

Willem van Schaik

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

6,670
citations

71004

43
h-index

81351

76
g-index

110
all docs

110
docs citations

110
times ranked

8513
citing authors

#	ARTICLE	IF	CITATIONS
1	Alcaligenes faecalis metallo-β-lactamase in extensively drug-resistant Pseudomonas aeruginosa isolates. <i>Clinical Microbiology and Infection</i> , 2022, 28, 880.e1-880.e8.	2.8	18
2	Effects of early-life antibiotics on the developing infant gut microbiome and resistome: a randomized trial. <i>Nature Communications</i> , 2022, 13, 893.	5.8	95
3	Phenotypic and Genotypic Characterization of a Hypervirulent Carbapenem-Resistant <i>Klebsiella pneumoniae</i> ST17-KL38 Clinical Isolate Harboring the Carbapenemase IMP-4. <i>Microbiology Spectrum</i> , 2022, 10, e0213421.	1.2	15
4	Enterobacteriaceae and Bacteroidaceae provide resistance to travel-associated intestinal colonization by multi-drug resistant Escherichia coli. <i>Gut Microbes</i> , 2022, 14, 2060676.	4.3	11
5	Baas Beeking meets One Health. <i>Nature Microbiology</i> , 2022, 7, 482-483.	5.9	3
6	Antibiotic resistance in the commensal human gut microbiota. <i>Current Opinion in Microbiology</i> , 2022, 68, 102150.	2.3	32
7	GR13-type plasmids in Acinetobacter potentiate the accumulation and horizontal transfer of diverse accessory genes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
8	Acquisition of a genomic resistance island (AbGRI5) from global clone 2 through homologous recombination in a clinical Acinetobacter baumannii isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 65-69.	1.3	13
9	Transferable Acinetobacter baumannii plasmid pDETAB2 encodes OXA-58 and NDM-1 and represents a new class of antibiotic resistance plasmids. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1130-1134.	1.3	27
10	Harder, better, faster, stronger: Colistin resistance mechanisms in Escherichia coli. <i>PLoS Genetics</i> , 2021, 17, e1009262.	1.5	13
11	Emergence of carbapenem-resistant <i>Klebsiella pneumoniae</i> harbouring bla OXA-48-like genes in China. <i>Journal of Medical Microbiology</i> , 2021, 70, .	0.7	13
12	Metagenome-Wide Analysis of Rural and Urban Surface Waters and Sediments in Bangladesh Identifies Human Waste as a Driver of Antibiotic Resistance. <i>MSystems</i> , 2021, 6, e0013721.	1.7	12
13	Functional characterization of a gene cluster responsible for inositol catabolism associated with hospital-adapted isolates of <i>Enterococcus faecium</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	0
14	Spread of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in an Intensive Care Unit: A Whole-Genome Sequence-Based Prospective Observational Study. <i>Microbiology Spectrum</i> , 2021, 9, e0005821.	1.2	12
15	Temperature-Regulated IncX3 Plasmid Characteristics and the Role of Plasmid-Encoded H-NS in Thermoregulation. <i>Frontiers in Microbiology</i> , 2021, 12, 765492.	1.5	8
16	Topical or oral antibiotics for children with acute otitis media presenting with ear discharge: study protocol of a randomised controlled non-inferiority trial. <i>BMJ Open</i> , 2021, 11, e052128.	0.8	1
17	Tandem amplification of the vanM gene cluster drives vancomycin resistance in vancomycin-variable enterococci. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 283-291.	1.3	16
18	Increased risk of acquisition and transmission of ESBL-producing Enterobacteriaceae in malnourished children exposed to amoxicillin. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 709-717.	1.3	16

