

Wolfgang Florian Fricke

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

6,824
citations

101543

36
h-index

106344

65
g-index

74
all docs

74
docs citations

74
times ranked

10284
citing authors

#	ARTICLE	IF	CITATIONS
1	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. <i>Journal of Bacteriology</i> , 2008, 190, 6881-6893.	2.2	763
2	Genome sequence of the bioplastic-producing <i>Ralstonia eutropha</i> H16. <i>Nature Biotechnology</i> , 2006, 24, 1257-1262.	17.5	527
3	The genome of <i>Clostridium kluyveri</i> , a strict anaerobe with unique metabolic features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2128-2133.	7.1	409
4	Complete genome sequence of the acetic acid bacterium <i>Gluconobacter oxydans</i> . <i>Nature Biotechnology</i> , 2005, 23, 195-200.	17.5	371
5	Score-based prediction of genomic islands in prokaryotic genomes using hidden Markov models. <i>BMC Bioinformatics</i> , 2006, 7, 142.	2.6	349
6	Multiple Antimicrobial Resistance in Plague: An Emerging Public Health Risk. <i>PLoS ONE</i> , 2007, 2, e309.	2.5	344
7	The genome sequence of <i>Clostridium tetani</i> , the causative agent of tetanus disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1316-1321.	7.1	324
8	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
9	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
10	Colonization patterns of soil microbial communities in the Atacama Desert. <i>Microbiome</i> , 2013, 1, 28.	11.1	215
11	Comparative Genomics of the Inca/C Multidrug Resistance Plasmid Family. <i>Journal of Bacteriology</i> , 2009, 191, 4750-4757.	2.2	199
12	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
13	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. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5963-5971.	3.1	160
14	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
15	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
16	Natural Transformation Facilitates Transfer of Transposons, Integrons and Gene Cassettes between Bacterial Species. <i>PLoS Pathogens</i> , 2012, 8, e1002837.	4.7	146
17	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. <i>Nature Reviews Genetics</i> , 2014, 15, 49-55.	16.3	141
18	Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. <i>ISME Journal</i> , 2013, 7, 1354-1366.	9.8	135

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19	What is new and relevant for sequencing-based microbiome research? A mini-review. <i>Journal of Advanced Research</i> , 2019, 19, 105-112.	9.5	105
20	Horizontal Gene Transfer of a ColV Plasmid Has Resulted in a Dominant Avian Clonal Type of <i>Salmonella enterica</i> Serovar Kentucky. <i>PLoS ONE</i> , 2010, 5, e15524.	2.5	101
21	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	3.8	100
22	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015, 6, 8754.	12.8	100
23	The Complete Genome Sequence of <i>Yersinia pseudotuberculosis</i> IP31758, the Causative Agent of Far East Scarlet-Like Fever. <i>PLoS Genetics</i> , 2007, 3, e142.	3.5	99
24	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
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. <i>Journal of Bacteriology</i> , 2008, 190, 6779-6794.	2.2	82
26	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. <i>PLoS ONE</i> , 2011, 6, e26624.	2.5	75
27	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
28	Origin and Variation of Tunicate Secondary Metabolites. <i>Journal of Natural Products</i> , 2012, 75, 295-304.	3.0	71
29	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019, 5, .	2.0	69
30	Variation in Tropical Reef Symbiont Metagenomes Defined by Secondary Metabolism. <i>PLoS ONE</i> , 2011, 6, e17897.	2.5	59
31	<i>Salmonella</i> 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
32	Gut microbiota-dependent modulation of innate immunity and lymph node remodeling affects cardiac allograft outcomes. <i>JCI Insight</i> , 2018, 3, .	5.0	53
33	Whole-Genome Sequences of <i>Bacillus subtilis</i> and Close Relatives. <i>Journal of Bacteriology</i> , 2012, 194, 2378-2379.	2.2	52
34	CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. <i>Microbiome</i> , 2013, 1, 6.	11.1	49
35	Microbiota implications for immunity and transplantation. <i>Nature Reviews Nephrology</i> , 2015, 11, 342-353.	9.6	47
36	Efficacy of Fecal Microbiota Transplantation in 2 Children With Recurrent <i>Clostridium difficile</i> Infection and Its Impact on Their Growth and Gut Microbiome. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2014, 59, 565-570.	1.8	39

