

# 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	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
2	Population Analysis of O26 Shiga Toxin-Producing <i>Escherichia coli</i> Causing Hemolytic Uremic Syndrome in Italy, 1989–2020, Through Whole Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 842508.	1.8	4
3	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
4	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
5	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
6	Assessment of the Feasibility of a Future Integrated Larger-Scale Epidemiological Study to Evaluate Health Risks of Air Pollution Episodes in Children. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8531.	1.2	1
7	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
8	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
9	Case Report: Multidrug Resistant <i>Raoultella ornithinolytica</i> in a Septicemic Calf. <i>Frontiers in Veterinary Science</i> , 2021, 8, 631716.	0.9	5
10	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
11	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
12	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a <i>Salmonella</i> food-borne outbreak. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
13	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical <i>Mycobacterium tuberculosis</i> 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
14	Development of a multiplex mass spectrometry method for simultaneous quantification of urinary proteins related to respiratory health. <i>Scientific Reports</i> , 2021, 11, 10107.	1.6	7
15	Epidemiology of the <i>Staphylococcus aureus</i> CA-MRSA USA300 in Belgium. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 2335-2347.	1.3	8
16	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
17	Coverage of the national surveillance system for human <i>Salmonella</i> infections, Belgium, 2016-2020. <i>PLoS ONE</i> , 2021, 16, e0256820.	1.1	4
18	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

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19	Whole-genome-based phylogenomic analysis of the Belgian 2016–2017 influenza A(H3N2) outbreak season allows improved surveillance. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
20	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
21	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
22	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
23	Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. <i>Frontiers in Microbiology</i> , 2021, 12, 750278.	1.5	7
24	Strategy to Develop and Evaluate a Multiplex RT-ddPCR in Response to SARS-CoV-2 Genomic Evolution. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1937-1949.	1.0	9
25	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
26	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
27	Whole-Genome Sequencing-Based Antimicrobial Resistance Characterization and Phylogenomic Investigation of 19 Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Positive <i>Escherichia coli</i> Strains Collected From Hospital Patients in Benin in 2019. <i>Frontiers in Microbiology</i> , 2021, 12, 752883.	1.5	8
28	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
29	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
30	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
31	A multiplex oligonucleotide ligation-PCR method for the genosertyping of common <i>Salmonella</i> using a liquid bead suspension assay. <i>Food Microbiology</i> , 2020, 87, 103394.	2.1	6
32	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
33	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
34	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
35	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
36	Gender-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

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37	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
38	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
39	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
40	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
41	Identification of an unauthorized genetically modified bacteria in food enzyme through whole-genome sequencing. <i>Scientific Reports</i> , 2020, 10, 7094.	1.6	14
42	Screening strategy targeting the presence of food enzyme-producing fungi in food enzyme preparations. <i>Food Control</i> , 2020, 117, 107295.	2.8	6
43	A genosotyping system for a fast and objective identification of <i>Salmonella</i> serotypes commonly isolated from poultry and pork food sectors in Belgium. <i>Food Microbiology</i> , 2020, 91, 103534.	2.1	12
44	Isolation of Drug-Resistant <i>Gallibacterium anatis</i> from Calves with Unresponsive Bronchopneumonia, Belgium. <i>Emerging Infectious Diseases</i> , 2020, 26, .	2.0	18
45	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
46	First detection of a plasmid located carbapenem resistant blaVIM-1 gene in <i>E. coli</i> isolated from meat products at retail in Belgium in 2015. <i>International Journal of Food Microbiology</i> , 2020, 324, 108624.	2.1	16
47	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
48	Whole-Genome Sequencing of Multidrug-Resistant <i>Escherichia coli</i> Strains Harboring the mcr-1 Gene, Isolated from Seawater of the Algiers Coast in Algeria. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
49	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
50	Development of a real-time PCR method for the genosotyping of <i>Salmonella</i> Paratyphi B variant Java. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4987-4996.	1.7	7
51	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
52	Shifting national surveillance of <i>Shigella</i> infections toward genosotyping by the development of a tailored Luminex assay and NGS workflow. <i>MicrobiologyOpen</i> , 2019, 8, e00807.	1.2	8
53	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: <i>Neisseria meningitidis</i> as a Proof of Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 2897.	1.5	8
54	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

