

Sigrid C J De Keersmaecker

List of Publications by Year in descending order

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141
papers

8,269
citations

53751

45
h-index

49868

87
g-index

147
all docs

147
docs citations

147
times ranked

8879
citing authors

#	ARTICLE	IF	CITATIONS
1	Host interactions of probiotic bacterial surface molecules: comparison with commensals and pathogens. <i>Nature Reviews Microbiology</i> , 2010, 8, 171-184.	13.6	828
2	Genes and Molecules of Lactobacilli Supporting Probiotic Action. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 728-764.	2.9	782
3	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a human-mucus binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17193-17198.	3.3	654
4	Salmonella biofilms: An overview on occurrence, structure, regulation and eradication. <i>Food Research International</i> , 2012, 45, 502-531.	2.9	406
5	Functional Analysis of <i>Lactobacillus rhamnosus</i> GG Pili in Relation to Adhesion and Immunomodulatory Interactions with Intestinal Epithelial Cells. <i>Applied and Environmental Microbiology</i> , 2012, 78, 185-193.	1.4	274
6	Strong antimicrobial activity of <i>Lactobacillus rhamnosus</i> GG against <i>Salmonella typhimurium</i> due to accumulation of lactic acid. <i>FEMS Microbiology Letters</i> , 2006, 259, 89-96.	0.7	257
7	Identification of a Gene Cluster for the Biosynthesis of a Long, Galactose-Rich Exopolysaccharide in <i>Lactobacillus rhamnosus</i> GG and Functional Analysis of the Priming Glycosyltransferase. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3554-3563.	1.4	234
8	Impact of Environmental and Genetic Factors on Biofilm Formation by the Probiotic Strain <i>Lactobacillus rhamnosus</i> GG. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6768-6775.	1.4	229
9	Brominated Furanones Inhibit Biofilm Formation by <i>Salmonella enterica</i> Serovar Typhimurium. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6639-6648.	1.4	184
10	Adherence factors of <i>Lactobacillus</i> in the human gastrointestinal tract. <i>FEMS Microbiology Letters</i> , 2007, 276, 140-148.	0.7	169
11	Detection, Localization, and Conformational Analysis of Single Polysaccharide Molecules on Live Bacteria. <i>ACS Nano</i> , 2008, 2, 1921-1929.	7.3	159
12	Let LuxS speak up in AI-2 signaling. <i>Trends in Microbiology</i> , 2006, 14, 114-119.	3.5	152
13	Exopolysaccharides of <i>Lactobacillus rhamnosus</i> GG form a protective shield against innate immune factors in the intestine. <i>Microbial Biotechnology</i> , 2011, 4, 368-374.	2.0	150
14	Concise and Diversity-Oriented Route toward Polysubstituted 2-Aminoimidazole Alkaloids and Their Analogues. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 9465-9468.	7.2	146
15	Functional Analysis of luxS in the Probiotic Strain <i>Lactobacillus rhamnosus</i> GG Reveals a Central Metabolic Role Important for Growth and Biofilm Formation. <i>Journal of Bacteriology</i> , 2007, 189, 860-871.	1.0	142
16	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
17	Chemical Synthesis of (S)-4,5-Dihydroxy-2,3-pentanedione, a Bacterial Signal Molecule Precursor, and Validation of Its Activity in <i>Salmonella typhimurium</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 19563-19568.	1.6	127
18	Targeting the 16S rRNA Gene for Bacterial Identification in Complex Mixed Samples: Comparative Evaluation of Second (Illumina) and Third (Oxford Nanopore Technologies) Generation Sequencing Technologies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 298.	1.8	117