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37	Characterization of the Bacterial Community of the Chemically Defended Hawaiian Sacoglossan <i>Elysia rufescens</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 7073-7081.	3.1	37
38	“Available upon request” not good enough for microbiome data!. <i>Microbiome</i> , 2018, 6, 8.	11.1	35
39	<i>Ralstonia eutropha</i> H16 Flagellation Changes According to Nutrient Supply and State of Poly(3-Hydroxybutyrate) Accumulation. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4477-4490.	3.1	34
40	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
41	Strain inheritance and neonatal gut microbiota development: A meta-analysis. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151483.	3.6	31
42	Microbiome or no microbiome: are we looking at the prenatal environment through the right lens?. <i>Microbiome</i> , 2021, 9, 9.	11.1	24
43	The Role of Genomics in the Identification, Prediction, and Prevention of Biological Threats. <i>PLoS Biology</i> , 2009, 7, e1000217.	5.6	23
44	High intake of orange juice and cola differently affects metabolic risk in healthy subjects. <i>Clinical Nutrition</i> , 2019, 38, 812-819.	5.0	22
45	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
46	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
47	Bacterial microbiota diversity and composition in red and white wines correlate with plant-derived DNA contributions and botrytis infection. <i>Scientific Reports</i> , 2020, 10, 13828.	3.3	19
48	Growth advantage of <i>Escherichia coli</i> O104:H4 strains on 5- N -acetyl-9- O -acetyl neuraminic acid as a carbon source is dependent on heterogeneous phage-Borne nanS-p esterases. <i>International Journal of Medical Microbiology</i> , 2018, 308, 459-468.	3.6	18
49	Genome sequences of 65 <i>Helicobacter pylori</i> strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. <i>Pathogens and Disease</i> , 2013, 68, 39-43.	2.0	17
50	The Genome Organization of <i>Ralstonia eutropha</i> Strain H16 and Related Species of the Burkholderiaceae. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 124-135.	1.0	16
51	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
52	Genome Sequence of <i>Ruegeria</i> sp. Strain KLH11, an N-Acylhomoserine Lactone-Producing Bacterium Isolated from the Marine Sponge <i>Mycale laxissima</i> . <i>Journal of Bacteriology</i> , 2011, 193, 5011-5012.	2.2	13
53	CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. <i>BMC Genomics</i> , 2017, 18, 332.	2.8	12
54	No Resistance Plasmid in <i>Yersinia pestis</i> , North America. <i>Emerging Infectious Diseases</i> , 2010, 16, 885-887.	4.3	10

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55	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. <i>PLoS Medicine</i> , 2014, 11, e1001627.	8.4	9
56	More data needed on neonatal microbiome seeding. <i>Microbiome</i> , 2022, 10, .	11.1	7
57	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
58	Checks and Balances"Microbiota Shifts in Immunosuppressed Mice. <i>Transplantation</i> , 2017, 101, 26-27.	1.0	5
59	P-value based visualization of codon usage data. <i>Algorithms for Molecular Biology</i> , 2006, 1, 10.	1.2	4
60	Genome Sequence of <i>Salmonella enterica</i> Serotype Tennessee Strain CDC07-0191, Implicated in the 2006-2007 Multistate Food-Borne Outbreak Linked to Peanut Butter in the United States. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
61	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 0, , .	0.1	4
62	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
63	CloVR-Microbe: Assembly, gene finding and functional annotation of raw sequence data from single microbial genome projects " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 0, , .	0.1	3
64	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.1. <i>Nature Precedings</i> , 0, , .	0.1	2
65	Food-Borne Outbreaks. , 2011, , 29-41.		2
66	When to suspect contamination rather than colonization " lessons from a putative fetal sheep microbiome. <i>Gut Microbes</i> , 2022, 14, 2005751.	9.8	2
67	CloVR-Metagenomics: Functional and taxonomic microbial community characterization from metagenomic whole-genome shotgun (WGS) sequences " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	1