Wolfgang Florian Fricke

List of Publications by Year
in descending order

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	Metagenomic strain detection with SameStr: identification of a persisting core gut microbiota transferable by fecal transplantation. Microbiome, 2022, 10, 53.	11.1	15
2	When to suspect contamination rather than colonization â€" lessons from a putative fetal sheep microbiome. Gut Microbes, 2022, 14, 2005751.	9.8	2
3	More data needed on neonatal microbiome seeding. Microbiome, 2022, 10, .	11.1	7
4	Microbiome or no microbiome: are we looking at the prenatal environment through the right lens?. Microbiome, 2021, 9, 9.	11.1	24
5	Strain inheritance and neonatal gut microbiota development: A meta-analysis. International Journal of Medical Microbiology, 2021, 311, 151483.	3.6	31
6	Bacterial microbiota diversity and composition in red and white wines correlate with plant-derived DNA contributions and botrytis infection. Scientific Reports, 2020, 10, 13828.	3.3	19
7	What is new and relevant for sequencing-based microbiome research? A mini-review. Journal of Advanced Research, 2019, 19, 105-112.	9.5	105
8	High intake of orange juice and cola differently affects metabolic risk in healthy subjects. Clinical Nutrition, 2019, 38, 812-819.	5.0	22
9	Global phylogenomics of multidrug-resistant Salmonella enterica serotype Kentucky ST198. Microbial Genomics, 2019, 5, .	2.0	69
10	Growth advantage of Escherichia coli 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. International Journal of Medical Microbiology, 2018, 308, 459-468.	3.6	18
11	Qualitative and Quantitative DNA- and RNA-Based Analysis of the Bacterial Stomach Microbiota in Humans, Mice, and Gerbils. MSystems, 2018, 3, .	3.8	21
12	â€œAvailable upon requestâ€¹ not good enough for microbiome data!. Microbiome, 2018, 6, 8.	11.1	35
13	Salmonella Activation of STAT3 Signaling by SarA Effector Promotes Intracellular Replication and Production of IL-10. Cell Reports, 2018, 23, 3525-3536.	6.4	57
14	Gut microbiotaâ€"dependent modulation of innate immunity and lymph node remodeling affects cardiac allograft outcomes. JCI Insight, 2018, 3, .	5.0	53
15	CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. BMC Genomics, 2017, 18, 332.	2.8	12
16	Checks and Balancesâ€"Microbiota Shifts in Immunosuppressed Mice. Transplantation, 2017, 101, 26-27.	1.0	5
17	Allelic variation contributes to bacterial host specificity. Nature Communications, 2015, 6, 8754.	12.8	100
18	Type 2 immunity-dependent reduction of segmented filamentous bacteria in mice infected with the helminthic parasite Nippostrongylus brasiliensis. Microbiome, 2015, 3, 40.	11.1	93

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19	Microbiota—implications for immunity and transplantation. Nature Reviews Nephrology, 2015, 11, 342-353.	9.6	47
20	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34
21	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. PLoS Medicine, 2014, 11, e1001627.	8.4	9
22	Efficacy of Fecal Microbiota Transplantation in 2 Children With Recurrent *Clostridium difficile* Infection and Its Impact on Their Growth and Gut Microbiome. Journal of Pediatric Gastroenterology and Nutrition, 2014, 59, 565-570.	1.8	39
23	The More the Merrier? Reduced Fecal Microbiota Diversity in Preterm Infants Treated with Antibiotics. Journal of Pediatrics, 2014, 165, 8-10.	1.8	19
24	Efficacy of Combined Jejunal and Colonic Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection. Clinical Gastroenterology and Hepatology, 2014, 12, 1572-1576.	4.4	74
25	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. Nature Reviews Genetics, 2014, 15, 49-55.	16.3	141
26	CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. Microbiome, 2013, 1, 6.	11.1	49
27	Characterization of the Bacterial Community of the Chemically Defended Hawaiian Sacoglossan Elysia rufescens. Applied and Environmental Microbiology, 2013, 79, 7073-7081.	3.1	37
28	Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. ISME Journal, 2013, 7, 1354-1366.	9.8	135
29	Genome sequences of 65 *Helicobacter pylori* strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. Pathogens and Disease, 2013, 68, 39-43.	2.0	17
30	Genome Sequence of Salmonella enterica Serotype Tennessee Strain CDC07-0191, Implicated in the 2006-2007 Multistate Food-Borne Outbreak Linked to Peanut Butter in the United States. Genome Announcements, 2013, 1, .	0.8	4
31	Colonization patterns of soil microbial communities in the Atacama Desert. Microbiome, 2013, 1, 28.	11.1	215
32	Microbiota Dynamics in Patients Treated with Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection. PLoS ONE, 2013, 8, e81330.	2.5	167
33	Natural Transformation Facilitates Transfer of Transposons, Integrons and Gene Cassettes between Bacterial Species. PLoS Pathogens, 2012, 8, e1002837.	4.7	146
34	Whole-Genome Sequences of Bacillus subtilis and Close Relatives. Journal of Bacteriology, 2012, 194, 2378-2379.	2.2	52
35	Origin and Variation of Tunicate Secondary Metabolites. Journal of Natural Products, 2012, 75, 295-304.	3.0	71
36	Proof of Concept of Microbiome-Metabolome Analysis and Delayed Gluten Exposure on Celiac Disease Autoimmunity in Genetically At-Risk Infants. PLoS ONE, 2012, 7, e33387.	2.5	219

