Wiep Klaas Smits

List of Publications by Year in Descending Order

64 papers	3,051 citations	26 h-index	55 g-index
76 ext. papers	3,796 ext. citations	8.3 avg, IF	5.31 L-index

#	Paper	IF	Citations
64	Practical observations on the use of fluorescent reporter systems in Clostridioides difficile.. *Antonie Van Leeuwenhoek*, **2022**, 115, 297	2.1	0
63	New insights into the Type A glycan modification of Clostridioides difficile flagellar protein flagellin C by phosphoproteomics analysis.. *Journal of Biological Chemistry*, **2022**, 101622	5.4	0
62	Clostridioides difficile Phosphoproteomics Shows an Expansion of Phosphorylated Proteins in Stationary Growth Phase.. *MSphere*, **2022**, e0091121	5	2
61	Plasmids of Clostridioides difficile. *Current Opinion in Microbiology*, **2021**, 65, 87-94	7.9	0
60	Haem is crucial for medium-dependent metronidazole resistance in clinical isolates of Clostridioides difficile. *Journal of Antimicrobial Chemotherapy*, **2021**, 76, 1731-1740	5.1	11
59	Distinct evolution of colistin resistance associated with experimental resistance evolution models in Klebsiella pneumoniae. *Journal of Antimicrobial Chemotherapy*, **2021**, 76, 533-535	5.1	5
58	Cyclodextrin/Adamantane-Mediated Targeting of Inoculated Bacteria in Mice. *Bioconjugate Chemistry*, **2021**, 32, 607-614	6.3	4
57	Fecal Microbiota Transplantation Influences Procarcinogenic Escherichia coli in Recipient Recurrent Clostridioides difficile Patients. *Gastroenterology*, **2021**, 161, 1218-1228.e5	13.3	7
56	COMPARISON OF WHOLE GENOME SEQUENCE-BASED METHODS AND PCR RIBOTYPING FOR SUBTYPING OF .. *Journal of Clinical Microbiology*, **2021**, JCM0173721	9.7	0
55	Host Immune Responses to : Toxins and Beyond.. *Frontiers in Microbiology*, **2021**, 12, 804949	5.7	2
54	Redefining the Clostridioides difficile Regulon: Activates Genes Involved in Detoxifying Radicals That Can Result from the Exposure to Antimicrobials and Hydrogen Peroxide. *MSphere*, **2020**, 5,	5	10
53	Plasmid-mediated metronidazole resistance in Clostridioides difficile. *Nature Communications*, **2020**, 11, 598	17.4	31
52	Identification of the Unwinding Region in the Chromosomal Origin of Replication. *Frontiers in Microbiology*, **2020**, 11, 581401	5.7	1
51	The C-Terminal Domain of Clostridioides difficile TcdC Is Exposed on the Bacterial Cell Surface. *Journal of Bacteriology*, **2020**, 202,	3.5	2
50	Fluorescent imaging of bacterial infections and recent advances made with multimodal radiopharmaceuticals. *Clinical and Translational Imaging*, **2019**, 7, 125-138	2	17
49	#EUROmicroMOOC: using Twitter to share trends in Microbiology worldwide. *FEMS Microbiology Letters*, **2019**, 366,	2.9	5
48	Microbial evolutionary medicine: from theory to clinical practice. *Lancet Infectious Diseases, The*, **2019**, 19, e273-e283	25.5	6

47	Multimodal Tracking of Controlled Infections in Mice. *ACS Infectious Diseases*, **2019**, 5, 1160-1168	5.5	5
46	An survey of extrachromosomal elements . *Microbial Genomics*, **2019**, 5,	4.4	5
45	Genome Location Dictates the Transcriptional Response to PolC Inhibition in. *Antimicrobial Agents and Chemotherapy*, **2019**, 63,	5.9	7
44	The Bacterial Chromatin Protein HupA Can Remodel DNA and Associates with the Nucleoid in Clostridium difficile. *Journal of Molecular Biology*, **2019**, 431, 653-672	6.5	14
43	A helicase-containing module defines a family of pCD630-like plasmids in Clostridium difficile. *Anaerobe*, **2018**, 49, 78-84	2.8	9
42	Mechanistic Insights in the Success of Fecal Microbiota Transplants for the Treatment of Infections. *Frontiers in Microbiology*, **2018**, 9, 1242	5.7	53
41	The evolving epidemic of Clostridium difficile 630. *Anaerobe*, **2018**, 53, 2-4	2.8	7
40	Characterization of the virulence of a non-RT027, non-RT078 and binary toxin-positive Clostridium difficile strain associated with severe diarrhea. *Emerging Microbes and Infections*, **2018**, 7, 211	18.9	9
39	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	4.9	4
38	DNA replication proteins as potential targets for antimicrobials in drug-resistant bacterial pathogens. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 1275-1284	5.1	35
37	Interspecies Interactions between and. *MSphere*, **2016**, 1,	5	53
36	Clostridium difficile infection. *Nature Reviews Disease Primers*, **2016**, 2, 16021	51.1	2
35	The Signal Sequence of the Abundant Extracellular Metalloprotease PPEP-1 Can Be Used to Secrete Synthetic Reporter Proteins in Clostridium difficile. *ACS Synthetic Biology*, **2016**, 5, 1376-1382	5.7	20
34	Primase is required for helicase activity and helicase alters the specificity of primase in the enteropathogen Clostridium difficile. *Open Biology*, **2016**, 6,	7	10
33	Clostridium difficile infection. *Nature Reviews Disease Primers*, **2016**, 2, 16020	51.1	342
32	Complete genome sequence of BS49 and draft genome sequence of BS34A, Bacillus subtilis strains carrying Tn916. *FEMS Microbiology Letters*, **2015**, 362, 1-4	2.9	9
31	Complete genome sequence of the Clostridium difficile laboratory strain 630Δerm reveals differences from strain 630, including translocation of the mobile element CTn5. *BMC Genomics*, **2015**, 16, 31	4.5	45
30	Functional genomics reveals that Clostridium difficile Spo0A coordinates sporulation, virulence and metabolism. *BMC Genomics*, **2014**, 15, 160	4.5	85

