

# W Florian Fricke

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

3,270  
citations

394421

19  
h-index

552781

26  
g-index

30  
all docs

30  
docs citations

30  
times ranked

5172  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic strain detection with SameStr: identification of a persisting core gut microbiota transferable by fecal transplantation. <i>Microbiome</i> , 2022, 10, 53.	11.1	15
2	Qualitative and Quantitative DNA- and RNA-Based Analysis of the Bacterial Stomach Microbiota in Humans, Mice, and Gerbils. <i>MSystems</i> , 2018, 3, .	3.8	21
3	Salmonella Activation of STAT3 Signaling by SarA Effector Promotes Intracellular Replication and Production of IL-10. <i>Cell Reports</i> , 2018, 23, 3525-3536.	6.4	57
4	CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. <i>BMC Genomics</i> , 2017, 18, 332.	2.8	12
5	Type 2 immunity-dependent reduction of segmented filamentous bacteria in mice infected with the helminthic parasite <i>Nippostrongylus brasiliensis</i> . <i>Microbiome</i> , 2015, 3, 40.	11.1	93
6	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. <i>PLoS Medicine</i> , 2014, 11, e1001627.	8.4	9
7	The More the Merrier? Reduced Fecal Microbiota Diversity in Preterm Infants Treated with Antibiotics. <i>Journal of Pediatrics</i> , 2014, 165, 8-10.	1.8	19
8	Efficacy of Combined Jejunal and Colonic Fecal Microbiota Transplantation for Recurrent <i>Clostridium difficile</i> Infection. <i>Clinical Gastroenterology and Hepatology</i> , 2014, 12, 1572-1576.	4.4	74
9	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. <i>Nature Reviews Genetics</i> , 2014, 15, 49-55.	16.3	141
10	Microbiota Dynamics in Patients Treated with Fecal Microbiota Transplantation for Recurrent <i>Clostridium difficile</i> Infection. <i>PLoS ONE</i> , 2013, 8, e81330.	2.5	167
11	Origin and Variation of Tunicate Secondary Metabolites. <i>Journal of Natural Products</i> , 2012, 75, 295-304.	3.0	71
12	Proof of Concept of Microbiome-Metabolome Analysis and Delayed Gluten Exposure on Celiac Disease Autoimmunity in Genetically At-Risk Infants. <i>PLoS ONE</i> , 2012, 7, e33387.	2.5	219
13	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	5
14	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	3
15	Variation in Tropical Reef Symbiont Metagenomes Defined by Secondary Metabolism. <i>PLoS ONE</i> , 2011, 6, e17897.	2.5	59
16	CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. <i>BMC Bioinformatics</i> , 2011, 12, 356.	2.6	246
17	Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1423-32.	7.1	146
18	Comparative Genomics of 28 <i>Salmonella enterica</i> Isolates: Evidence for CRISPR-Mediated Adaptive Sublineage Evolution. <i>Journal of Bacteriology</i> , 2011, 193, 3556-3568.	2.2	159

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19	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624.	2.5	75
20	Horizontal Gene Transfer of a ColV Plasmid Has Resulted in a Dominant Avian Clonal Type of Salmonella enterica Serovar Kentucky. PLoS ONE, 2010, 5, e15524.	2.5	101
21	No Resistance Plasmid in <i>Yersinia pestis</i> , North America. Emerging Infectious Diseases, 2010, 16, 885-887.	4.3	10
22	Antimicrobial Resistance-Confering Plasmids with Similarity to Virulence Plasmids from Avian Pathogenic <i>Escherichia coli</i> Strains in <i>Salmonella enterica</i> Serovar Kentucky Isolates from Poultry. Applied and Environmental Microbiology, 2009, 75, 5963-5971.	3.1	160
23	Comparative Genomics of the IncA/C Multidrug Resistance Plasmid Family. Journal of Bacteriology, 2009, 191, 4750-4757.	2.2	199
24	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. Journal of Bacteriology, 2008, 190, 6881-6893.	2.2	763
25	Insights into the Environmental Resistance Gene Pool from the Genome Sequence of the Multidrug-Resistant Environmental Isolate <i>Escherichia coli</i> SMS-3-5. Journal of Bacteriology, 2008, 190, 6779-6794.	2.2	82
26	Multiple Antimicrobial Resistance in Plague: An Emerging Public Health Risk. PLoS ONE, 2007, 2, e309.	2.5	344
27	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing – standard operating procedure, version 1.0. Nature Precedings, 0, , .	0.1	4