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19	Comparison of the PhoPQ Regulon in <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> . <i>Journal of Molecular Evolution</i> , 2005, 60, 462-474.	0.8	106
20	Functional Analysis of d-Alanylation of Lipoteichoic Acid in the Probiotic Strain <i>Lactobacillus rhamnosus</i> GG. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3595-3604.	1.4	98
21	Stretching polysaccharides on live cells using single molecule force spectroscopy. <i>Nature Protocols</i> , 2009, 4, 939-946.	5.5	97
22	Impact of lipoteichoic acid modification on the performance of the probiotic <i>Lactobacillus rhamnosus</i> GG in experimental colitis. <i>Clinical and Experimental Immunology</i> , 2010, 162, 306-314.	1.1	92
23	Functional Characterization of a Mucus-Specific LPXTG Surface Adhesin from Probiotic <i>Lactobacillus rhamnosus</i> GG. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4465-4472.	1.4	90
24	Characterization of MabA, a modulator of <i>Lactobacillus rhamnosus</i> GG adhesion and biofilm formation. <i>FEMS Immunology and Medical Microbiology</i> , 2010, 59, 386-398.	2.7	82
25	Genetic and Biochemical Characterization of the Cell Wall Hydrolase Activity of the Major Secreted Protein of <i>Lactobacillus rhamnosus</i> GG. <i>PLoS ONE</i> , 2012, 7, e31588.	1.1	77
26	The major secreted protein Msp1/p75 is O-glycosylated in <i>Lactobacillus rhamnosus</i> GG. <i>Microbial Cell Factories</i> , 2012, 11, 15.	1.9	72
27	Lipoteichoic acid is an important microbe-associated molecular pattern of <i>Lactobacillus rhamnosus</i> GG. <i>Microbial Cell Factories</i> , 2012, 11, 161.	1.9	70
28	Impact of <i>luxS</i> and Suppressor Mutations on the Gastrointestinal Transit of <i>Lactobacillus rhamnosus</i> GG. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4711-4718.	1.4	68
29	Delineation of the <i>Salmonella enterica</i> Serovar Typhimurium HilA Regulon through Genome-Wide Location and Transcript Analysis. <i>Journal of Bacteriology</i> , 2007, 189, 4587-4596.	1.0	65
30	Synthesis of N-Acyl Homoserine Lactone Analogues Reveals Strong Activators of SdiA, the <i>Salmonella enterica</i> Serovar Typhimurium LuxR Homologue. <i>Applied and Environmental Microbiology</i> , 2007, 73, 535-544.	1.4	63
31	Structure-activity relationship of brominated 3-alkyl-5-methylene-2(5H)-furanones and alkylmaleic anhydrides as inhibitors of <i>Salmonella</i> biofilm formation and quorum sensing regulated bioluminescence in <i>Vibrio harveyi</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 5224-5233.	1.4	61
32	How to Deal with the Upcoming Challenges in GMO Detection in Food and Feed. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-11.	3.0	61
33	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified <i>Bacillus</i> . <i>Scientific Reports</i> , 2020, 10, 4310.	1.6	57
34	Next-generation sequencing as a tool for the molecular characterisation and risk assessment of genetically modified plants: Added value or not?. <i>Trends in Food Science and Technology</i> , 2015, 45, 319-326.	7.8	55
35	Structure-Activity Relationship of 4(5)-Aryl-2-amino-1H-imidazoles, N-1-Substituted 2-Aminoimidazoles and Imidazo[1,2-a]pyrimidinium Salts as Inhibitors of Biofilm Formation by <i>Salmonella</i> Typhimurium and <i>Pseudomonas aeruginosa</i> . <i>Journal of Medicinal Chemistry</i> , 2011, 54, 472-484.	2.9	54
36	Comparative Study of Seven Commercial Kits for Human DNA Extraction from Urine Samples Suitable for DNA Biomarker-Based Public Health Studies. <i>Journal of Biomolecular Techniques</i> , 2014, 25, jbt.14-2504-002.	0.8	54

