

Christian H Ahrens

List of Publications by Year in descending order

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76
papers

6,295
citations

87723

38
h-index

74018

75
g-index

86
all docs

86
docs citations

86
times ranked

8640
citing authors

#	ARTICLE	IF	CITATIONS
1	A Practical Guide to Small Protein Discovery and Characterization Using Mass Spectrometry. Journal of Bacteriology, 2022, 204, JB0035321.	1.0	30
2	Role of the flagellar hook in the structural development and antibiotic tolerance of <i>Pseudomonas aeruginosa</i> biofilms. ISME Journal, 2022, 16, 1176-1186.	4.4	18
3	Genome sequence data of the antagonistic soil-borne yeast <i>Cyberlindnera sargentensis</i> (SHA 17.2). Data in Brief, 2022, 40, 107799.	0.5	2
4	Salt- and osmo-responsive sensor histidine kinases activate the <i>Bradyrhizobium diazoefficiens</i> general stress response to initiate functional symbiosis. Molecular Plant-Microbe Interactions, 2022, , .	1.4	1
5	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. Microbiome, 2021, 9, 55.	4.9	24
6	Towards the characterization of the hidden world of small proteins in <i>Staphylococcus aureus</i> , a proteogenomics approach. PLoS Genetics, 2021, 17, e1009585.	1.5	23
7	Differential Expression of <i>Paraburkholderia phyumatum</i> Type VI Secretion Systems (T6SS) Suggests a Role of T6SS-b in Early Symbiotic Interaction. Frontiers in Plant Science, 2021, 12, 699590.	1.7	10
8	Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus <i>Aureobasidium pullulans</i> to identify potential biocontrol genes. Microbial Cell, 2021, 8, 184-202.	1.4	17
9	Indicative bacterial communities and taxa of disease-suppressing and growth-promoting composts and their associations to the rhizosphere. FEMS Microbiology Ecology, 2021, 97, .	1.3	4
10	Harnessing the Microbiomes of Suppressive Composts for Plant Protection: From Metagenomes to Beneficial Microorganisms and Reliable Diagnostics. Frontiers in Microbiology, 2020, 11, 1810.	1.5	34
11	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. Scientific Data, 2020, 7, 324.	2.4	33
12	Optimized Proteomics Workflow for the Detection of Small Proteins. Journal of Proteome Research, 2020, 19, 4004-4018.	1.8	28
13	An integrated model system to gain mechanistic insights into biofilm-associated antimicrobial resistance in <i>Pseudomonas aeruginosa</i> MPAO1. Npj Biofilms and Microbiomes, 2020, 6, 46.	2.9	31
14	Linking Comparative Genomics of Nine Potato-Associated <i>Pseudomonas</i> Isolates With Their Differing Biocontrol Potential Against Late Blight. Frontiers in Microbiology, 2020, 11, 857.	1.5	32
15	The Leader Peptide <i>peTrpL</i> Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. MBio, 2020, 11, .	1.8	10
16	Complete genome sequence and epigenetic profile of <i>Bacillus velezensis</i> UCMB5140 used for plant and crop protection in comparison with other plant-associated <i>Bacillus</i> strains. Applied Microbiology and Biotechnology, 2020, 104, 7643-7656.	1.7	10
17	A Proteogenomic Resource Enabling Integrated Analysis of <i>Listeria</i> Genotype-Phenotype Relationships. Journal of Proteome Research, 2020, 19, 1647-1662.	1.8	10
18	Genetic, Epigenetic and Phenotypic Diversity of Four <i>Bacillus velezensis</i> Strains Used for Plant Protection or as Probiotics. Frontiers in Microbiology, 2019, 10, 2610.	1.5	34