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55	Whole-Genome Sequencing of Six Strains of <i>Salmonella enterica</i> Isolated from Imported Meat in Algeria. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
56	CHAPTER 8. GMO Detection and Identification Using Next-generation Sequencing. <i>Food Chemistry, Function and Analysis</i> , 2019, , 96-106.	0.1	3
57	A novel genotoxin-specific qPCR array based on the metabolically competent human HepaRG <sup>®</sup> 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
58	Detection and discrimination of five <i>E. coli</i> pathotypes using a combinatory SYBR <sup>®</sup> Green qPCR screening system. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3267-3285.	1.7	17
59	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
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	The genetic structure of the Belgian population. <i>Human Genomics</i> , 2018, 12, 6.	1.4	7
62	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
63	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
64	Molecular Subtyping of <i>Salmonella</i> Typhimurium with Multiplex Oligonucleotide Ligation-PCR (MOL-PCR). <i>Methods in Molecular Biology</i> , 2017, 1616, 39-69.	0.4	1
65	Discrimination of three genetically close <i>Aspergillus</i> species by using high resolution melting analysis applied to indoor air as case study. <i>BMC Microbiology</i> , 2017, 17, 84.	1.3	11
66	Development and performance assessment of a luminex xMAP <sup>®</sup> direct hybridization assay for the detection and identification of indoor air fungal contamination. <i>PLoS ONE</i> , 2017, 12, e0173390.	1.1	5
67	Development of a Luminex xTAG <sup>®</sup> assay for cost-effective multiplex detection of $\beta$ -lactamases in Gram-negative bacteria. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2479-2483.	1.3	17
68	Optimized MOL-PCR for Characterization of Microbial Pathogens. <i>Current Protocols in Cytometry</i> , 2016, 75, 13.15.1-13.15.15.	3.7	0
69	FabR regulates <i>Salmonella</i> biofilm formation via its direct target FabB. <i>BMC Genomics</i> , 2016, 17, 253.	1.2	9
70	A molecular approach for the rapid, selective and sensitive detection of <i>Exophiala jeanselmei</i> in environmental samples: development and performance assessment of a real-time PCR assay. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1377-1392.	1.7	11
71	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. <i>Food Chemistry</i> , 2016, 192, 788-798.	4.2	47
72	Experimental approaches to identify small RNA s 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

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73	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
74	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
75	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
76	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
77	A multiplex oligonucleotide ligation-PCR as a complementary tool for subtyping of <i>Salmonella</i> Typhimurium. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8137-8149.	1.7	12
78	Development and performance assessment of a qualitative SYBR <sup>®</sup> green real-time PCR assay for the detection of <i>Aspergillus versicolor</i> in indoor air. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7267-7282.	1.7	15
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	<i>Salmonella</i> biofilms: An overview on occurrence, structure, regulation and eradication. <i>Food Research International</i> , 2012, 45, 502-531.	2.9	406
87	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
88	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
89	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
90	Identification and characterization of 4-[4-(3-phenyl-2-propen-1-yl)-1-piperazinyl]-5H-pyrimido[5,4-b]indole derivatives as <i>Salmonella</i> biofilm inhibitors. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 65, 390-394.	2.7	8

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91	A combined approach to study the protein glycosylation potential of <i>Lactobacillus rhamnosus</i> GG (LGG). <i>Communications in Agricultural and Applied Biological Sciences</i> , 2012, 77, 15-9.	0.0	1
92	Structure-Activity Relationship of 4(5)-Aryl-2-amino-1 <i>H</i> -imidazoles, <i>N</i> -1-Substituted 2-Aminoimidazoles and Imidazo[1,2- <i>a</i> ]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
93	Gene expression analysis of monospecies <i>Salmonella</i> Typhimurium biofilms using Differential Fluorescence Induction. <i>Journal of Microbiological Methods</i> , 2011, 84, 467-478.	0.7	16
94	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
95	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
96	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella</i> Typhimurium LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
97	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
98	Structure-activity relationship of 2-hydroxy-2-aryl-2,3-dihydro-imidazo[1,2- <i>a</i> ]pyrimidinium salts and 2 <i>N</i> -substituted 4(5)-aryl-2-amino-1 <i>H</i> -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
99	Functional Characterization of a Mucus-Specific LPXTC Surface Adhesin from Probiotic <i>Lactobacillus rhamnosus</i> GG. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4465-4472.	1.4	90
100	Adaptation factors of the probiotic <i>Lactobacillus rhamnosus</i> GG. <i>Beneficial Microbes</i> , 2010, 1, 335-342.	1.0	28
101	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
102	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
103	Structure-activity relationship of brominated 3-alkyl-5-methylene-2(5 <i>H</i> )-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
104	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
105	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
106	Host interactions of probiotic bacterial surface molecules: comparison with commensals and pathogens. <i>Nature Reviews Microbiology</i> , 2010, 8, 171-184.	13.6	828
107	The AI-2-dependent regulator LsrR has a limited regulon in <i>Salmonella</i> Typhimurium. <i>Cell Research</i> , 2010, 20, 966-969.	5.7	8
108	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