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37	In silico identification and experimental validation of PmrAB targets in <i>Salmonella typhimurium</i> by regulatory motif detection. <i>Genome Biology</i> , 2004, 5, R9.	13.9	53
38	DISTILLER: a data integration framework to reveal condition dependency of complex regulons in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2009, 10, R27.	13.9	52
39	Validation of a Bioinformatics Workflow for Routine Analysis of Whole-Genome Sequencing Data and Related Challenges for Pathogen Typing in a European National Reference Center: <i>Neisseria meningitidis</i> as a Proof-of-Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 362.	1.5	51
40	Microarray Analysis and Motif Detection Reveal New Targets of the <i>Salmonella enterica</i> Serovar Typhimurium HilA Regulatory Protein, Including hilA Itself. <i>Journal of Bacteriology</i> , 2005, 187, 4381-4391.	1.0	50
41	Detection of Plasmid-Mediated Colistin Resistance, <i>mcr-1</i> and <i>mcr-2</i> Genes, in <i>Salmonella</i> spp. Isolated from Food at Retail in Belgium from 2012 to 2015. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 114-117.	0.8	50
42	Integration of omics data: how well does it work for bacteria?. <i>Molecular Microbiology</i> , 2006, 62, 1239-1250.	1.2	49
43	Flow Cytometric Testing of Green Fluorescent Protein-Tagged <i>Lactobacillus rhamnosus</i> GG for Response to Defensins. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4923-4930.	1.4	48
44	The small regulatory RNA molecule MicA is involved in <i>Salmonella enterica</i> serovar Typhimurium biofilm formation. <i>BMC Microbiology</i> , 2010, 10, 276.	1.3	48
45	FISH analysis of <i>Lactobacillus</i> biofilms in the gastrointestinal tract of different hosts. <i>Letters in Applied Microbiology</i> , 2011, 52, 220-226.	1.0	48
46	Identification and characterization of starter lactic acid bacteria and probiotics from Columbian dairy products. <i>Journal of Applied Microbiology</i> , 2007, 103, 666-674.	1.4	47
47	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. <i>Food Chemistry</i> , 2016, 192, 788-798.	4.2	47
48	The proteome of <i>Salmonella</i> Typhimurium grown under <i>in vivo</i> mimicking conditions. <i>Proteomics</i> , 2009, 9, 565-579.	1.3	46
49	Small Molecules for Interference with Cell-Cell-Communication Systems in Gram-Negative Bacteria. <i>Current Medicinal Chemistry</i> , 2008, 15, 2144-2156.	1.2	43
50	MLVA as a Tool for Public Health Surveillance of Human <i>Salmonella</i> Typhimurium: Prospective Study in Belgium and Evaluation of MLVA Loci Stability. <i>PLoS ONE</i> , 2013, 8, e84055.	1.1	40
51	Structure-activity relationship of 2-hydroxy-2-aryl-2,3-dihydro-imidazo[1,2-a]pyrimidinium salts and 2N-substituted 4(5)-aryl-2-amino-1H-imidazoles as inhibitors of biofilm formation by <i>Salmonella</i> Typhimurium and <i>Pseudomonas aeruginosa</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2011, 19, 3462-3473.	1.4	39
52	Lessons from probiotic-host interaction studies in murine models of experimental colitis. <i>Molecular Nutrition and Food Research</i> , 2011, 55, 1441-1453.	1.5	38
53	Integration of omics data: does it lead to new insights into host-microbe interactions?. <i>Future Microbiology</i> , 2010, 5, 313-328.	1.0	32
54	Impact of DNA extraction on whole genome sequencing analysis for characterization and relatedness of Shiga toxin-producing <i>Escherichia coli</i> isolates. <i>Scientific Reports</i> , 2020, 10, 14649.	1.6	32

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55	Genome-specific higher-order background models to improve motif detection. <i>Trends in Microbiology</i> , 2003, 11, 61-66.	3.5	29
56	Comparison of SNP-based subtyping workflows for bacterial isolates using WGS data, applied to <i>Salmonella enterica</i> serotype Typhimurium and serotype 1,4,[5],12:i:-. <i>PLoS ONE</i> , 2018, 13, e0192504.	1.1	29
57	Large diversity of linezolid-resistant isolates discovered in food-producing animals through linezolid selective monitoring in Belgium in 2019. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 77, 49-57.	1.3	29
58	Whole Genome Sequence Analysis of <i>Salmonella</i> Enteritidis PT4 Outbreaks from a National Reference Laboratory's Viewpoint. <i>PLOS Currents</i> , 2015, 7, .	1.4	29
59	Adaptation factors of the probiotic <i>Lactobacillus rhamnosus</i> GG. <i>Beneficial Microbes</i> , 2010, 1, 335-342.	1.0	28
60	Nanopore sequencing technology: a new route for the fast detection of unauthorized GMO. <i>Scientific Reports</i> , 2018, 8, 7903.	1.6	26
61	Genomic epidemiology of emerging ESBL-producing <i>Salmonella</i> Kentucky blaCTX-M-14b in Europe. <i>Emerging Microbes and Infections</i> , 2020, 9, 2124-2135.	3.0	26
62	Deepening of In Silico Evaluation of SARS-CoV-2 Detection RT-qPCR Assays in the Context of New Variants. <i>Genes</i> , 2021, 12, 565.	1.0	26
63	A GFP promoter fusion library for the study of <i>Salmonella</i> biofilm formation and the mode of action of biofilm inhibitors. <i>Biofouling</i> , 2014, 30, 605-625.	0.8	25
64	Use of next generation sequencing data to develop a qPCR method for specific detection of EU-unauthorized genetically modified <i>Bacillus subtilis</i> overproducing riboflavin. <i>BMC Biotechnology</i> , 2015, 15, 103.	1.7	25
65	Genome Sequence of EU-Unauthorized Genetically Modified <i>Bacillus subtilis</i> Strain 2014-3557 Overproducing Riboflavin, Isolated from a Vitamin B2 80% Feed Additive. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
66	The Benefits of Whole Genome Sequencing for Foodborne Outbreak Investigation from the Perspective of a National Reference Laboratory in a Smaller Country. <i>Foods</i> , 2020, 9, 1030.	1.9	23
67	Use of Whole Genome Sequencing Data for a First in Silico Specificity Evaluation of the RT-qPCR Assays Used for SARS-CoV-2 Detection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5585.	1.8	23
68	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing <i>Escherichia coli</i> using a reference collection extensively characterized with conventional methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	20
69	High-resolution melting PCR analysis for rapid genotyping of <i>Burkholderia mallei</i> . <i>Infection, Genetics and Evolution</i> , 2018, 63, 1-4.	1.0	19
70	Towards Real-Time and Affordable Strain-Level Metagenomics-Based Foodborne Outbreak Investigations Using Oxford Nanopore Sequencing Technologies. <i>Frontiers in Microbiology</i> , 2021, 12, 738284.	1.5	19
71	Experimental approaches to identify small RNAs and their diverse roles in bacteria – what we have learnt in one decade of MicA research. <i>MicrobiologyOpen</i> , 2015, 4, 699-711.	1.2	18
72	MinION sequencing technology to characterize unauthorized GM petunia plants circulating on the European Union market. <i>Scientific Reports</i> , 2019, 9, 7141.	1.6	18

