

Katharina Riedel

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

2,977
citations

186265

28
h-index

189892

50
g-index

86
all docs

86
docs citations

86
times ranked

4653
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellulose and hemicellulose decomposition by forest soil bacteria proceeds by the action of structurally variable enzymatic systems. <i>Scientific Reports</i> , 2016, 6, 25279.	3.3	328
2	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. <i>ISME Journal</i> , 2015, 9, 412-424.	9.8	238
3	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	4.1	219
4	Identification of Proteins Associated with the <i>Pseudomonas aeruginosa</i> Biofilm Extracellular Matrix. <i>Journal of Proteome Research</i> , 2012, 11, 4906-4915.	3.7	198
5	Molecular mechanisms underlying the close association between soil <i>Burkholderia</i> and fungi. <i>ISME Journal</i> , 2016, 10, 253-264.	9.8	118
6	Fungal volatile compounds induce production of the secondary metabolite Sodorifen in <i>Serratia plymuthica</i> PRI-2C. <i>Scientific Reports</i> , 2017, 7, 862.	3.3	115
7	Deciphering functional diversification within the lichen microbiota by meta-omics. <i>Microbiome</i> , 2017, 5, 82.	11.1	91
8	The Lichens™ Microbiota, Still a Mystery?. <i>Frontiers in Microbiology</i> , 2021, 12, 623839.	3.5	85
9	Virulence Factors Produced by <i>Staphylococcus aureus</i> Biofilms Have a Moonlighting Function Contributing to Biofilm Integrity. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1036-1053.	3.8	82
10	Holistic Assessment of Rumen Microbiome Dynamics through Quantitative Metatranscriptomics Reveals Multifunctional Redundancy during Key Steps of Anaerobic Feed Degradation. <i>MSystems</i> , 2018, 3, .	3.8	74
11	A Metaproteomics Approach to Elucidate Host and Pathogen Protein Expression during Catheter-Associated Urinary Tract Infections (CAUTIs). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 989-1008.	3.8	63
12	Deletion of membrane-associated <i>Asp</i> ₂₃ leads to upregulation of cell wall stress genes in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2014, 93, 1259-1268.	2.5	58
13	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus</i> O199. <i>Biotechnology for Biofuels</i> , 2016, 9, 104.	6.2	56
14	Soil and leaf litter metaproteomics—a brief guideline from sampling to understanding. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw180.	2.7	54
15	Metaproteomics to unravel major microbial players in leaf litter and soil environments: challenges and perspectives. <i>Proteomics</i> , 2013, 13, 2895-2909.	2.2	51
16	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49
17	Microbial functionality as affected by experimental warming of a temperate mountain forest soil—A metaproteomics survey. <i>Applied Soil Ecology</i> , 2017, 117-118, 196-202.	4.3	48
18	A Core Genome Multilocus Sequence Typing Scheme for <i>Enterococcus faecalis</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	47

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19	Highly Precise Quantification of Protein Molecules per Cell During Stress and Starvation Responses in <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2260-2276.	3.8	44
20	Symbiotic Interplay of Fungi, Algae, and Bacteria within the Lung Lichen <i>Lobaria pulmonaria</i> L. Hoffm. as Assessed by State-of-the-Art Metaproteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2160-2173.	3.7	43
21	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophan. <i>Nature Protocols</i> , 2020, 15, 3212-3239.	12.0	42
22	The HIPPO Transducer YAP and Its Targets CTGF and Cyr61 Drive a Paracrine Signalling in Cold Atmospheric Plasma-Mediated Wound Healing. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-14.	4.0	40
23	Enhancing Recombinant Protein Yields in the <i>E. coli</i> Periplasm by Combining Signal Peptide and Production Rate Screening. <i>Frontiers in Microbiology</i> , 2019, 10, 1511.	3.5	39
24	Costs of life - Dynamics of the protein inventory of <i>Staphylococcus aureus</i> during anaerobiosis. <i>Scientific Reports</i> , 2016, 6, 28172.	3.3	38
25	The protein inventory of <i>Clostridium difficile</i> grown in complex and minimal medium. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1068-1072.	1.6	36
26	Proteomic analysis of the food spoiler <i>Pseudomonas fluorescens</i> ITEM 17298 reveals the antibiofilm activity of the pepsin-digested bovine lactoferrin. <i>Food Microbiology</i> , 2019, 82, 177-193.	4.2	36
27	Response of Microbial Communities and Their Metabolic Functions to Drying/Rewetting Stress in a Temperate Forest Soil. <i>Microorganisms</i> , 2019, 7, 129.	3.6	35
28	Milk-deteriorating exoenzymes from <i>Pseudomonas fluorescens</i> 041 isolated from refrigerated raw milk. <i>Brazilian Journal of Microbiology</i> , 2015, 46, 207-217.	2.0	29
29	Aureolib – A Proteome Signature Library: Towards an Understanding of <i>Staphylococcus aureus</i> Pathophysiology. <i>PLoS ONE</i> , 2013, 8, e70669.	2.5	28
30	Life Stage-specific Proteomes of <i>Legionella pneumophila</i> Reveal a Highly Differential Abundance of Virulence-associated Dot/Icm effectors. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 177-200.	3.8	27
31	Editorial: Bioactive Compounds from Microbes. <i>Frontiers in Microbiology</i> , 2017, 8, 392.	3.5	26
32	Biofilm and Pathogenesis-Related Proteins in the Foodborne <i>P. fluorescens</i> ITEM 17298 With Distinctive Phenotypes During Cold Storage. <i>Frontiers in Microbiology</i> , 2020, 11, 991.	3.5	26
33	Differential View on the Bile Acid Stress Response of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 258.	3.5	24
34	A sulfur-containing volatile emitted by potato-associated bacteria confers protection against late blight through direct anti-oomycete activity. <i>Scientific Reports</i> , 2019, 9, 18778.	3.3	23
35	Data visualization in environmental proteomics. <i>Proteomics</i> , 2013, 13, 2805-2821.	2.2	21
36	Proteome and carbon flux analysis of <i>Pseudomonas aeruginosa</i> clinical isolates from different infection sites. <i>Proteomics</i> , 2016, 16, 1381-1385.	2.2	21

