

Hendrik C Den Bakker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4352288/publications.pdf>

Version: 2024-02-01

74
papers

4,730
citations

81900

39
h-index

102487

66
g-index

76
all docs

76
docs citations

76
times ranked

4839
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Listeria monocytogenes</i> lineages: Genomics, evolution, ecology, and phenotypic characteristics. <i>International Journal of Medical Microbiology</i> , 2011, 301, 79-96.	3.6	628
2	<i>Listeria marthii</i> sp. nov., isolated from the natural environment, Finger Lakes National Forest. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1280-1288.	1.7	185
3	SeqSero2: Rapid and Improved <i>Salmonella</i> Serotype Determination Using Whole-Genome Sequencing Data. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	185
4	Comparative genomics of the bacterial genus <i>Listeria</i> : Genome evolution is characterized by limited gene acquisition and limited gene loss. <i>BMC Genomics</i> , 2010, 11, 688.	2.8	174
5	Identification and Characterization of Psychrotolerant Sporeformers Associated with Fluid Milk Production and Processing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1853-1864.	3.1	160
6	Rapid Whole-Genome Sequencing for Surveillance of <i>Salmonella enterica</i> Serovar Enteritidis. <i>Emerging Infectious Diseases</i> , 2014, 20, 1306-1314.	4.3	155
7	Genomic Epidemiology: Whole-Genome-Sequencingâ€‘Powered Surveillance and Outbreak Investigation of Foodborne Bacterial Pathogens. <i>Annual Review of Food Science and Technology</i> , 2016, 7, 353-374.	9.9	152
8	Mashtree: a rapid comparison of whole genome sequence files. <i>Journal of Open Source Software</i> , 2019, 4, 1762.	4.6	138
9	Genome sequencing reveals diversification of virulence factor content and possible host adaptation in distinct subpopulations of <i>Salmonella enterica</i> . <i>BMC Genomics</i> , 2011, 12, 425.	2.8	133
10	Whole-Genome Sequencing Allows for Improved Identification of Persistent <i>Listeria monocytogenes</i> in Food-Associated Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6024-6037.	3.1	127
11	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	17.5	123
12	Dissemination of the <i>mcr-1</i> colistin resistance gene. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 144-145.	9.1	119
13	<i>Listeria floridensis</i> sp. nov., <i>Listeria aquatica</i> sp. nov., <i>Listeria cornellensis</i> sp. nov., <i>Listeria riparia</i> sp. nov. and <i>Listeria grandensis</i> sp. nov., from agricultural and natural environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 1882-1889.	1.7	114
14	A Whole-Genome Single Nucleotide Polymorphism-Based Approach To Trace and Identify Outbreaks Linked to a Common <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Montevideo Pulsed-Field Gel Electrophoresis Type. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8648-8655.	3.1	100
15	<i>Listeria booriae</i> sp. nov. and <i>Listeria newyorkensis</i> sp. nov., from food processing environments in the USA. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 286-292.	1.7	100
16	Lineage specific recombination rates and microevolution in <i>Listeria monocytogenes</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 277.	3.2	96
17	A Population Genetics-Based and Phylogenetic Approach to Understanding the Evolution of Virulence in the Genus <i>Listeria</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 6085-6100.	3.1	94
18	Comparison of Typing Methods with a New Procedure Based on Sequence Characterization for <i>Salmonella</i> Serovar Prediction. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1786-1797.	3.9	92