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19	Microevolution of acquired colistin resistance in Enterobacteriaceae from ICU patients receiving selective decontamination of the digestive tract. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3135-3143.	1.3	18
20	Evolution of Colistin Resistance in the <i>Klebsiella pneumoniae</i> Complex Follows Multiple Evolutionary Trajectories with Variable Effects on Fitness and Virulence Characteristics. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	12
21	Conditionally essential genes for survival during starvation in <i>Enterococcus faecium</i> E745. <i>BMC Genomics</i> , 2020, 21, 568.	1.2	12
22	Plasmids Shaped the Recent Emergence of the Major Nosocomial Pathogen <i>Enterococcus faecium</i> . <i>MBio</i> , 2020, 11, .	1.8	91
23	Nonclonal Emergence of Colistin Resistance Associated with Mutations in the BasRS Two-Component System in <i>Escherichia coli</i> Bloodstream Isolates. <i>MSphere</i> , 2020, 5, .	1.3	19
24	Horizontal transfer of antibiotic resistance genes in the human gut microbiome. <i>Current Opinion in Microbiology</i> , 2020, 53, 35-43.	2.3	191
25	A Pilot Integrative Analysis of Colonic Gene Expression, Gut Microbiota, and Immune Infiltration in Primary Sclerosing Cholangitis-Inflammatory Bowel Disease: Association of Disease With Bile Acid Pathways. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 935-947.	0.6	81
26	Cointegration as a mechanism for the evolution of a KPC-producing multidrug resistance plasmid in <i>Proteus mirabilis</i> . <i>Emerging Microbes and Infections</i> , 2020, 9, 1206-1218.	3.0	30
27	Gut Microbiota and Colonization Resistance against Bacterial Enteric Infection. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	2.9	272
28	Do we really understand how faecal microbiota transplantation works?. <i>EBioMedicine</i> , 2019, 42, 39.	2.7	1
29	CRISPR-Cas9-mediated genome editing in vancomycin-resistant <i>Enterococcus faecium</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	22
30	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	5.9	129
31	<i>Enterococcus faecium</i> genome dynamics during long-term asymptomatic patient gut colonization. <i>Microbial Genomics</i> , 2019, 5, .	1.0	18
32	Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients. <i>Microbial Genomics</i> , 2019, 5, .	1.0	59
33	OWE-014...Whole transcriptome shotgun sequencing reveals significant upregulation of colonic mucosal immune-mediated anti-microbial mechanisms in psc-uc. , 2018, , .		0
34	Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	72
35	Rapid resistome mapping using nanopore sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw1328.	6.5	62
36	Challenges and opportunities for whole-genome sequencing-based surveillance of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 108-120.	1.8	87

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37	The Two-Component System ChtRS Contributes to Chlorhexidine Tolerance in <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	33
38	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2017, 30, 1015-1063.	5.7	310
39	Characterization of <i>Enterococcus</i> Isolates Colonizing the Intestinal Tract of Intensive Care Unit Patients Receiving Selective Digestive Decontamination. <i>Frontiers in Microbiology</i> , 2017, 8, 1596.	1.5	18
40	Comparative gut microbiota and resistome profiling of intensive care patients receiving selective digestive tract decontamination and healthy subjects. <i>Microbiome</i> , 2017, 5, 88.	4.9	90
41	RNA-seq and Tn-seq reveal fitness determinants of vancomycin-resistant <i>Enterococcus faecium</i> during growth in human serum. <i>BMC Genomics</i> , 2017, 18, 893.	1.2	57
42	On the (im)possibility of reconstructing plasmids from whole-genome short-read sequencing data. <i>Microbial Genomics</i> , 2017, 3, e000128.	1.0	198
43	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. <i>Frontiers in Microbiology</i> , 2016, 7, 788.	1.5	248
44	Complement resistance mechanisms of <i>Klebsiella pneumoniae</i> . <i>Immunobiology</i> , 2016, 221, 1102-1109.	0.8	87
45	The N-terminal domain of the thermo-regulated surface protein PrpA of <i>Enterococcus faecium</i> binds to fibrinogen, fibronectin and platelets. <i>Scientific Reports</i> , 2016, 5, 18255.	1.6	12
46	Genomic Characterization of Colistin Heteroresistance in <i>Klebsiella pneumoniae</i> during a Nosocomial Outbreak. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6837-6843.	1.4	80
47	Genome-wide Screening Identifies Phosphotransferase System Permease BepA to Be Involved in <i>Enterococcus faecium</i> Endocarditis and Biofilm Formation. <i>Journal of Infectious Diseases</i> , 2016, 214, 189-195.	1.9	36
48	The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62.	0.8	13
49	Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. <i>Scientific Reports</i> , 2015, 5, 11981.	1.6	50
50	The human gut resistome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140087.	1.8	275
51	Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of <i>Enterococcus faecium</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3788-3797.	1.8	240
52	Investigating the mobilome in clinically important lineages of <i>Enterococcus faecium</i> and <i>Enterococcus faecalis</i> . <i>BMC Genomics</i> , 2015, 16, 282.	1.2	82
53	Deletions in a ribosomal protein-coding gene are associated with tigecycline resistance in <i>Enterococcus faecium</i> . <i>International Journal of Antimicrobial Agents</i> , 2015, 46, 572-575.	1.1	32
54	Loss of Antibiotic Tolerance in Sod-Deficient Mutants Is Dependent on the Energy Source and Arginine Catabolism in Enterococci. <i>Journal of Bacteriology</i> , 2015, 197, 3283-3293.	1.0	16