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37	CloVR-Metagenomics: Functional and taxonomic microbial community characterization from metagenomic whole-genome shotgun (WGS) sequences â€" standard operating procedure, version 1.0. Nature Precedings, 2011, , .	0.1	1
38	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€" standard operating procedure, version1.0. Nature Precedings, 2011, , .	0.1	5
39	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€" standard operating procedure, version 1.0. Nature Precedings, 2011, , .	0.1	3
40	Food-Borne Outbreaks. , 2011, , 29-41.		2
41	Variation in Tropical Reef Symbiont Metagenomes Defined by Secondary Metabolism. PLoS ONE, 2011, 6, e17897.	2.5	59
42	CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. BMC Bioinformatics, 2011, 12, 356.	2.6	246
43	Genome Sequence of Ruegeria sp. Strain KLH11, an *N*-Acylhomoserine Lactone-Producing Bacterium Isolated from the Marine Sponge Mycale laxissima. Journal of Bacteriology, 2011, 193, 5011-5012.	2.2	13
44	Complex microbiome underlying secondary and primary metabolism in the tunicate- *Prochloron* symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1423-32.	7.1	146
45	Comparative Genomics of 28 Salmonella enterica Isolates: Evidence for CRISPR-Mediated Adaptive Sublineage Evolution. Journal of Bacteriology, 2011, 193, 3556-3568.	2.2	159
46	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624.	2.5	75
47	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
48	No Resistance Plasmid in *Yersinia pestis,* North America. Emerging Infectious Diseases, 2010, 16, 885-887.	4.3	10
49	Antimicrobial Resistance-Conferring Plasmids with Similarity to Virulence Plasmids from Avian Pathogenic *Escherichia coli* Strains in *Salmonella enterica* Serovar Kentucky Isolates from Poultry. Applied and Environmental Microbiology, 2009, 75, 5963-5971.	3.1	160
50	Comparative Genomics of the IncA/C Multidrug Resistance Plasmid Family. Journal of Bacteriology, 2009, 191, 4750-4757.	2.2	199
51	The Genome Organization of <i>Ralstonia eutropha</i> Strain H16 and Related Species of the <i>Burkholderiaceae</i>. Journal of Molecular Microbiology and Biotechnology, 2009, 16, 124-135.	1.0	16
52	Genome sequence of *Desulfobacterium autotrophicum* HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. Environmental Microbiology, 2009, 11, 1038-1055.	3.8	100
53	The Role of Genomics in the Identification, Prediction, and Prevention of Biological Threats. PLoS Biology, 2009, 7, e1000217.	5.6	23
54	The Pangenome Structure of *Escherichia coli*: Comparative Genomic Analysis of *E. coli* Commensal and Pathogenic Isolates. Journal of Bacteriology, 2008, 190, 6881-6893.	2.2	763

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55	Insights into the Environmental Resistance Gene Pool from the Genome Sequence of the Multidrug-Resistant Environmental Isolate *Escherichia coli* SMS-3-5. Journal of Bacteriology, 2008, 190, 6779-6794.	2.2	82
56	*Ralstonia eutropha* H16 Flagellation Changes According to Nutrient Supply and State of Poly(3-Hydroxybutyrate) Accumulation. Applied and Environmental Microbiology, 2008, 74, 4477-4490.	3.1	34
57	The genome of *Clostridium kluyveri*, a strict anaerobe with unique metabolic features. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2128-2133.	7.1	409
58	The Complete Genome Sequence of Yersinia pseudotuberculosis IP31758, the Causative Agent of Far East Scarlet-Like Fever. PLoS Genetics, 2007, 3, e142.	3.5	99
59	Multiple Antimicrobial Resistance in Plague: An Emerging Public Health Risk. PLoS ONE, 2007, 2, e309.	2.5	344
60	P-value based visualization of codon usage data. Algorithms for Molecular Biology, 2006, 1, 10.	1.2	4
61	Genome sequence of the bioplastic-producing â€œKnallgasâ€•bacterium Ralstonia eutropha H16. Nature Biotechnology, 2006, 24, 1257-1262.	17.5	527
62	Score-based prediction of genomic islands in prokaryotic genomes using hidden Markov models. BMC Bioinformatics, 2006, 7, 142.	2.6	349
63	Complete genome sequence of the acetic acid bacterium Gluconobacter oxydans. Nature Biotechnology, 2005, 23, 195-200.	17.5	371
64	The genome sequence of *Clostridium tetani*, the causative agent of tetanus disease. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1316-1321.	7.1	324
65	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€" standard operating procedure, version 1.1. Nature Precedings, 0, , .	0.1	2
66	CloVR-Microbe: Assembly, gene finding and functional annotation of raw sequence data from single microbial genome projects â€" standard operating procedure, version 1.0. Nature Precedings, 0, , .	0.1	3
67	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€" standard operating procedure, version 1.0. Nature Precedings, 0, , .	0.1	4