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37	Comprehensive Redox Profiling of the Thiol Proteome of <i>Clostridium difficile</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1035-1046.	3.8	21
38	Antimicrobial effects of microwave-induced plasma torch (MiniMIP) treatment on <i>Candida albicans</i> biofilms. <i>Microbial Biotechnology</i> , 2019, 12, 1034-1048.	4.2	18
39	An optimized metaproteomics protocol for a holistic taxonomic and functional characterization of microbial communities from marine particles. <i>Environmental Microbiology Reports</i> , 2020, 12, 367-376.	2.4	18
40	Carbon Source-Dependent Reprogramming of Anaerobic Metabolism in <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	17
41	Biotransformation and reduction of estrogenicity of bisphenol A by the biphenyl-degrading <i>Cupriavidus basilensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3743-3758.	3.6	16
42	Metabolic Rearrangements Causing Elevated Proline and Polyhydroxybutyrate Accumulation During the Osmotic Adaptation Response of <i>Bacillus megaterium</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 47.	4.1	16
43	Antibacterial Metabolites and Bacteriolytic Enzymes Produced by <i>Bacillus pumilus</i> During Bacteriolysis of <i>Arthrobacter citreus</i> . <i>Marine Biotechnology</i> , 2015, 17, 290-304.	2.4	15
44	Quorum Sensing and Spoilage Potential of Psychrotrophic Enterobacteriaceae Isolated from Milk. <i>BioMed Research International</i> , 2018, 2018, 1-13.	1.9	15
45	A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. <i>Microorganisms</i> , 2020, 8, 1887.	3.6	15
46	Characterization of Antimicrobial Effects of Plasma-Treated Water (PTW) Produced by Microwave-Induced Plasma (MidiPLexc) on <i>Pseudomonas fluorescens</i> Biofilms. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 3118.	2.5	15
47	Impact of Different Trace Elements on the Growth and Proteome of Two Strains of <i>Granulicella</i> , Class "Acidobacteria". <i>Frontiers in Microbiology</i> , 2020, 11, 1227.	3.5	15
48	Proteomic Signatures of <i>Clostridium difficile</i> Stressed with Metronidazole, Vancomycin, or Fidaxomicin. <i>Cells</i> , 2018, 7, 213.	4.1	14
49	Influenza A H1N1 Induced Disturbance of the Respiratory and Fecal Microbiome of German Landrace Pigs – a Multi-Omics Characterization. <i>Microbiology Spectrum</i> , 2021, 9, e0018221.	3.0	14
50	Reducing the genetic code induces massive rearrangement of the proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17206-17211.	7.1	13
51	Time-Resolved Analysis of Cytosolic and Surface-Associated Proteins of <i>Staphylococcus aureus</i> HG001 under Planktonic and Biofilm Conditions. <i>Journal of Proteome Research</i> , 2015, 14, 3804-3822.	3.7	13
52	Proteogenomics Uncovers Critical Elements of Host Response in Bovine Soft Palate Epithelial Cells Following In Vitro Infection with Foot-And-Mouth Disease Virus. <i>Viruses</i> , 2019, 11, 53.	3.3	13
53	Comparative proteome analysis in an <i>Escherichia coli</i> CyDisCo strain identifies stress responses related to protein production, oxidative stress and accumulation of misfolded protein. <i>Microbial Cell Factories</i> , 2019, 18, 19.	4.0	13
54	What's a Biofilm? How the Choice of the Biofilm Model Impacts the Protein Inventory of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 682111.	3.5	13

