8.	1.8	21
67	Draft Genome Sequence of a 94-Year-Old <i>Listeria monocytogenes</i> Isolate, SLCC208. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
68	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
69	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
70	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
71	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
72	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

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73	Whole genome sequence-based serogrouping of <i>Listeria monocytogenes</i> isolates. <i>Journal of Biotechnology</i> , 2016, 235, 181-186.	1.9	45
74	Draft Genome Sequence of a Vancomycin-Resistant and Vancomycin-Dependent <i>Enterococcus faecium</i> Isolate. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
75	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
76	Accuracy of conventional identification methods used for Enterobacteriaceae isolates in three Nigerian hospitals. <i>PeerJ</i> , 2016, 4, e2511.	0.9	16
77	Improved Protocol for Rapid Identification of Certain Spa Types Using High Resolution Melting Curve Analysis. <i>PLoS ONE</i> , 2015, 10, e0116713.	1.1	14
78	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
79	Ongoing outbreak of invasive listeriosis, Germany, 2012 to 2015. <i>Eurosurveillance</i> , 2015, 20, .	3.9	20
80	Evaluation of Adh1 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
81	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
82	One-Step Triplex High-Resolution Melting Analysis for Rapid Identification and Simultaneous Subtyping of Frequently Isolated <i>Salmonella</i> Serovars. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3352-3360.	1.4	19
83	Gene Scanning of an Internalin B Gene Fragment Using High-Resolution Melting Curve Analysis as a Tool for Rapid Typing of <i>Listeria monocytogenes</i> . <i>Journal of Molecular Diagnostics</i> , 2011, 13, 57-63.	1.2	19
84	Characterization of selected Gram-negative non-fermenting bacteria isolated from honey bees ( <i>Apis mellifera</i> ) in Germany. <i>Journal of Applied Microbiology</i> , 2011, 110, 107-114.	0.9	14
85	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
86	Listeriosis outbreak caused by acid curd cheese 'Quargel', Austria and Germany 2009. <i>Eurosurveillance</i> , 2010, 15, .	3.9	62
87	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
88	Listeriosis outbreak caused by acid curd cheese Quargel, Austria and Germany 2009. <i>Eurosurveillance</i> , 2010, 15, .	3.9	28
89	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
90	Rapid identification of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates by rpoB gene scanning using high-resolution melting curve PCR analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 436-436.	1.3	0

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91	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
92	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
93	Methicillin-resistant <i>Staphylococcus aureus</i> : a new zoonotic agent?. <i>Wiener Klinische Wochenschrift</i> , 2009, 121, 86-90.	1.0	67
94	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
95	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
96	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
97	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
98	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 <i>PVL</i> genes. <i>International Journal of Antimicrobial Agents</i> , 2007, 29, S359-S360.	1.1	1
99	Suitability of partial 16S ribosomal RNA gene sequence analysis for the identification of dangerous bacterial pathogens. <i>Journal of Applied Microbiology</i> , 2007, 102, 852-859.	1.4	17
100	Meticillin-resistant <i>Staphylococcus aureus</i> : occurrence of a new <i>spa</i> type in two acute care hospitals in Austria. <i>Journal of Hospital Infection</i> , 2007, 67, 316-322.	1.4	12
101	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
102	Outbreak of acute gastroenteritis in an Austrian boarding school, September 2006. <i>Eurosurveillance</i> , 2007, 12, 7-8.	3.9	24
103	Occurrence of the USA300 community-acquired <i>Staphylococcus aureus</i> clone in Austria. , 2007, 12, E071025.1.		23
104	Outbreak of acute gastroenteritis in an Austrian boarding school, September 2006. <i>Eurosurveillance</i> , 2007, 12, 224.	3.9	7
105	TEN YEARS OF FIRE BLIGHT IN AUSTRIA: SURVEY AND CONTROL MEASURES. <i>Acta Horticulturae</i> , 2006, , 43-50.	0.1	2
106	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
107	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
108	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

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109	STABILITY OF SHORT SEQUENCE REPEATS AND SUITABILITY OF SSR, AFLP AND RAPD FOR THE CHARACTERIZATION OF ERWINIA AMYLOVORA STRAINS. <i>Acta Horticulturae</i> , 2006, , 75-86.	0.1	1
110	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
111	A rapid and sensitive method for the detection of <i>Xanthomonas fragariae</i> , causal agent of angular leafspot disease in strawberry plants. <i>Journal of Microbiological Methods</i> , 2004, 58, 281-284.	0.7	20
112	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
113	Overexpressed thioredoxin compensates Fanconi anemia related chromosomal instability. <i>Oncogene</i> , 2002, 21, 2406-2412.	2.6	29
114	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
115	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
116	Involvement of the Fanconi anemia protein FA-C in repair processes of oxidative DNA damages. <i>FEBS Letters</i> , 1998, 440, 103-106.	1.3	21
117	The role of oxygen metabolism for the pathological phenotype of Fanconi anemia. <i>Human Genetics</i> , 1997, 99, 710-719.	1.8	56
118	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
119	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
120	Activity of Ternary Gelatinase A-TIMP-2- Matrix Metallo-Proteinase Complexes. <i>Biological Chemistry Hoppe-Seyler</i> , 1994, 375, 589-596.	1.4	8
121	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