#	ARTICLE	IF	CITATIONS
19	Genomic Epidemiology of <i>Salmonella enterica</i> Serotype Enteritidis based on Population Structure of Prevalent Lineages. <i>Emerging Infectious Diseases</i> , 2014, 20, 1481-1489.	4.3	87
20	Genomic characterization provides new insight into <i>Salmonella</i> phage diversity. <i>BMC Genomics</i> , 2013, 14, 481.	2.8	80
21	Selection and Characterization of Phage-Resistant Mutant Strains of <i>Listeria monocytogenes</i> Reveal Host Genes Linked to Phage Adsorption. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4295-4305.	3.1	78
22	Salt Stress Phenotypes in <i>Listeria monocytogenes</i> Vary by Genetic Lineage and Temperature. <i>Foodborne Pathogens and Disease</i> , 2010, 7, 1537-1549.	1.8	75
23	Zoonotic Source Attribution of <i>Salmonella enterica</i> Serotype Typhimurium Using Genomic Surveillance Data, United States. <i>Emerging Infectious Diseases</i> , 2019, 25, 82-91.	4.3	75
24	Evolution and host specificity in the ectomycorrhizal genus <i>Leccinum</i> . <i>New Phytologist</i> , 2004, 163, 201-215.	7.3	74
25	Precision food safety: A systems approach to food safety facilitated by genomics tools. <i>TrAC - Trends in Analytical Chemistry</i> , 2017, 96, 52-61.	11.4	74
26	Comparative Genomic and Morphological Analyses of <i>Listeria</i> Phages Isolated from Farm Environments. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4616-4625.	3.1	72
27	Clonality and Recombination in the Life History of an Asexual Arbuscular Mycorrhizal Fungus. <i>Molecular Biology and Evolution</i> , 2010, 27, 2474-2486.	8.9	67
28	Carbapenem-Resistant Bacteria Recovered from Faeces of Dairy Cattle in the High Plains Region of the USA. <i>PLoS ONE</i> , 2016, 11, e0147363.	2.5	64
29	Evolutionary Dynamics of the Accessory Genome of <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e67511.	2.5	63
30	Identification and Characterization of Novel <i>Salmonella</i> Mobile Elements Involved in the Dissemination of Genes Linked to Virulence and Transmission. <i>PLoS ONE</i> , 2012, 7, e41247.	2.5	61
31	Transcriptomic Analysis of the Adaptation of <i>Listeria monocytogenes</i> to Growth on Vacuum-Packed Cold Smoked Salmon. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6812-6824.	3.1	61
32	Equine Stomachs Harbor an Abundant and Diverse Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2522-2532.	3.1	60
33	Determination of Evolutionary Relationships of Outbreak-Associated <i>Listeria monocytogenes</i> Strains of Serotypes 1/2a and 1/2b by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 928-938.	3.1	58
34	Silage Collected from Dairy Farms Harbors an Abundance of <i>Listeria</i> Phages with Considerable Host Range and Genome Size Diversity. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8666-8675.	3.1	47
35	Genome sequencing identifies <i>Listeria fleischmannii</i> subsp. <i>coloradonensis</i> subsp. nov., isolated from a ranch. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3257-3268.	1.7	46
36	Multilocus Sequence Typing of Outbreak-Associated <i>Listeria monocytogenes</i> Isolates to Identify Epidemic Clones. <i>Foodborne Pathogens and Disease</i> , 2010, 7, 257-265.	1.8	43

#	ARTICLE	IF	CITATIONS
37	FSL J1-208, a Virulent Uncommon Phylogenetic Lineage IV <i>Listeria monocytogenes</i> Strain with a Small Chromosome Size and a Putative Virulence Plasmid Carrying Internalin-Like Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1876-1889.	3.1	43
38	<i>Salmonella</i> bacteriophage diversity reflects host diversity on dairy farms. <i>Food Microbiology</i> , 2013, 36, 275-285.	4.2	43
39	Characterization of the cytolethal distending toxin (typhoid toxin) in non-typhoidal <i>Salmonella</i> serovars. <i>Gut Pathogens</i> , 2015, 7, 19.	3.4	43
40	Listeriosis Outbreak in Dairy Cattle Caused by an Unusual <i>Listeria Monocytogenes</i> Serotype 4b Strain. <i>Journal of Veterinary Diagnostic Investigation</i> , 2011, 23, 155-158.	1.1	41
41	<i>Listeria monocytogenes</i> and hemolytic <i>Listeria innocua</i> in poultry. <i>Poultry Science</i> , 2012, 91, 2158-2163.	3.4	33
42	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	31
43	Molecular evolution patterns reveal life history features of mycoplasma-related endobacteria associated with arbuscular mycorrhizal fungi. <i>Molecular Ecology</i> , 2015, 24, 3485-3500.	3.9	29
44	An ITS phylogeny of <i>Leccinum</i> and an analysis of the evolution of minisatellite-like sequences within ITS1. <i>Mycologia</i> , 2004, 96, 102-118.	1.9	28
45	Genomic comparison of sporeforming bacilli isolated from milk. <i>BMC Genomics</i> , 2014, 15, 26.	2.8	27
46	CRISPR-based assay for the molecular identification of highly prevalent <i>Salmonella</i> serotypes. <i>Food Microbiology</i> , 2018, 71, 8-16.	4.2	27
47	Targeted Amplicon Sequencing for Single-Nucleotide-Polymorphism Genotyping of Attaching and Effacing <i>Escherichia coli</i> O26:H11 Cattle Strains via a High-Throughput Library Preparation Technique. <i>Applied and Environmental Microbiology</i> , 2016, 82, 640-649.	3.1	26
48	RIBOSOMAL RNA GENE DIVERSITY, EFFECTIVE POPULATION SIZE, AND EVOLUTIONARY LONGEVITY IN ASEXUAL GLOMEROMYCOTA. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 207-224.	2.3	24
49	Genomic Diversity of <i>Listeria monocytogenes</i> Isolated from Clinical and Non-Clinical Samples in Chile. <i>Genes</i> , 2018, 9, 396.	2.4	24
50	Genomics tools in microbial food safety. <i>Current Opinion in Food Science</i> , 2015, 4, 105-110.	8.0	22
51	Pre-harvest internalization and surface survival of <i>Salmonella</i> and <i>Escherichia coli</i> O157:H7 sprayed onto different lettuce cultivars under field and growth chamber conditions. <i>International Journal of Food Microbiology</i> , 2019, 291, 197-204.	4.7	22
52	<i>Listeria monocytogenes</i> is prevalent in retail produce environments but <i>Salmonella enterica</i> is rare. <i>Food Control</i> , 2020, 113, 107173.	5.5	21
53	A phylogenetic study of <i>Boletus</i> section <i>Boletus</i> in Europe. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2008, 20, 1-7.	4.4	20
54	Genomic characterization of <i>Salmonella</i> Cerro ST367, an emerging <i>Salmonella</i> subtype in cattle in the United States. <i>BMC Genomics</i> , 2014, 15, 427.	2.8	19