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55	Dissemination of Cephalosporin Resistance Genes between <i>Escherichia coli</i> Strains from Farm Animals and Humans by Specific Plasmid Lineages. <i>PLoS Genetics</i> , 2014, 10, e1004776.	1.5	276
56	Effects of selective digestive decontamination (SDD) on the gut resistome. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2215-2223.	1.3	90
57	Functional genomic analysis of bile salt resistance in <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2013, 14, 299.	1.2	29
58	Genomic transition of enterococci from gut commensals to leading causes of multidrug-resistant hospital infection in the antibiotic era. <i>Current Opinion in Microbiology</i> , 2013, 16, 10-16.	2.3	220
59	The cell wall architecture of <i>Enterococcus faecium</i> : from resistance to pathogenesis. <i>Future Microbiology</i> , 2013, 8, 993-1010.	1.0	33
60	Antibiotic resistant enterococci – Tales of a drug resistance gene trafficker. <i>International Journal of Medical Microbiology</i> , 2013, 303, 360-379.	1.5	139
61	Identification of a Genetic Determinant in Clinical <i>Enterococcus faecium</i> Strains That Contributes to Intestinal Colonization During Antibiotic Treatment. <i>Journal of Infectious Diseases</i> , 2013, 207, 1780-1786.	1.9	79
62	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in <i>Enterococcus faecium</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1524-1535.	1.1	87
63	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	1.8	336
64	Identification of CodY Targets in <i>Bacillus anthracis</i> by Genome-Wide In Vitro Binding Analysis. <i>Journal of Bacteriology</i> , 2013, 195, 1204-1213.	1.0	33
65	The <i>Enterococcus faecium</i> Enterococcal Biofilm Regulator, EbrB, Regulates the esp Operon and Is Implicated in Biofilm Formation and Intestinal Colonization. <i>PLoS ONE</i> , 2013, 8, e65224.	1.1	45
66	A LacI-Family Regulator Activates Maltodextrin Metabolism of <i>Enterococcus faecium</i> . <i>PLoS ONE</i> , 2013, 8, e72285.	1.1	8
67	Genome-Wide Identification of Ampicillin Resistance Determinants in <i>Enterococcus faecium</i> . <i>PLoS Genetics</i> , 2012, 8, e1002804.	1.5	83
68	Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12.	1.8	177
69	Hospital and Community Ampicillin-Resistant <i>Enterococcus faecium</i> Are Evolutionarily Closely Linked but Have Diversified through Niche Adaptation. <i>PLoS ONE</i> , 2012, 7, e30319.	1.1	45
70	A multiresistance megaplasmid pLG1 bearing a hylEfm genomic island in hospital <i>Enterococcus faecium</i> isolates. <i>International Journal of Medical Microbiology</i> , 2011, 301, 165-175.	1.5	66
71	A genetic element present on megaplasms allows <i>Enterococcus faecium</i> to use raffinose as carbon source. <i>Environmental Microbiology</i> , 2011, 13, 518-528.	1.8	48
72	The Recombinase IntA Is Required for Excision of esp -Containing ICE Efm1 in <i>Enterococcus faecium</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1003-1006.	1.0	22

