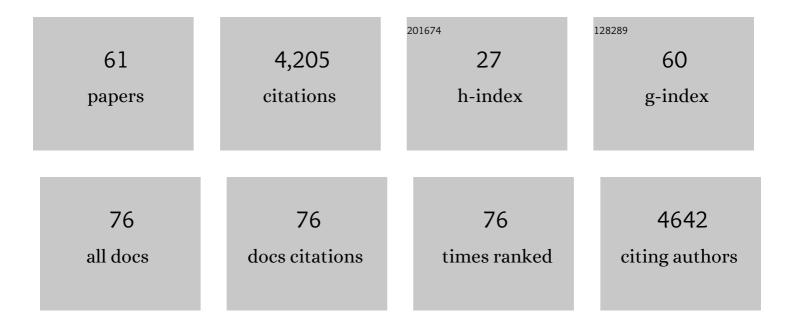
Wiep Klaas Smits

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Bistability, Epigenetics, and Bet-Hedging in Bacteria. Annual Review of Microbiology, 2008, 62, 193-210. | 7.3 | 907 |
| 2 | Clostridium difficile infection. Nature Reviews Disease Primers, 2016, 2, 16020. | 30.5 | 588 |
| 3 | Phenotypic variation in bacteria: the role of feedback regulation. Nature Reviews Microbiology, 2006, 4, 259-271. | 28.6 | 443 |
| 4 | StrippingBacillus: ComK auto-stimulation is responsible for the bistable response in competence development. Molecular Microbiology, 2005, 56, 604-614. | 2.5 | 178 |
| 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, 5517-5528. | 14.5 | 147 |
| 6 | Functional genomics reveals that Clostridium difficileSpo0A coordinates sporulation, virulence and metabolism. BMC Genomics, 2014, 15, 160. | 2.8 | 145 |
| 7 | Genome2D: a visualization tool for the rapid analysis of bacterial transcriptome data. Genome Biology, 2004, 5, R37. | 9.6 | 93 |
| 8 | 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 |
| 9 | Plasmid-mediated metronidazole resistance in Clostridioides difficile. Nature Communications, 2020, 11, 598. | 12.8 | 79 |
| 10 | 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. | 2.8 | 76 |
| 11 | C. difficile 630Δerm SpoOA 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 |
| 12 | The Rok Protein of Bacillus subtilis Represses Genes for Cell Surface and Extracellular Functions. Journal of Bacteriology, 2005, 187, 2010-2019. | 2.2 | 74 |
| 13 | Interspecies Interactions between Clostridium difficile and Candida albicans. MSphere, 2016, 1, . | 2.9 | 74 |
| 14 | Temporal separation of distinct differentiation pathways by a dual specificity Rap-Phr system inBacillus subtilis. Molecular Microbiology, 2007, 65, 103-120. | 2.5 | 73 |
| 15 | 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 |
| 16 | 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 |
| 17 | Chromosomal Replication Initiation Machinery of Low-G+C-Content Firmicutes. Journal of Bacteriology, 2012, 194, 5162-5170. | 2.2 | 65 |
| 18 | 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 |