#	ARTICLE	IF	CITATIONS
55	Population dynamics of enteric Salmonella in response to antimicrobial use in beef feedlot cattle. <i>Scientific Reports</i> , 2017, 7, 14310.	3.3	19
56	Morphological and molecular evidence supporting an arbutoid mycorrhizal relationship in the Costa Rican <i>Áramo</i> . <i>Mycorrhiza</i> , 2007, 17, 217-222.	2.8	15
57	Phylogeographic patterns in <i>Leccinum</i> sect. <i>Scabra</i> and the status of the arctic-alpine species <i>L. rotundifoliae</i> . <i>Mycological Research</i> , 2007, 111, 663-672.	2.5	14
58	<i>Salmonella enterica</i> and <i>Escherichia coli</i> in Wheat Flour: Detection and Serotyping by a Quasimetagenomic Approach Assisted by Magnetic Capture, Multiple-Displacement Amplification, and Real-Time Sequencing. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	13
59	An ITS Phylogeny of <i>Leccinum</i> and an Analysis of the Evolution of Minisatellite-like Sequences within ITS1. <i>Mycologia</i> , 2004, 96, 102.	1.9	12
60	Complete Genome Sequence of the Porcine Strain <i>Brachyspira pilosicoli</i> P43/6/78 ^T. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
61	Two Draft Genome Sequences of a New Serovar of <i>Salmonella enterica</i> , Serovar Lubbock. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
62	Quantitative dynamics of <i>Salmonella</i> and <i>E. coli</i> in feces of feedlot cattle treated with ceftiofur and chlortetracycline. <i>PLoS ONE</i> , 2019, 14, e0225697.	2.5	11
63	Survival of <i>Salmonella enterica</i> and <i>Escherichia coli</i> O157:H7 Sprayed onto the Foliage of Field-Grown Cabbage Plants. <i>Journal of Food Protection</i> , 2019, 82, 479-485.	1.7	8
64	An ITS phylogeny of <i>Leccinum</i> and an analysis of the evolution of minisatellite-like sequences within ITS1. <i>Mycologia</i> , 2004, 96, 102-18.	1.9	8
65	High-Resolution Genomic Comparisons within <i>Salmonella enterica</i> Serotypes Derived from Beef Feedlot Cattle: Parsing the Roles of Cattle Source, Pen, Animal, Sample Type, and Production Period. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0048521.	3.1	6
66	Phenotypic characterization and analysis of complete genomes of two distinct strains of the proposed species <i>L. swaminathanii</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	6
67	Molecular Source Tracking and Molecular Subtyping. , 2019, , 971-988.		3
68	Complete Genome Sequences of Three <i>Listeria monocytogenes</i> Bacteriophage Propagation Strains. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
69	Complete Genome Sequence of a Serotype 7 <i>Listeria monocytogenes</i> Strain, FSL R9-0915. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
70	SneakerNet: A modular quality assurance and quality check workflow for primary genomic and metagenomic read data. <i>Journal of Open Source Software</i> , 2021, 6, 2334.	4.6	1
71	Phylogeny of the <i>Bacillus altitudinis</i> Complex and Characterization of a Newly Isolated Strain with Antilisterial Activity. <i>Journal of Food Protection</i> , 2021, 84, 1321-1332.	1.7	1
72	Heat Inactivation of <i>Listeria monocytogenes</i> on Pecans, Macadamia Nuts, and Sunflower Seeds. <i>Microbiology Spectrum</i> , 2021, 9, e0113421.	3.0	1

#	ARTICLE	IF	CITATIONS
73	Draft Genome Sequences of Two <i>Lactobacillus johnsonii</i> and Three <i>Ligilactobacillus salivarius</i> Strains Isolated from Intestinal Microbiomes of Chickens. <i>Microbiology Resource Announcements</i> , 2022, 11, e0092521.	0.6	1
74	Sepia, a taxonomy oriented read classifier in Rust. <i>Journal of Open Source Software</i> , 2021, 6, 3839.	4.6	1