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109	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
110	2D proteome analysis initiates new Insights on the SalmonellaTyphimurium LuxS protein. <i>BMC Microbiology</i> , 2009, 9, 198.	1.3	17
111	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
112	Stretching polysaccharides on live cells using single molecule force spectroscopy. <i>Nature Protocols</i> , 2009, 4, 939-946.	5.5	97
113	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
114	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
115	Detection, Localization, and Conformational Analysis of Single Polysaccharide Molecules on Live Bacteria. <i>ACS Nano</i> , 2008, 2, 1921-1929.	7.3	159
116	Genes and Molecules of Lactobacilli Supporting Probiotic Action. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 728-764.	2.9	782
117	A simple structured model for growth and AI-2 mediated cell-cell communication of Salmonella Typhimurium. , 2008, , .		0
118	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
119	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
120	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
121	Functional Analysis of <i>luxS</i> 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
122	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
123	Delineation of the <i>Salmonella enterica</i> Serovar Typhimurium <i>HilA</i> Regulon through Genome-Wide Location and Transcript Analysis. <i>Journal of Bacteriology</i> , 2007, 189, 4587-4596.	1.0	65
124	Synthesis of N-Acyl Homoserine Lactone Analogues Reveals Strong Activators of <i>SdiA</i> , the <i>Salmonella enterica</i> Serovar Typhimurium <i>LuxR</i> Homologue. <i>Applied and Environmental Microbiology</i> , 2007, 73, 535-544.	1.4	63
125	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
126	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



#	ARTICLE	IF	CITATIONS
127	Adherence factors of <i>Lactobacillus</i> in the human gastrointestinal tract. FEMS Microbiology Letters, 2007, 276, 140-148.	0.7	169
128	Let LuxS speak up in AI-2 signaling. Trends in Microbiology, 2006, 14, 114-119.	3.5	152
129	Strong antimicrobial activity of <i>Lactobacillus rhamnosus</i> GG against <i>Salmonella typhimurium</i> due to accumulation of lactic acid. FEMS Microbiology Letters, 2006, 259, 89-96.	0.7	257
130	Integration of omics data: how well does it work for bacteria?. Molecular Microbiology, 2006, 62, 1239-1250.	1.2	49
131	More robust detection of motifs in coexpressed genes by using phylogenetic information. BMC Bioinformatics, 2006, 7, 160.	1.2	16
132	Flow Cytometric Testing of Green Fluorescent Protein-Tagged <i>Lactobacillus rhamnosus</i> GG for Response to Defensins. Applied and Environmental Microbiology, 2006, 72, 4923-4930.	1.4	48
133	IDENTIFYING NEW DRUG TARGETS TO COMBAT PATHOGENIC INFECTIONS: AN INTERDISCIPLINARY APPROACH. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 121-126.	0.4	0
134	Influence of genetic background on transformation and expression of Green Fluorescent Protein in <i>Actinobacillus actinomycetemcomitans</i> . Oral Microbiology and Immunology, 2005, 20, 274-281.	2.8	3
135	Comparison of the PhoPQ Regulon in <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> . Journal of Molecular Evolution, 2005, 60, 462-474.	0.8	106
136	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> . Journal of Biological Chemistry, 2005, 280, 19563-19568.	1.6	127
137	Microarray Analysis and Motif Detection Reveal New Targets of the <i>Salmonella enterica</i> Serovar Typhimurium HilA Regulatory Protein, Including hilA Itself. Journal of Bacteriology, 2005, 187, 4381-4391.	1.0	50
138	Synthesis of Vinyl 1,2-Diketones.. ChemInform, 2004, 35, no.	0.1	0
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140	In silico identification and experimental validation of PmrAB targets in <i>Salmonella typhimurium</i> by regulatory motif detection. Genome Biology, 2004, 5, R9.	13.9	53
141	Genome-specific higher-order background models to improve motif detection. Trends in Microbiology, 2003, 11, 61-66.	3.5	29