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73	CodY regulation is required for full virulence and heme iron acquisition in <i>Bacillus anthracis</i> . FASEB Journal, 2011, 25, 4445-4456.	0.2	39
74	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen <i>Enterococcus faecium</i> and identification of a large transferable pathogenicity island. BMC Genomics, 2010, 11, 239.	1.2	190
75	Comparative analysis of transcriptional and physiological responses of <i>Bacillus cereus</i> to organic and inorganic acid shocks. International Journal of Food Microbiology, 2010, 137, 13-21.	2.1	45
76	Genome-based insights into the evolution of enterococci. Clinical Microbiology and Infection, 2010, 16, 527-532.	2.8	72
77	A novel hybrid kinase is essential for regulating the σ^B -mediated stress response of <i>Bacillus cereus</i> . Environmental Microbiology, 2010, 12, 730-745.	1.8	30
78	Differential PilA pilus assembly by a hospital-acquired and a community-derived <i>Enterococcus faecium</i> isolate. Microbiology (United Kingdom), 2010, 156, 2649-2659.	0.7	17
79	Genome-based insights into the evolution of enterococci.. Clinical Microbiology and Infection, 2010, , .	2.8	1
80	The Global Regulator CodY Regulates Toxin Gene Expression in <i>Bacillus anthracis</i> and Is Required for Full Virulence. Infection and Immunity, 2009, 77, 4437-4445.	1.0	81
81	LPxTG surface proteins of enterococci. Trends in Microbiology, 2009, 17, 423-430.	3.5	106
82	Transition of <i>Enterococcus faecium</i> from commensal organism to nosocomial pathogen. Future Microbiology, 2009, 4, 1125-1135.	1.0	151
83	Identification of a Novel Genomic Island Specific to Hospital-Acquired Clonal Complex 17 <i>Enterococcus faecium</i> Isolates. Applied and Environmental Microbiology, 2008, 74, 7094-7097.	1.4	41
84	Identification of the σ^B Regulon of <i>Bacillus cereus</i> and Conservation of σ^B -Regulated Genes in Low-GC-Content Gram-Positive Bacteria. Journal of Bacteriology, 2007, 189, 4384-4390.	1.0	53
85	The role of σ^B in the stress response of Gram-positive bacteria – targets for food preservation and safety. Current Opinion in Biotechnology, 2005, 16, 218-224.	3.3	161
86	Deletion of σ^B in <i>Bacillus cereus</i> affects spore properties. FEMS Microbiology Letters, 2005, 252, 169-173.	0.7	11
87	Deletion of the σ^B Gene in <i>Bacillus cereus</i> ATCC 14579 Leads to Hydrogen Peroxide Hyperresistance. Applied and Environmental Microbiology, 2005, 71, 6427-6430.	1.4	18
88	Analysis of the Role of RsbV, RsbW, and RsbY in Regulating σ^B Activity in <i>Bacillus cereus</i> . Journal of Bacteriology, 2005, 187, 5846-5851.	1.0	43
89	The Alternative Sigma Factor σ^B of <i>Bacillus cereus</i> : Response to Stress and Role in Heat Adaptation. Journal of Bacteriology, 2004, 186, 316-325.	1.0	72
90	Identification of σ^B -Dependent Genes in <i>Bacillus cereus</i> by Proteome and In Vitro Transcription Analysis. Journal of Bacteriology, 2004, 186, 4100-4109.	1.0	26

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91	Impact of genomics on microbial food safety. Trends in Biotechnology, 2004, 22, 653-660.	4.9	40
92	Progress in Food-related Research Focussing on Bacillus cereus. Microbes and Environments, 2004, 19, 265-269.	0.7	5
93	Identification of Proteins Involved in the Heat Stress Response of Bacillus cereus ATCC 14579. Applied and Environmental Microbiology, 2002, 68, 3486-3495.	1.4	117
94	Acid-Adapted Listeria monocytogenes Displays Enhanced Tolerance against the Lantibiotics Nisin and Lacticin 3147. Journal of Food Protection, 1999, 62, 536-540.	0.8	122