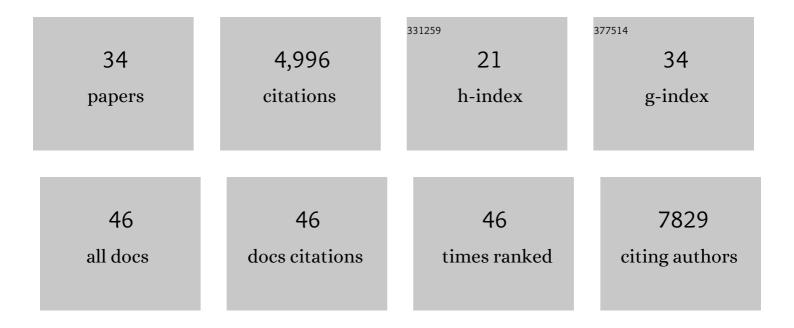
## Sünje Johanna Pamp

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mucosal microbiotas and their role in stem cell transplantation. Apmis, 2022, , .	0.9	3
2	Library Preparation and Sequencing Platform Introduce Bias in Metagenomic-Based Characterizations of Microbiomes. Microbiology Spectrum, 2022, 10, e0009022.	1.2	12
3	Extended-spectrum beta-lactamase-producing Escherichia coli and antimicrobial resistance in municipal and hospital wastewaters in Czech Republic: Culture-based and metagenomic approaches. Environmental Research, 2021, 193, 110487.	3.7	24
4	Glycerol–Silicone Membranes for Sustained and Controlled Topical Delivery of Antimicrobial and Painâ€Relief Drugs. Advanced Materials Interfaces, 2021, 8, 2001873.	1.9	6
5	Simultaneous delivery of several antimicrobial drugs from multiâ€compartment glycerolâ€silicone membranes. Journal of Applied Polymer Science, 2021, 138, 50780.	1.3	0
6	Reconstruction of ancient microbial genomes from the human gut. Nature, 2021, 594, 234-239.	13.7	139
7	A Peek into the Plasmidome of Global Sewage. MSystems, 2021, 6, e0028321.	1.7	14
8	Microbiota long-term dynamics and prediction of acute graft-versus-host disease in pediatric allogeneic stem cell transplantation. Microbiome, 2021, 9, 148.	4.9	35
9	Standard Sample Storage Conditions Have an Impact on Inferred Microbiome Composition and Antimicrobial Resistance Patterns. Microbiology Spectrum, 2021, 9, e0138721.	1.2	24
10	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	1.6	4
11	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	1.5	7
12	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. Frontiers in Public Health, 2020, 8, 38.	1.3	11
13	Gastrointestinal toxicity during induction treatment for childhood acute lymphoblastic leukemia: The impact of the gut microbiota. International Journal of Cancer, 2020, 147, 1953-1962.	2.3	32
14	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	1.1	24
15	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131.	4.9	65
16	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	5.8	612
17	Genomics-Based Identification of Microorganisms in Human Ocular Body Fluid. Scientific Reports, 2018, 8, 4126.	1.6	69
18	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908.	5.9	230

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19	Draft Genome Sequence of Acinetobacter johnsonii C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions. Genome Announcements, 2017, 5, .	0.8	7
20	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. Journal of Antimicrobial Chemotherapy, 2017, 72, 385-392.	1.3	89
21	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. MSystems, 2016, 1, .	1.7	153
22	Comparative genomics of toxigenic and non-toxigenic Staphylococcus hyicus. Veterinary Microbiology, 2016, 185, 34-40.	0.8	9
23	Development of Spatial Distribution Patterns by Biofilm Cells. Applied and Environmental Microbiology, 2015, 81, 6120-6128.	1.4	30
24	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and S.Âaureus Carriage. Cell Host and Microbe, 2013, 14, 631-640.	5.1	294
25	Single-cell sequencing provides clues about the host interactions of segmented filamentous bacteria (SFB). Genome Research, 2012, 22, 1107-1119.	2.4	108
26	Gut Immune Maturation Depends on Colonization with a Host-Specific Microbiota. Cell, 2012, 149, 1578-1593.	13.5	1,050
27	The metabolically active subpopulation in <i>Pseudomonas aeruginosa</i> biofilms survives exposure to membrane-targeting antimicrobials via distinct molecular mechanisms. FEMS Immunology and Medical Microbiology, 2012, 65, 245-256.	2.7	54
28	An update on <i>Pseudomonas aeruginosa</i> biofilm formation, tolerance, and dispersal. FEMS Immunology and Medical Microbiology, 2010, 59, 253-268.	2.7	288
29	Insight into the microbial multicellular lifestyle via flowâ€cell technology and confocal microscopy. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 90-103.	1.1	118
30	Inactivation of the <i>rhlA</i> gene in <i>Pseudomonas aeruginosa</i> prevents rhamnolipid production, disabling the protection against polymorphonuclear leukocytes. Apmis, 2009, 117, 537-546.	0.9	177
31	Roles of type IV pili, flagellumâ€mediated motility and extracellular DNA in the formation of mature multicellular structures in <i>Pseudomonas aeruginosa</i> biofilms. Environmental Microbiology, 2008, 10, 2331-2343.	1.8	345
32	Tolerance to the antimicrobial peptide colistin in <i>Pseudomonas aeruginosa</i> biofilms is linked to metabolically active cells, and depends on the <i>pmr</i> and <i>mexABâ€oprM</i> genes. Molecular Microbiology, 2008, 68, 223-240.	1.2	430
33	Multiple Roles of Biosurfactants in Structural Biofilm Development by Pseudomonas aeruginosa. Journal of Bacteriology, 2007, 189, 2531-2539.	1.0	352
34	Spx Is a Global Effector Impacting Stress Tolerance and Biofilm Formation in Staphylococcus aureus. Journal of Bacteriology, 2006, 188, 4861-4870.	1.0	150