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55	Detailed Soluble Proteome Analyses of a Dairy-Isolated <i>Enterococcus faecalis</i> : A Possible Approach to Assess Food Safety and Potential Probiotic Value. <i>Frontiers in Nutrition</i> , 2019, 6, 71.	3.7	11
56	Investigation of the chemical composition of plasma-treated water by MidiPlexc and its antimicrobial effect on <i>L. monocytogenes</i> and <i>Pseudomonas fluorescens</i> monospecies suspension cultures. <i>Journal Physics D: Applied Physics</i> , 2020, 53, 305204.	2.8	11
57	Plasma-Treated Water Affects <i>Listeria monocytogenes</i> Vitality and Biofilm Structure. <i>Frontiers in Microbiology</i> , 2021, 12, 652481.	3.5	10
58	Sample Preparation for Metaproteome Analyses of Soil and Leaf Litter. <i>Methods in Molecular Biology</i> , 2018, 1841, 303-318.	0.9	9
59	Effects of adult temperature on gene expression in a butterfly: identifying pathways associated with thermal acclimation. <i>BMC Evolutionary Biology</i> , 2019, 19, 32.	3.2	8
60	Model of persistent foot-and-mouth disease virus infection in multilayered cells derived from bovine dorsal soft palate. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 133-148.	3.0	8
61	<i>Escherichia coli</i> Can Adapt Its Protein Translocation Machinery for Enhanced Periplasmic Recombinant Protein Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 465.	4.1	8
62	Responses of <i>Acidobacteria Granulicella</i> sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. <i>Microorganisms</i> , 2020, 8, 244.	3.6	8
63	Non-invasive and label-free 3D-visualization shows in vivo oligomerization of the staphylococcal alkaline shock protein 23 (Asp23). <i>Scientific Reports</i> , 2020, 10, 125.	3.3	8
64	The hidden lipoproteome of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 569-581.	3.6	7
65	Fibronectin rescues aberrant phenotype of endothelial cells lacking either CCM1, CCM2 or CCM3. <i>FASEB Journal</i> , 2020, 34, 9018-9033.	0.5	7
66	Far-reaching cellular consequences of <i>tat</i> deletion in <i>Escherichia coli</i> revealed by comprehensive proteome analyses. <i>Microbiological Research</i> , 2019, 218, 97-107.	5.3	6
67	A Point Mutation in the Transcriptional Repressor PerR Results in a Constitutive Oxidative Stress Response in <i>Clostridioides difficile</i> 630 ^{ATCC} <i>erm</i> . <i>MSphere</i> , 2021, 6, .	2.9	6
68	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050421.	0.6	6
69	An Innovative Protocol for Metaproteomic Analyses of Microbial Pathogens in Cystic Fibrosis Sputum. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 724569.	3.9	6
70	The Involvement of the McsB Arginine Kinase in Clp-Dependent Degradation of the MgsR Regulator in <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 900.	3.5	5
71	<i>Moniliella spathulata</i> , an oil-degrading yeast, which promotes growth of barley in oil-polluted soil. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 401-415.	3.6	5
72	Myxopyronin B inhibits growth of a Fidaxomicin-resistant <i>Clostridioides difficile</i> isolate and interferes with toxin synthesis. <i>Gut Pathogens</i> , 2022, 14, 4.	3.4	5

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73	Bioinformatic analysis of fold-type III PLP-dependent enzymes discovers multimeric racemases. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1499-1507.	3.6	4
74	Updating the proteome of the uncultivable hemotrophic <i>Mycoplasma</i> in experimentally infected pigs. <i>Proteomics</i> , 2016, 16, 609-613.	2.2	3
75	Identification of AHL- and BDSF-Controlled Proteins in <i>Burkholderia cenocepacia</i> by Proteomics. <i>Methods in Molecular Biology</i> , 2018, 1673, 193-202.	0.9	2
76	Polymer drug release system for biofilm inhibition in medical application. <i>Current Directions in Biomedical Engineering</i> , 2018, 4, 213-216.	0.4	2
77	Complementation studies with human ClpP in <i>Bacillus subtilis</i> . <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118744.	4.1	2
78	Insights into the Degradation of Medium-Chain-Length Dicarboxylic Acids in <i>Cupriavidus necator</i> H16 Reveal $\hat{1}^2$ -Oxidation Differences between Dicarboxylic Acids and Fatty Acids. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0187321.	3.1	2
79	Protein expression profiling of <i>Staphylococcus aureus</i> in response to the bacteriocin bovicin HC5. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7857-7869.	3.6	0
80	Complete Genome Sequence of <i>Escherichia coli</i> GW-AmxH19, Isolated from Hospital Wastewater in Greifswald, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
81	Metaproteomics of Litter-Associated Fungi. , 2020, , 369-383.		0
82	Inactivation of antibiotic-resistant microorganisms by physical plasma. <i>Access Microbiology</i> , 2022, 4, .	0.5	0