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73	Strategy for the identification of micro-organisms producing food and feed products: Bacteria producing food enzymes as study case. <i>Food Chemistry</i> , 2020, 305, 125431.	4.2	18
74	Isolation of Drug-Resistant <i>Gallibacterium anatis</i> from Calves with Unresponsive Bronchopneumonia, Belgium. <i>Emerging Infectious Diseases</i> , 2020, 26, .	2.0	18
75	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical Mycobacterium tuberculosis Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and <i>In Silico</i> Approaches. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	18
76	2D proteome analysis initiates new Insights on the SalmonellaTyphimurium LuxS protein. <i>BMC Microbiology</i> , 2009, 9, 198.	1.3	17
77	Development of a Luminex xTAG [®] assay for cost-effective multiplex detection of β -lactamases in Gram-negative bacteria. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2479-2483.	1.3	17
78	A novel genotoxin-specific qPCR array based on the metabolically competent human HepaRG _h cell line as a rapid and reliable tool for improved in vitro hazard assessment. <i>Archives of Toxicology</i> , 2018, 92, 1593-1608.	1.9	17
79	Detection and discrimination of five E. coli pathotypes using a combinatory SYBR [®] Green qPCR screening system. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3267-3285.	1.7	17
80	More robust detection of motifs in coexpressed genes by using phylogenetic information. <i>BMC Bioinformatics</i> , 2006, 7, 160.	1.2	16
81	Gene expression analysis of monospecies Salmonella Typhimurium biofilms using Differential Fluorescence Induction. <i>Journal of Microbiological Methods</i> , 2011, 84, 467-478.	0.7	16
82	First detection of a plasmid located carbapenem resistant blaVIM-1 gene in E. coli isolated from meat products at retail in Belgium in 2015. <i>International Journal of Food Microbiology</i> , 2020, 324, 108624.	2.1	16
83	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a Salmonella food-borne outbreak. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
84	Guidelines for Optimisation of a Multiplex Oligonucleotide Ligation-PCR for Characterisation of Microbial Pathogens in a Microsphere Suspension Array. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	15
85	Development and performance assessment of a qualitative SYBR [®] green real-time PCR assay for the detection of Aspergillus versicolor in indoor air. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7267-7282.	1.7	15
86	Strategy and Performance Evaluation of Low-Frequency Variant Calling for SARS-CoV-2 Using Targeted Deep Illumina Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 747458.	1.5	15
87	Strain-Level Metagenomic Data Analysis of Enriched In Vitro and In Silico Spiked Food Samples: Paving the Way towards a Culture-Free Foodborne Outbreak Investigation Using STEC as a Case Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5688.	1.8	14
88	A Practical Method to Implement Strain-Level Metagenomics-Based Foodborne Outbreak Investigation and Source Tracking in Routine. <i>Microorganisms</i> , 2020, 8, 1191.	1.6	14
89	Identification of an unauthorized genetically modified bacteria in food enzyme through whole-genome sequencing. <i>Scientific Reports</i> , 2020, 10, 7094.	1.6	14
90	Development of an NGS-Based Workflow for Improved Monitoring of Circulating Plasmids in Support of Risk Assessment of Antimicrobial Resistance Gene Dissemination. <i>Antibiotics</i> , 2020, 9, 503.	1.5	13

