

# Dirk Benndorf

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9106585/publications.pdf>

Version: 2024-02-01

39  
papers

1,433  
citations

430754

18  
h-index

345118

36  
g-index

42  
all docs

42  
docs citations

42  
times ranked

1640  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Pout2Prot</i>: An Efficient Tool to Create Protein (Sub)groups from Percolator Output Files. <i>Journal of Proteome Research</i> , 2022, 21, 1175-1180.	1.8	4
2	Absolute quantification of viral proteins during single-round replication of MDCK suspension cells. <i>Journal of Proteomics</i> , 2022, 259, 104544.	1.2	5
3	Lignocellulose Fermentation Products Generated by Giant Panda Gut Microbiomes Depend Ultimately on pH Rather than Portion of Bamboo: A Preliminary Study. <i>Microorganisms</i> , 2022, 10, 978.	1.6	0
4	OP7, a novel influenza A virus defective interfering particle: production, purification, and animal experiments demonstrating antiviral potential. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 129-146.	1.7	25
5	An Investigation of Alternatives to Transform Protein Sequence Databases to a Columnar Index Schema. <i>Algorithms</i> , 2021, 14, 59.	1.2	0
6	Tracking changes in adaptation to suspension growth for MDCK cells: cell growth correlates with levels of metabolites, enzymes and proteins. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1861-1874.	1.7	2
7	The structure and function of soil archaea across biomes. <i>Journal of Proteomics</i> , 2021, 237, 104147.	1.2	10
8	Fecal Metaproteomics Reveals Reduced Gut Inflammation and Changed Microbial Metabolism Following Lifestyle-Induced Weight Loss. <i>Biomolecules</i> , 2021, 11, 726.	1.8	11
9	smORFer: a modular algorithm to detect small ORFs in prokaryotes. <i>Nucleic Acids Research</i> , 2021, 49, e89-e89.	6.5	16
10	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. <i>Microorganisms</i> , 2021, 9, 1457.	1.6	8
11	Integrated Cycles for Urban Biomass as a Strategy to Promote a CO2-Neutral Societyâ€”A Feasibility Study. <i>Sustainability</i> , 2021, 13, 9505.	1.6	2
12	Triangulation of microbial fingerprinting in anaerobic digestion reveals consistent fingerprinting profiles. <i>Water Research</i> , 2021, 202, 117422.	5.3	12
13	MPA_Pathway_Tool: User-Friendly, Automatic Assignment of Microbial Community Data on Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10992.	1.8	2
14	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	5.8	34
15	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	4.9	36
16	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophane. <i>Nature Protocols</i> , 2020, 15, 3212-3239.	5.5	42
17	The Role of <i>Petrimonas mucosa</i> ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , 2020, 8, 2024.	1.6	23
18	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. <i>Journal of Proteome Research</i> , 2020, 19, 3562-3566.	1.8	11

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19	The Impact of <i>ackA</i> , <i>pta</i> , and <i>ackA-pta</i> Mutations on Growth, Gene Expression and Protein Acetylation in <i>Escherichia coli</i> K-12. <i>Frontiers in Microbiology</i> , 2020, 11, 233.	1.5	30
20	Impact of feeding and stirring regimes on the internal stratification of microbial communities in the fermenter of anaerobic digestion plants. <i>Bioresource Technology</i> , 2020, 314, 123679.	4.8	5
21	Substrate-Dependent Fermentation of Bamboo in Giant Panda Gut Microbiomes: Leaf Primarily to Ethanol and Pith to Lactate. <i>Frontiers in Microbiology</i> , 2020, 11, 530.	1.5	7
22	A Robust and Universal Metaproteomics Workflow for Research Studies and Routine Diagnostics Within 24 h Using Phenol Extraction, FASP Digest, and the MetaProteomeAnalyzer. <i>Frontiers in Microbiology</i> , 2019, 10, 1883.	1.5	66
23	Augmenting Biogas Process Modeling by Resolving Intracellular Metabolic Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1095.	1.5	14
24	RedCom: A strategy for reduced metabolic modeling of complex microbial communities and its application for analyzing experimental datasets from anaerobic digestion. <i>PLoS Computational Biology</i> , 2019, 15, e1006759.	1.5	29
25	A robust, cost-effective method for DNA, RNA and protein co-extraction from soil, other complex microbiomes and pure cultures. <i>Molecular Ecology Resources</i> , 2019, 19, 439-455.	2.2	43
26	Reduced TCA cycle rates at high hydrostatic pressure hinder hydrocarbon degradation and obligate oil degraders in natural, deep-sea microbial communities. <i>ISME Journal</i> , 2019, 13, 1004-1018.	4.4	14
27	MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go. <i>Analytical Chemistry</i> , 2018, 90, 685-689.	3.2	65
28	SDS-PAGE fractionation to increase metaproteomic insight into the taxonomic and functional composition of microbial communities for biogas plant samples. <i>Engineering in Life Sciences</i> , 2018, 18, 498-509.	2.0	27
29	FMNH2-dependent monooxygenases initiate catabolism of sulfonamides in <i>Microbacterium</i> sp. strain BR1 subsisting on sulfonamide antibiotics. <i>Scientific Reports</i> , 2017, 7, 15783.	1.6	66
30	Challenges and perspectives of metaproteomic data analysis. <i>Journal of Biotechnology</i> , 2017, 261, 24-36.	1.9	195
31	Metaproteomics Applied to Activated Sludge for Industrial Wastewater Treatment Revealed a Dominant Methylophilic Metabolism of <i>Hyphomicrobium zavarzinii</i> . <i>Microbial Ecology</i> , 2016, 72, 9-13.	1.4	12
32	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. <i>Proteomics</i> , 2015, 15, 3585-3589.	1.3	14
33	Metaproteomics of activated sludge from a wastewater treatment plant – A pilot study. <i>Proteomics</i> , 2015, 15, 3596-3601.	1.3	52
34	Monitoring changes in proteome during stepwise adaptation of a MDCK cell line from adherence to growth in suspension. <i>Vaccine</i> , 2015, 33, 4269-4280.	1.7	19
35	The MetaProteomeAnalyzer: A Powerful Open-Source Software Suite for Metaproteomics Data Analysis and Interpretation. <i>Journal of Proteome Research</i> , 2015, 14, 1557-1565.	1.8	169
36	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7791-7803.	1.7	64

#	ARTICLE	IF	CITATIONS
37	Metaproteomics of complex microbial communities in biogas plants. <i>Microbial Biotechnology</i> , 2015, 8, 749-763.	2.0	98
38	Proteomics in environmental and technical microbiology. <i>Engineering in Life Sciences</i> , 2014, 14, 27-46.	2.0	6
39	Metagenome and metaproteome analyses of microbial communities in mesophilic biogas-producing anaerobic batch fermentations indicate concerted plant carbohydrate degradation. <i>Systematic and Applied Microbiology</i> , 2013, 36, 330-338.	1.2	182