

Flavia Huygens

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,295
citations

218381

26
h-index

223531

46
g-index

53
all docs

53
docs citations

53
times ranked

3264
citing authors

#	ARTICLE	IF	CITATIONS
1	Decay of SARS-CoV-2 and surrogate murine hepatitis virus RNA in untreated wastewater to inform application in wastewater-based epidemiology. <i>Environmental Research</i> , 2020, 191, 110092.	3.7	285
2	Isolation of Nontuberculous Mycobacteria (NTM) from Household Water and Shower Aerosols in Patients with Pulmonary Disease Caused by NTM. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3006-3011.	1.8	179
3	Genetic Diversity among Community Methicillin-Resistant <i>Staphylococcus aureus</i> Strains Causing Outpatient Infections in Australia. <i>Journal of Clinical Microbiology</i> , 2004, 42, 4735-4743.	1.8	150
4	Use of a Single-Nucleotide Polymorphism Genotyping System To Demonstrate the Unique Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in Remote Aboriginal Communities. <i>Journal of Clinical Microbiology</i> , 2006, 44, 3720-3727.	1.8	113
5	High-Resolution DNA Melt Curve Analysis of the Clustered, Regularly Interspaced Short-Palindromic-Repeat Locus of <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3431-3436.	1.4	105
6	Factors associated with the isolation of Nontuberculous mycobacteria (NTM) from a large municipal water system in Brisbane, Australia. <i>BMC Microbiology</i> , 2013, 13, 89.	1.3	93
7	<i>Mycobacterium abscessus</i> isolated from municipal water - a potential source of human infection. <i>BMC Infectious Diseases</i> , 2013, 13, 241.	1.3	80
8	<i>Staphylococcus epidermidis</i> as a cause of bacteremia. <i>Future Microbiology</i> , 2015, 10, 1859-1879.	1.0	80
9	Incidence and risk factors for developing infection in patients presenting with uninfected diabetic foot ulcers. <i>PLoS ONE</i> , 2017, 12, e0177916.	1.1	79
10	<i>Staphylococcus aureus</i> Genotyping Using Novel Real-Time PCR Formats. <i>Journal of Clinical Microbiology</i> , 2006, 44, 3712-3719.	1.8	68
11	High-Resolution Melting Analysis of the <i>spa</i> Repeat Region of <i>Staphylococcus aureus</i> . <i>Clinical Chemistry</i> , 2008, 54, 432-436.	1.5	68
12	Identification and interrogation of highly informative single nucleotide polymorphism sets defined by bacterial multilocus sequence typing databases. <i>Journal of Medical Microbiology</i> , 2004, 53, 35-45.	0.7	67
13	Phylogenetically Distinct <i>Staphylococcus aureus</i> Lineage Prevalent among Indigenous Communities in Northern Australia. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2295-2300.	1.8	67
14	Antimicrobial and Immunomodulatory Surface-Functionalized Electrospun Membranes for Bone Regeneration. <i>Advanced Healthcare Materials</i> , 2017, 6, 1601345.	3.9	66
15	Methicillin-resistant <i>Staphylococcus aureus</i> genotyping using a small set of polymorphisms. <i>Journal of Medical Microbiology</i> , 2006, 55, 43-51.	0.7	63
16	A role for the endometrial microbiome in dysfunctional menstrual bleeding. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 933-943.	0.7	60
17	Firmicutes dominate the bacterial taxa within sugar-cane processing plants. <i>Scientific Reports</i> , 2013, 3, 3107.	1.6	58
18	The fallopian tube microbiome: implications for reproductive health. <i>Oncotarget</i> , 2018, 9, 21541-21551.	0.8	40