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91	A multiplex oligonucleotide ligation-PCR as a complementary tool for subtyping of Salmonella Typhimurium. Applied Microbiology and Biotechnology, 2015, 99, 8137-8149.	1.7	12
92	A genoserotyping system for a fast and objective identification of Salmonella serotypes commonly isolated from poultry and pork food sectors in Belgium. Food Microbiology, 2020, 91, 103534.	2.1	12
93	A molecular approach for the rapid, selective and sensitive detection of Exophiala jeanselmei in environmental samples: development and performance assessment of a real-time PCR assay. Applied Microbiology and Biotechnology, 2016, 100, 1377-1392.	1.7	11
94	Discrimination of three genetically close Aspergillus species by using high resolution melting analysis applied to indoor air as case study. BMC Microbiology, 2017, 17, 84.	1.3	11
95	Synthesis of vinyl 1,2-diketones. Tetrahedron Letters, 2004, 45, 4057-4059.	0.7	10
96	FabR regulates Salmonella biofilm formation via its direct target FabB. BMC Genomics, 2016, 17, 253.	1.2	9
97	Strategy to Develop and Evaluate a Multiplex RT-ddPCR in Response to SARS-CoV-2 Genomic Evolution. Current Issues in Molecular Biology, 2021, 43, 1937-1949.	1.0	9
98	The AI-2-dependent regulator LsrR has a limited regulon in Salmonella Typhimurium. Cell Research, 2010, 20, 966-969.	5.7	8
99	Identification and characterization of 4-[4-(3-phenyl-2-propen-1-yl)-1-piperazinyl]-5H-pyrimido[5,4-b]indole derivatives as Salmonella biofilm inhibitors. FEMS Immunology and Medical Microbiology, 2012, 65, 390-394.	2.7	8
100	Shifting national surveillance of Shigella infections toward genoserotyping by the development of a tailored Luminex assay and NGS workflow. MicrobiologyOpen, 2019, 8, e00807.	1.2	8
101	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: Neisseria meningitidis as a Proof of Concept. Frontiers in Microbiology, 2019, 10, 2897.	1.5	8
102	Epidemiology of the Staphylococcus aureus CA-MRSA USA300 in Belgium. European Journal of Clinical Microbiology and Infectious Diseases, 2021, 40, 2335-2347.	1.3	8
103	Whole-Genome Sequencing-Based Antimicrobial Resistance Characterization and Phylogenomic Investigation of 19 Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Positive Escherichia coli Strains Collected From Hospital Patients in Benin in 2019. Frontiers in Microbiology, 2021, 12, 752883.	1.5	8
104	The genetic structure of the Belgian population. Human Genomics, 2018, 12, 6.	1.4	7
105	Development of a real-time PCR method for the genoserotyping of Salmonella Paratyphi B variant Java. Applied Microbiology and Biotechnology, 2019, 103, 4987-4996.	1.7	7
106	Development of a multiplex mass spectrometry method for simultaneous quantification of urinary proteins related to respiratory health. Scientific Reports, 2021, 11, 10107.	1.6	7
107	Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. Frontiers in Microbiology, 2021, 12, 750278.	1.5	7
108	Whole-Genome Sequencing of Multidrug-Resistant Escherichia coli Strains Harboring the mcr-1 Gene, Isolated from Seawater of the Algiers Coast in Algeria. Microbiology Resource Announcements, 2019, 8, .	0.3	6