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19	Long-read based de novo assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. BMC Microbiology, 2019, 19, 143.	1.3	104
20	An Integrated Systems Approach Unveils New Aspects of Microoxia-Mediated Regulation in Bradyrhizobium diazoefficiens. Frontiers in Microbiology, 2019, 10, 924.	1.5	31
21	Snf2 controls pulcherriminic acid biosynthesis and antifungal activity of the biocontrol yeast <i>Metschnikowia pulcherrima</i> . Molecular Microbiology, 2019, 112, 317-332.	1.2	64
22	Seasonal Dynamics of Glyphosate and AMPA in Lake Greifensee: Rapid Microbial Degradation in the Epilimnion During Summer. Environmental Science & Technology, 2018, 52, 4641-4649.	4.6	48
23	Pushing the limits of de novo genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. Nucleic Acids Research, 2018, 46, 8953-8965.	6.5	104
24	Comparative Genomics of Completely Sequenced Lactobacillus helveticus Genomes Provides Insights into Strain-Specific Genes and Resolves Metagenomics Data Down to the Strain Level. Frontiers in Microbiology, 2018, 9, 63.	1.5	73
25	Pseudomonas orientalis F9: A Potent Antagonist against Phytopathogens with Phytotoxic Effect in the Apple Flower. Frontiers in Microbiology, 2018, 9, 145.	1.5	34
26	Metabolomics and Transcriptomics Identify Multiple Downstream Targets of Paraburkholderia phymatum If54 During Symbiosis with Phaseolus vulgaris. International Journal of Molecular Sciences, 2018, 19, 1049.	1.8	11
27	Long-Chain Alkyl Cyanides: Unprecedented Volatile Compounds Released by <i>Pseudomonas</i> and <i>Micromonospora</i> Bacteria. Angewandte Chemie - International Edition, 2017, 56, 4342-4346.	7.2	26
28	Langkettige Alkylcyanide, beispiellose flüchtige Verbindungen aus <i>Pseudomonas</i> und <i>Micromonospora</i> Bakterien. Angewandte Chemie, 2017, 129, 4406-4410.	1.6	2
29	Biofilm Formation Potential of Heat-Resistant Escherichia coli Dairy Isolates and the Complete Genome of Multidrug-Resistant, Heat-Resistant Strain FAM21845. Applied and Environmental Microbiology, 2017, 83, .	1.4	29
30	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. Genome Research, 2017, 27, 2083-2095.	2.4	112
31	Competition assays and physiological experiments of soil and phyllosphere yeasts identify Candida subhashii as a novel antagonist of filamentous fungi. BMC Microbiology, 2017, 17, 4.	1.3	77
32	Metabolomic Profiling of Bradyrhizobium diazoefficiens-Induced Root Nodules Reveals Both Host Plant-Specific and Developmental Signatures. International Journal of Molecular Sciences, 2016, 17, 815.	1.8	52
33	Complete genome sequence of Pseudomonas citronellolis P3B5, a candidate for microbial phyllo-remediation of hydrocarbon-contaminated sites. Standards in Genomic Sciences, 2016, 11, 75.	1.5	49
34	Genome-wide transcription start site mapping of Bradyrhizobium japonicum grown free-living or in symbiosis – a rich resource to identify new transcripts, proteins and to study gene regulation. BMC Genomics, 2016, 17, 302.	1.2	70
35	Short communication: Heat-resistant Escherichia coli as potential persistent reservoir of extended-spectrum β -lactamases and Shiga toxin-encoding phages in dairy. Journal of Dairy Science, 2016, 99, 8622-8632.	1.4	30
36	Explosive cell lysis as a mechanism for the biogenesis of bacterial membrane vesicles and biofilms. Nature Communications, 2016, 7, 11220.	5.8	487

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37	A Peptidomimetic Antibiotic Targets Outer Membrane Proteins and Disrupts Selectively the Outer Membrane in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 1921-1932.	1.6	97
38	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
39	Volatile Organic Compounds from Native Potato-associated <i>Pseudomonas</i> as Potential Anti-oomycete Agents. <i>Frontiers in Microbiology</i> , 2015, 6, 1295.	1.5	134
40	Īf ⁵⁴ -Dependent Response to Nitrogen Limitation and Virulence in <i>Burkholderia cenocepacia</i> Strain H111. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4077-4089.	1.4	44
41	Protter: interactive protein feature visualization and integration with experimental proteomic data. <i>Bioinformatics</i> , 2014, 30, 884-886.	1.8	1,090
42	A Link between Arabinose Utilization and Oxalotrophy in <i>Bradyrhizobium japonicum</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 2094-2101.	1.4	28
43	Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism. <i>Journal of Proteomics</i> , 2014, 99, 123-137.	1.2	55
44	Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. <i>Journal of Proteomics</i> , 2014, 108, 269-283.	1.2	43
45	Proteomics Analysis of <i>Psychotria</i> Leaf Nodule Symbiosis: Improved Genome Annotation and Metabolic Predictions. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1325-1333.	1.4	27
46	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. <i>Genome Research</i> , 2013, 23, 1916-1927.	2.4	91
47	The Hemolymph Proteome of Fed and Starved <i>Drosophila</i> Larvae. <i>PLoS ONE</i> , 2013, 8, e67208.	1.1	55
48	Response of <i>Burkholderia cenocepacia</i> H111 to Micro-Oxia. <i>PLoS ONE</i> , 2013, 8, e72939.	1.1	46
49	Cis-2-dodecenoic acid receptor RpfR links quorum-sensing signal perception with regulation of virulence through cyclic dimeric guanosine monophosphate turnover. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15479-15484.	3.3	145
50	The AHL- and BDSF-Dependent Quorum Sensing Systems Control Specific and Overlapping Sets of Genes in <i>Burkholderia cenocepacia</i> H111. <i>PLoS ONE</i> , 2012, 7, e49966.	1.1	70
51	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	1.3	9
52	A Mighty Small Heart: The Cardiac Proteome of Adult <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2011, 6, e18497.	1.1	81
53	Model organism proteomics. <i>Journal of Proteomics</i> , 2010, 73, 2051-2053.	1.2	4
54	An integrated proteomics and transcriptomics reference data set provides new insights into the <i>Bradyrhizobium japonicum</i> bacteroid metabolism in soybean root nodules. <i>Proteomics</i> , 2010, 10, 1391-1400.	1.3	111