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|----|--|------|-----------|
| 19 | TcdC Does Not Significantly Repress Toxin Expression in Clostridium difficile 630ΔErm. PLoS ONE, 2012, 7, e43247. | 2.5 | 64 |
| 20 | 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 |
| 21 | 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 |
| 22 | DNA replication proteins as potential targets for antimicrobials in drug-resistant bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw548. | 3.0 | 58 |
| 23 | 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 |
| 24 | Hype or hypervirulence. Virulence, 2013, 4, 592-596. | 4.4 | 41 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Antirepression as a second mechanism of transcriptional activation by a minor groove binding protein. Molecular Microbiology, 2007, 64, 368-381. | 2.5 | 32 |
| 29 | 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 |
| 30 | Production and Secretion Stress Caused by Overexpression of Heterologous α-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 |
| 31 | 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 |
| 32 | The HtrA-Like Protease CD3284 Modulates Virulence of Clostridium difficile. Infection and Immunity, 2014, 82, 4222-4232. | 2.2 | 25 |
| 33 | Fluorescent imaging of bacterial infections and recent advances made with multimodal radiopharmaceuticals. Clinical and Translational Imaging, 2019, 7, 125-138. | 2.1 | 22 |
| 34 | 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 |
| 35 | Host Immune Responses to Clostridioides difficile: Toxins and Beyond. Frontiers in Microbiology, 2021, 12, 804949. | 3.5 | 19 |
| 36 | Fecal Microbiota Transplantation Influences Procarcinogenic Escherichia coli in Recipient Recurrent Clostridioides difficile Patients. Gastroenterology, 2021, 161, 1218-1228.e5. | 1.3 | 18 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | Genome Location Dictates the Transcriptional Response to PolC Inhibition in <i>Clostridium difficile</i> . Antimicrobial Agents and Chemotherapy, 2019, 63, . | 3.2 | 15 |
| 40 | Redefining the Clostridioides difficile σ ^B Regulon: σ ^B Activates Genes Involved in Detoxifying Radicals That Can Result from the Exposure to Antimicrobials and Hydrogen Peroxide. MSphere, 2020, 5, . | 2.9 | 15 |
| 41 | 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 |
| 42 | Cyclodextrin/Adamantane-Mediated Targeting of Inoculated Bacteria in Mice. Bioconjugate Chemistry, 2021, 32, 607-614. | 3.6 | 14 |
| 43 | 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 |
| 44 | A helicase-containing module defines a family of pCD630-like plasmids in Clostridium difficile. Anaerobe, 2018, 49, 78-84. | 2.1 | 13 |
| 45 | Multimodal Tracking of Controlled <i>Staphylococcus aureus</i> Infections in Mice. ACS Infectious Diseases, 2019, 5, 1160-1168. | 3.8 | 13 |
| 46 | 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 |
| 47 | Microbial evolutionary medicine: from theory to clinical practice. Lancet Infectious Diseases, The, 2019, 19, e273-e283. | 9.1 | 11 |
| 48 | 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 |
| 49 | The evolving epidemic of Clostridium difficile 630. Anaerobe, 2018, 53, 2-4. | 2.1 | 10 |
| 50 | The C-Terminal Domain of Clostridioides difficile TcdC Is Exposed on the Bacterial Cell Surface. Journal of Bacteriology, 2020, 202, . | 2.2 | 9 |
| 51 | Plasmids of Clostridioides difficile. Current Opinion in Microbiology, 2022, 65, 87-94. | 5.1 | 8 |
| 52 | Clostridioides difficile Phosphoproteomics Shows an Expansion of Phosphorylated Proteins in Stationary Growth Phase. MSphere, 2022, 7, e0091121. | 2.9 | 8 |
| 53 | #EUROmicroMOOC: using Twitter to share trends in Microbiology worldwide. FEMS Microbiology Letters, 2019, 366, . | 1.8 | 7 |
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54 Phenotypic Variation and Bistable Switching in Bacteria. , 2008, , 339-365.

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|----|--|------|-----------|
| 55 | 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 |
| 56 | An in silico survey of Clostridioides difficile extrachromosomal elements. Microbial Genomics, 2019, 5, . | 2.0 | 6 |
| 57 | Practical observations on the use of fluorescent reporter systems in Clostridioides difficile. Antonie Van Leeuwenhoek, 2022, 115, 297-323. | 1.7 | 6 |
| 58 | 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 |
| 59 | Clostridium difficile infection. Nature Reviews Disease Primers, 2016, 2, 16021. | 30.5 | 3 |
| 60 | SNP-ing out the differences: Investigating differences between <i>Clostridium difficile</i> lab strains. Virulence, 2017, 8, 613-617. | 4.4 | 3 |
| 61 | Identification of the Unwinding Region in the Clostridioides difficile Chromosomal Origin of Replication. Frontiers in Microbiology, 2020, 11, 581401. | 3.5 | 1 |