29	The HtrA-like protease CD3284 modulates virulence of Clostridium difficile. *Infection and Immunity*, **2014**, 82, 4222-32	3.7	16
28	Hype or hypervirulence: a reflection on problematic C. difficile strains. *Virulence*, **2013**, 4, 592-6	4.7	35
27	TcdC does not significantly repress toxin expression in Clostridium difficile 630Δerm. *PLoS ONE*, **2012**, 7, e43247	3.7	59
26	C. difficile 630Δerm Spo0A regulates sporulation, but does not contribute to toxin production, by direct high-affinity binding to target DNA. *PLoS ONE*, **2012**, 7, e48608	3.7	54
25	Untwisting of the DNA helix stimulates the endonuclease activity of Bacillus subtilis Nth at AP sites. *Nucleic Acids Research*, **2012**, 40, 739-50	20.1	12
24	Chromosomal replication initiation machinery of low-G+C-content Firmicutes. *Journal of Bacteriology*, **2012**, 194, 5162-70	3.5	39
23	Primosomal proteins DnaD and DnaB are recruited to chromosomal regions bound by DnaA in Bacillus subtilis. *Journal of Bacteriology*, **2011**, 193, 640-8	3.5	31
22	Ordered association of helicase loader proteins with the Bacillus subtilis origin of replication in vivo. *Molecular Microbiology*, **2010**, 75, 452-61	4.1	51
21	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, 6930-42	20.1	18
20	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	6	69
19	Ubiquitous late competence genes in Bacillus species indicate the presence of functional DNA uptake machineries. *Environmental Microbiology*, **2009**, 11, 1911-22	5.2	41
18	Phenotypic Variation and Bistable Switching in Bacteria **2008**, 339-365		3
17	Bistability, epigenetics, and bet-hedging in bacteria. *Annual Review of Microbiology*, **2008**, 62, 193-210	17.5	717
16	Antirepression as a second mechanism of transcriptional activation by a minor groove binding protein. *Molecular Microbiology*, **2007**, 64, 368-81	4.1	31
15	Temporal separation of distinct differentiation pathways by a dual specificity Rap-Phr system in Bacillus subtilis. *Molecular Microbiology*, **2007**, 65, 103-20	4.1	69
14	Production and secretion stress caused by overexpression of heterologous alpha-amylase leads to inhibition of sporulation and a prolonged motile phase in Bacillus subtilis. *Applied and Environmental Microbiology*, **2007**, 73, 5354-62	4.8	23
13	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, 4718-28	3.5	11
12	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, 531-41	4.7	56

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11	Phenotypic variation in bacteria: the role of feedback regulation. *Nature Reviews Microbiology*, **2006**, 4, 259-71	22.2	381
10	Stripping Bacillus: ComK auto-stimulation is responsible for the bistable response in competence development. *Molecular Microbiology*, **2005**, 56, 604-14	4.1	162
9	The Rok protein of Bacillus subtilis represses genes for cell surface and extracellular functions. *Journal of Bacteriology*, **2005**, 187, 2010-9	3.5	68
8	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, 3921-30	3.5	32
7	Genome2D: a visualization tool for the rapid analysis of bacterial transcriptome data. *Genome Biology*, **2004**, 5, R37	18.3	78
6	Visualization of differential gene expression by improved cyan fluorescent protein and yellow fluorescent protein production in Bacillus subtilis. *Applied and Environmental Microbiology*, **2004**, 70, 6809-15	4.8	55
5	Improving the predictive value of the competence transcription factor (ComK) binding site in Bacillus subtilis using a genomic approach. *Nucleic Acids Research*, **2002**, 30, 5517-28	20.1	117
4	Heme is crucial for medium-dependent metronidazole resistance in clinical isolates of C. difficile		1
3	Anin silicosurvey ofClostridioides difficileextrachromosomal elements		1
2	Genome location dictates the transcriptional response to PolC-inhibition inClostridium difficile		1
1	Plasmid-mediated metronidazole resistance in Clostridioides difficile		1