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109	A multiplex oligonucleotide ligation-PCR method for the genosertotyping of common Salmonella using a liquid bead suspension assay. <i>Food Microbiology</i> , 2020, 87, 103394.	2.1	6
110	Screening strategy targeting the presence of food enzyme-producing fungi in food enzyme preparations. <i>Food Control</i> , 2020, 117, 107295.	2.8	6
111	First detection of a plasmid-encoded New-Delhi metallo-beta-lactamase-1 (NDM-1) producing <i>Acinetobacter baumannii</i> using whole genome sequencing, isolated in a clinical setting in Benin. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 5.	1.7	6
112	Whole-genome-based phylogenomic analysis of the Belgian 2016â€“2017 influenza A(H3N2) outbreak season allows improved surveillance. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
113	Development and performance assessment of a luminex xMAPÂ® direct hybridization assay for the detection and identification of indoor air fungal contamination. <i>PLoS ONE</i> , 2017, 12, e0173390.	1.1	5
114	Exploiting the Advantages of Molecular Tools for the Monitoring of Fungal Indoor Air Contamination: First Detection of <i>Exophiala jeanselmei</i> in Indoor Air of Air-Conditioned Offices. <i>Microorganisms</i> , 2019, 7, 674.	1.6	5
115	Genderâ€“dependent association between exhaled nitric oxide and the CC16 38AA genotype in young school children. <i>Immunity, Inflammation and Disease</i> , 2020, 8, 497-505.	1.3	5
116	Case Report: Multidrug Resistant <i>Raoultella ornithinolytica</i> in a Septicemic Calf. <i>Frontiers in Veterinary Science</i> , 2021, 8, 631716.	0.9	5
117	A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100023.	0.9	5
118	Retrospective evaluation of routine whole genome sequencing of <i>Mycobacterium tuberculosis</i> at the Belgian National Reference Center, 2019. <i>Acta Clinica Belgica</i> , 2022, 77, 853-860.	0.5	5
119	Urinary CC16, a potential indicator of lung integrity and inflammation, increases in children after short-term exposure to PM2.5/PM10 and is driven by the CC16 38GG genotype. <i>Environmental Research</i> , 2022, 212, 113272.	3.7	5
120	Whole-genome sequencing of <i>Listeria monocytogenes</i> serotype 4b isolated from ready-to-eat lentil salad in Algiers, Algeria. <i>New Microbes and New Infections</i> , 2020, 33, 100628.	0.8	4
121	Phylogenomic Investigation of Increasing Fluoroquinolone Resistance among Belgian Cases of Shigellosis between 2013 and 2018 Indicates Both Travel-Related Imports and Domestic Circulation. <i>Microorganisms</i> , 2021, 9, 767.	1.6	4
122	Coverage of the national surveillance system for human Salmonella infections, Belgium, 2016-2020. <i>PLoS ONE</i> , 2021, 16, e0256820.	1.1	4
123	Selection of a Noninvasive Source of Human DNA Envisaging Genotyping Assays in Epidemiological Studies: Urine or Saliva?. <i>Journal of Biomolecular Techniques</i> , 2020, 31, 27-35.	0.8	4
124	Characterization of Genetically Modified Microorganisms Using Short- and Long-Read Whole-Genome Sequencing Reveals Contaminations of Related Origin in Multiple Commercial Food Enzyme Products. <i>Foods</i> , 2021, 10, 2637.	1.9	4
125	Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
126	Population Analysis of O26 Shiga Toxin-Producing <i>Escherichia coli</i> Causing Hemolytic Uremic Syndrome in Italy, 1989â€“2020, Through Whole Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 842508.	1.8	4

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127	Influence of genetic background on transformation and expression of Green Fluorescent Protein in <i>Actinobacillus actinomycetemcomitans</i> . <i>Oral Microbiology and Immunology</i> , 2005, 20, 274-281.	2.8	3
128	NGS for (Hemato-) Oncology in Belgium: Evaluation of Laboratory Performance and Feasibility of a National External Quality Assessment Program. <i>Cancers</i> , 2020, 12, 3180.	1.7	3
129	Evaluation of the added value of viral genomic information for predicting severity of influenza infection. <i>BMC Infectious Diseases</i> , 2021, 21, 785.	1.3	3
130	CHAPTER 8. GMO Detection and Identification Using Next-generation Sequencing. <i>Food Chemistry, Function and Analysis</i> , 2019, , 96-106.	0.1	3
131	Genome Sequence of the <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Namur Strain 05-2929, Lacking the <i>Salmonella</i> Atypical Fimbrial Operon. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
132	Detection and identification of authorized and unauthorized GMOs using high-throughput sequencing with the support of a sequence-based GMO database. <i>Food Chemistry Molecular Sciences</i> , 2022, 4, 100096.	0.9	2
133	Whole-Genome Sequence Approach and Phylogenomic Stratification Improve the Association Analysis of Mutations With Patient Data in Influenza Surveillance. <i>Frontiers in Microbiology</i> , 2022, 13, 809887.	1.5	2
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138	Synthesis of Vinyl 1,2-Diketones.. <i>ChemInform</i> , 2004, 35, no.	0.1	0
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