Wiep Klaas Smits

List of Publications by Year
in descending order

61 papers	4,205 citations	201674 27 h-index	128289 60 g-index
76 all docs	76 docs citations	76 times ranked	4642 citing authors

#	Article	IF	Citations
1	Plasmids of Clostridioides difficile. Current Opinion in Microbiology, 2022, 65, 87-94.	5.1	8
2	Clostridioides difficile Phosphoproteomics Shows an Expansion of Phosphorylated Proteins in Stationary Growth Phase. MSphere, 2022, 7, e0091121.	2.9	8
3	Practical observations on the use of fluorescent reporter systems in Clostridioides difficile. Antonie Van Leeuwenhoek, 2022, 115, 297-323.	1.7	6
4	New insights into the type A glycan modification of Clostridioides difficile flagellar protein flagellin C by phosphoproteomics analysis. Journal of Biological Chemistry, 2022, 298, 101622.	3.4	4
5	Comparison of Whole-Genome Sequence-Based Methods and PCR Ribotyping for Subtyping of Clostridioides difficile. Journal of Clinical Microbiology, 2022, 60, JCM0173721.	3.9	22
6	Distinct evolution of colistin resistance associated with experimental resistance evolution models in Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2021, 76, 533-535.	3.0	6
7	Cyclodextrin/Adamantane-Mediated Targeting of Inoculated Bacteria in Mice. Bioconjugate Chemistry, 2021, 32, 607-614.	3.6	14
8	Haem is crucial for medium-dependent metronidazole resistance in clinical isolates of <i>Clostridioides difficile</i>. Journal of Antimicrobial Chemotherapy, 2021, 76, 1731-1740.	3.0	34
9	Fecal Microbiota Transplantation Influences Procarcinogenic Escherichia coli in Recipient Recurrent Clostridioides difficile Patients. Gastroenterology, 2021, 161, 1218-1228.e5.	1.3	18
10	Host Immune Responses to Clostridioides difficile: Toxins and Beyond. Frontiers in Microbiology, 2021, 12, 804949.	3.5	19
11	Identification of the Unwinding Region in the Clostridioides difficile Chromosomal Origin of Replication. Frontiers in Microbiology, 2020, 11, 581401.	3.5	1
12	The C-Terminal Domain of Clostridioides difficile TcdC Is Exposed on the Bacterial Cell Surface. Journal of Bacteriology, 2020, 202, .	2.2	9
13	Plasmid-mediated metronidazole resistance in Clostridioides difficile. Nature Communications, 2020, 11, 598.	12.8	79
14	Redefining the Clostridioides difficile Ïƒ ^B Regulon: Ïƒ ^B Activates Genes Involved in Detoxifying Radicals That Can Result from the Exposure to Antimicrobials and Hydrogen Peroxide. MSphere, 2020, 5, .	2.9	15
15	Fluorescent imaging of bacterial infections and recent advances made with multimodal radiopharmaceuticals. Clinical and Translational Imaging, 2019, 7, 125-138.	2.1	22
16	#EUROmicroMOOC: using Twitter to share trends in Microbiology worldwide. FEMS Microbiology Letters, 2019, 366, .	1.8	7
17	Microbial evolutionary medicine: from theory to clinical practice. Lancet Infectious Diseases, The, 2019, 19, e273-e283.	9.1	11
18	Multimodal Tracking of Controlled <i>Staphylococcus aureus</i> Infections in Mice. ACS Infectious Diseases, 2019, 5, 1160-1168.	3.8	13

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19	Genome Location Dictates the Transcriptional Response to PolC Inhibition in <i>Clostridium difficile</i>. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	15
20	The Bacterial Chromatin Protein HupA Can Remodel DNA and Associates with the Nucleoid in Clostridium difficile. Journal of Molecular Biology, 2019, 431, 653-672.	4.2	28
21	An in silico survey of Clostridioides difficile extrachromosomal elements. Microbial Genomics, 2019, 5, .	2.0	6
22	A helicase-containing module defines a family of pCD630-like plasmids in Clostridium difficile. Anaerobe, 2018, 49, 78-84.	2.1	13
23	Characterization of the virulence of a non-RT027, non-RT078 and binary toxin-positive <i>Clostridium difficile</i> strain associated with severe diarrhea. Emerging Microbes and Infections, 2018, 7, 1-11.	6.5	17
24	Proteomic identification of Axc, a novel beta-lactamase with carbapenemase activity in a meropenem-resistant clinical isolate of Achromobacter xylosoxidans. Scientific Reports, 2018, 8, 8181.	3.3	10
25	Mechanistic Insights in the Success of Fecal Microbiota Transplants for the Treatment of Clostridium difficile Infections. Frontiers in Microbiology, 2018, 9, 1242.	3.5	69
26	The evolving epidemic of Clostridium difficile 630. Anaerobe, 2018, 53, 2-4.	2.1	10
27	DNA replication proteins as potential targets for antimicrobials in drug-resistant bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw548.	3.0	58
28	SNP-ing out the differences: Investigating differences between <i>Clostridium difficile</i> lab strains. Virulence, 2017, 8, 613-617.	4.4	3
29	Primase is required for helicase activity and helicase alters the specificity of primase in the enteropathogen <i>Clostridium difficile</i>. Open Biology, 2016, 6, 160272.	3.6	14
30	Clostridium difficile infection. Nature Reviews Disease Primers, 2016, 2, 16020.	30.5	588
31	Interspecies Interactions between Clostridium difficile and Candida albicans. MSphere, 2016, 1, .	2.9	74
32	Clostridium difficile infection. Nature Reviews Disease Primers, 2016, 2, 16021.	30.5	3
33	The Signal Sequence of the Abundant Extracellular Metalloprotease PPEP-1 Can Be Used to Secrete Synthetic Reporter Proteins in <i>Clostridium difficile</i>. ACS Synthetic Biology, 2016, 5, 1376-1382.	3.8	34
34	Complete genome sequence of BS49 and draft genome sequence of BS34A, Bacillus subtilis strains carrying Tn916. FEMS Microbiology Letters, 2015, 362, 1-4.	1.8	13
35	Complete genome sequence of the Clostridium difficile laboratory strain 630Î”erm reveals differences from strain 630, including translocation of the mobile element CTn5. BMC Genomics, 2015, 16, 31.	2.8	76
36	Functional genomics reveals that Clostridium difficileSpo0A coordinates sporulation, virulence and metabolism. BMC Genomics, 2014, 15, 160.	2.8	145