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19	Carriage of methicillin-resistant <i>Staphylococcus aureus</i> in a Queensland Indigenous community. <i>Medical Journal of Australia</i> , 2006, 184, 556-559.	0.8	38
20	<i>Mycobacterium lentiflavum</i> in Drinking Water Supplies, Australia. <i>Emerging Infectious Diseases</i> , 2011, 17, 395-402.	2.0	35
21	<i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Genotyping by High-Resolution Melting Analysis of a <i>flaA</i> Fragment. <i>Applied and Environmental Microbiology</i> , 2010, 76, 493-499.	1.4	34
22	<i>bla</i> SHV Genes in <i>Klebsiella pneumoniae</i> : Different Allele Distributions Are Associated with Different Promoters within Individual Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 256-263.	1.4	33
23	Genotyping of <i>Campylobacter jejuni</i> using seven single-nucleotide polymorphisms in combination with <i>flaA</i> short variable region sequencing. <i>Journal of Medical Microbiology</i> , 2006, 55, 1061-1070.	0.7	31
24	Fingerprinting of <i>Campylobacter jejuni</i> by Using Resolution-Optimized Binary Gene Targets Derived from Comparative Genome Hybridization Studies. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7793-7803.	1.4	30
25	The impact of flood and post-flood cleaning on airborne microbiological and particle contamination in residential houses. <i>Environment International</i> , 2014, 69, 9-17.	4.8	30
26	GABA receptor α -subunit proteins in human chronic alcoholics. <i>Journal of Neurochemistry</i> , 2001, 78, 424-434.	2.1	27
27	Strain variation amongst clinical and potable water isolates of <i>M. kansasii</i> using automated repetitive unit PCR. <i>International Journal of Medical Microbiology</i> , 2014, 304, 484-489.	1.5	26
28	Computer-aided identification of polymorphism sets diagnostic for groups of bacterial and viral genetic variants. <i>BMC Bioinformatics</i> , 2007, 8, 278.	1.2	23
29	Systematic Derivation of Marker Sets for Staphylococcal Cassette Chromosome <i>mec</i> Typing. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 2954-2964.	1.4	22
30	Highly Discriminatory Single-Nucleotide Polymorphism Interrogation of <i>Escherichia coli</i> by Use of Allele-Specific Real-Time PCR and eBURST Analysis. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4337-4345.	1.4	21
31	Replacement of healthcare-associated MRSA by community-associated MRSA in Queensland: Confirmation by genotyping. <i>Journal of Infection</i> , 2013, 67, 439-447.	1.7	21
32	Pan-proteomics, a concept for unifying quantitative proteome measurements when comparing closely-related bacterial strains. <i>Expert Review of Proteomics</i> , 2016, 13, 355-365.	1.3	20
33	Assignment of <i>Streptococcus agalactiae</i> isolates to clonal complexes using a small set of single nucleotide polymorphisms. <i>BMC Microbiology</i> , 2008, 8, 140.	1.3	18
34	SNP diversity of <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> in a South East Queensland waterway, Australia, and associated antibiotic resistance gene profiles. <i>BMC Microbiology</i> , 2011, 11, 201.	1.3	18
35	<i>mecA</i> Locus Diversity in Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates in Brisbane, Australia, and the Development of a Novel Diagnostic Procedure for the Western Samoan Phage Pattern Clone. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1947-1955.	1.8	17
36	Genotyping of Methicillin-Resistant <i>Staphylococcus aureus</i> by Assaying for the Presence of Variable Elements Associated with <i>mecA</i> . <i>Journal of Clinical Microbiology</i> , 2002, 40, 3093-3097.	1.8	14

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37	CRISPR Diversity in <i>E. coli</i> Isolates from Australian Animals, Humans and Environmental Waters. <i>PLoS ONE</i> , 2015, 10, e0124090.	1.1	14
38	Culture-independent detection of chlorhexidine resistance genes <i>qacA/B</i> and <i>smr</i> in bacterial DNA recovered from body sites treated with chlorhexidine-containing dressings. <i>Journal of Medical Microbiology</i> , 2017, 66, 447-453.	0.7	14
39	Characterisation of chicken <i>Campylobacter jejuni</i> isolates using resolution optimised single nucleotide polymorphisms and binary gene markers. <i>International Journal of Food Microbiology</i> , 2008, 128, 304-308.	2.1	13
40	Proteomic and Bioinformatics Tools to Understand Virulence Mechanisms in <i>Staphylococcus aureus</i> . <i>Current Proteomics</i> , 2012, 9, 2-8.	0.1	13
41	Antimicrobial Activities of Seven Novel Tetramethylpiperidine-Substituted Phenazines against Multiple-Drug-Resistant Gram-Positive Bacteria. <i>Chemotherapy</i> , 2005, 51, 263-267.	0.8	9
42	Fallopian tube microbiota: evidence beyond DNA. <i>Future Microbiology</i> , 2018, 13, 1355-1361.	1.0	9
43	Genotyping <i>Streptococcus pneumoniae</i> . <i>Future Microbiology</i> , 2015, 10, 653-664.	1.0	8
44	Limitations of 16S rRNA Gene Sequencing to Characterize <i>Lactobacillus</i> Species in the Upper Genital Tract. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 641921.	1.8	7
45	Typing early Australian healthcare-associated MRSA: confirmation of major clones and emergence of ST1-MRSA-IV and novel ST2249-MRSA-III. <i>Pathology</i> , 2013, 45, 492-494.	0.3	6
46	Molecular Prediction of the O157:H-Negative Phenotype Prevalent in Australian Shiga Toxin-Producing <i>Escherichia coli</i> Cases Improves Concordance of In Silico Serotyping with Phenotypic Motility. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	5
47	Human-Specific <i>E. coli</i> Single Nucleotide Polymorphism (SNP) Genotypes Detected in a South East Queensland Waterway, Australia. <i>Environmental Science & Technology</i> , 2011, 45, 10331-10336.	4.6	4
48	<i>Pseudomonas aeruginosa</i> Trent and zinc homeostasis. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	4
49	Antimicrobial responses of peripheral and central nervous system glia against <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2021, 11, 10722.	1.6	4
50	Core and Accessory Genome Comparison of Australian and International Strains of O157 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 566415.	1.5	3
51	Modified MLVA for Genotyping Queensland Invasive <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0121870.	1.1	2
52	Signature-based clustering for analysis of the wound microbiome. , 2017, , .		1