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55	PeptideClassifier for protein inference and targeted quantitative proteomics. Nature Biotechnology, 2010, 28, 647-650.	9.4	92
56	Generating and navigating proteome maps using mass spectrometry. Nature Reviews Molecular Cell Biology, 2010, 11, 789-801.	16.1	181
57	Protein and gene model inference based on statistical modeling in k-partite graphs. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12101-12106.	3.3	39
58	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. Genome Research, 2009, 19, 1786-1800.	2.4	151
59	Identification and Functional Characterization of N-Terminally Acetylated Proteins in Drosophila melanogaster. PLoS Biology, 2009, 7, e1000236.	2.6	149
60	Comparative Functional Analysis of the Caenorhabditis elegans and Drosophila melanogaster Proteomes. PLoS Biology, 2009, 7, e1000048.	2.6	208
61	A Proteome Catalog of Drosophila melanogaster: An Essential Resource for Targeted Quantitative Proteomics. Fly, 2007, 1, 182-186.	0.9	15
62	Genome-Wide Transcript Analysis of <i>Bradyrhizobium japonicum</i> Bacteroids in Soybean Root Nodules. Molecular Plant-Microbe Interactions, 2007, 20, 1353-1363.	1.4	187
63	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 854, 173-182.	1.2	13
64	A high-quality catalog of the Drosophila melanogaster proteome. Nature Biotechnology, 2007, 25, 576-583.	9.4	247
65	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. , 2007, 97, 277-307.		7
66	Experimental Peptide Identification Repository (EPIR). Molecular and Cellular Proteomics, 2004, 3, 1023-1038.	2.5	38
67	WNT1 inducible signaling pathway protein 3, WISP-3, a novel target gene in colorectal carcinomas with microsatellite instability. Gastroenterology, 2001, 121, 1275-1280.	0.6	62
68	The Sequence of the Orgyia pseudotsugata Multinucleocapsid Nuclear Polyhedrosis Virus Genome. Virology, 1997, 229, 381-399.	1.1	260
69	The DNA polymerase and helicase genes of a baculovirus of Orgyia pseudotsugata. Journal of General Virology, 1996, 77, 825-837.	1.3	40
70	Identification and Characterization of a Second Putative Origin of DNA Replication in a Baculovirus of Orgyia pseudotsugata. Virology, 1995, 207, 572-576.	1.1	35
71	Identification, Sequence, and Transcriptional Analysis of lef-3, a Gene Essential for Orgyia pseudotsugata Baculovirus DNA Replication. Virology, 1995, 210, 372-382.	1.1	24
72	Replication of Orgyia pseudotsugata Baculovirus DNA: lef-2 and ie-1 Are Essential and ie-2, p34, and Op-iap Are Stimulatory Genes. Virology, 1995, 212, 650-662.	1.1	48

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73	Replication of baculovirus DNA. <i>Journal of General Virology</i> , 1995, 76, 2103-2118.	1.3	129
74	Identification of Essential trans-Acting Regions Required for DNA Replication of the <i>Orgyia pseudotsugata</i> Multinucleocapsid Nuclear Polyhedrosis Virus: lef-1 Is an Essential Replication Gene. <i>Virology</i> , 1995, 207, 417-428.	1.1	18
75	Identification of genes involved in DNA replication of the <i>Autographa californica</i> baculovirus.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11212-11216.	3.3	293
76	Identification and Characterization of a Putative Origin of DNA Replication in the Genome of a Baculovirus Pathogenic for <i>Orgyia pseudotsugata</i> . <i>Virology</i> , 1993, 197, 715-725.	1.1	74