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37	The HtrA-Like Protease CD3284 Modulates Virulence of Clostridium difficile. Infection and Immunity, 2014, 82, 4222-4232.	2.2	25
38	Hype or hypervirulence. Virulence, 2013, 4, 592-596.	4.4	41
39	Untwisting of the DNA helix stimulates the endonuclease activity of Bacillus subtilis Nth at AP sites. Nucleic Acids Research, 2012, 40, 739-750.	14.5	17
40	Chromosomal Replication Initiation Machinery of Low-G+C-Content Firmicutes. Journal of Bacteriology, 2012, 194, 5162-5170.	2.2	65
41	TcdC Does Not Significantly Repress Toxin Expression in Clostridium difficile 630Î”Erm. PLoS ONE, 2012, 7, e43247.	2.5	64
42	C. difficile 630Î”erm Spo0A Regulates Sporulation, but Does Not Contribute to Toxin Production, by Direct High-Affinity Binding to Target DNA. PLoS ONE, 2012, 7, e48608.	2.5	75
43	Primosomal Proteins DnaD and DnaB Are Recruited to Chromosomal Regions Bound by DnaA in<i>Bacillus subtilis</i>. Journal of Bacteriology, 2011, 193, 640-648.	2.2	42
44	Ordered association of helicase loader proteins with the <i>Bacillus subtilis</i> origin of replication <i>in vivo</i>. Molecular Microbiology, 2010, 75, 452-461.	2.5	63
45	When simple sequence comparison fails: the cryptic case of the shared domains of the bacterial replication initiation proteins DnaB and DnaD. Nucleic Acids Research, 2010, 38, 6930-6942.	14.5	26
46	The Transcriptional Regulator Rok Binds A+T-Rich DNA and Is Involved in Repression of a Mobile Genetic Element in Bacillus subtilis. PLoS Genetics, 2010, 6, e1001207.	3.5	90
47	Ubiquitous late competence genes in <i>Bacillus</i> species indicate the presence of functional DNA uptake machineries. Environmental Microbiology, 2009, 11, 1911-1922.	3.8	60
48	Phenotypic Variation and Bistable Switching in Bacteria. , 2008, , 339-365.		6
49	Bistability, Epigenetics, and Bet-Hedging in Bacteria. Annual Review of Microbiology, 2008, 62, 193-210.	7.3	907
50	Production and Secretion Stress Caused by Overexpression of Heterologous Î±-Amylase Leads to Inhibition of Sporulation and a Prolonged Motile Phase in Bacillus subtilis. Applied and Environmental Microbiology, 2007, 73, 5354-5362.	3.1	27
51	A Single, Specific Thymine Mutation in the ComK-Binding Site Severely Decreases Binding and Transcription Activation by the Competence Transcription Factor ComK of Bacillus subtilis. Journal of Bacteriology, 2007, 189, 4718-4728.	2.2	11
52	Antirepression as a second mechanism of transcriptional activation by a minor groove binding protein. Molecular Microbiology, 2007, 64, 368-381.	2.5	32
53	Temporal separation of distinct differentiation pathways by a dual specificity Rap-Phr system inBacillus subtilis. Molecular Microbiology, 2007, 65, 103-120.	2.5	73
54	Single cell analysis of gene expression patterns of competence development and initiation of sporulation in Bacillus subtilis grown on chemically defined media. Journal of Applied Microbiology, 2006, 101, 531-541.	3.1	66

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55	Phenotypic variation in bacteria: the role of feedback regulation. Nature Reviews Microbiology, 2006, 4, 259-271.	28.6	443
56	StrippingBacillus: ComK auto-stimulation is responsible for the bistable response in competence development. Molecular Microbiology, 2005, 56, 604-614.	2.5	178
57	The Rok Protein of Bacillus subtilis Represses Genes for Cell Surface and Extracellular Functions. Journal of Bacteriology, 2005, 187, 2010-2019.	2.2	74
58	Tricksy Business: Transcriptome Analysis Reveals the Involvement of Thioredoxin A in Redox Homeostasis, Oxidative Stress, Sulfur Metabolism, and Cellular Differentiation in Bacillus subtilis. Journal of Bacteriology, 2005, 187, 3921-3930.	2.2	36
59	Genome2D: a visualization tool for the rapid analysis of bacterial transcriptome data. Genome Biology, 2004, 5, R37.	9.6	93
60	Visualization of Differential Gene Expression by Improved Cyan Fluorescent Protein and Yellow Fluorescent Protein Production in Bacillus subtilis. Applied and Environmental Microbiology, 2004, 70, 6809-6815.	3.1	64
61	Improving the predictive value of the competence transcription factor (ComK) binding site in Bacillus subtilis using a genomic approach. Nucleic Acids Research, 2002, 30, 5517-5528.	14.5	147